



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 9, 2016 – 01:15 PM BST

PDB ID : 5L8W
Title : Structure of USP12-UB-PRG/UAF1
Authors : Dharadhar, S.; Sixma, T.
Deposited on : 2016-06-08
Resolution : 2.79 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

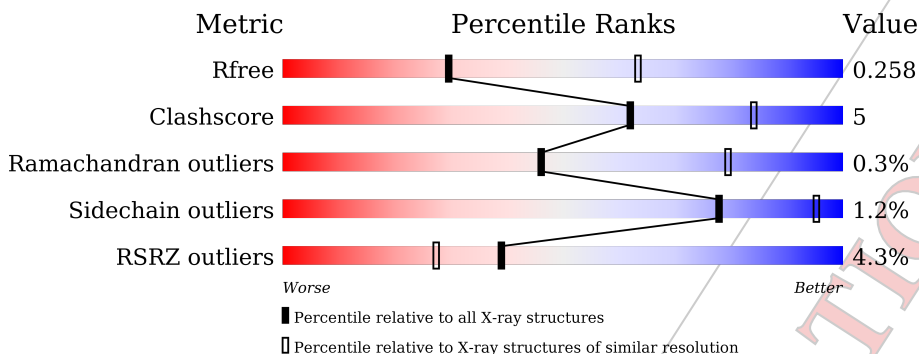
MolProbity : 4.02b-467
Mogul : unknown
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027674
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027674

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.79 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	376	 3% 73% 11% 15%
2	B	580	 5% 76% 12% 12%
3	C	75	 95% 5%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	AYE	A	401	-	-	X	X

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2 Entry composition i

There are 7 unique types of molecules in this entry. The entry contains 7287 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Ubiquitin carboxyl-terminal hydrolase 12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	319	2631	1675	448	492	16	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	HIS	-	expression tag	UNP O75317
A	-4	HIS	-	expression tag	UNP O75317
A	-3	HIS	-	expression tag	UNP O75317
A	-2	HIS	-	expression tag	UNP O75317
A	-1	HIS	-	expression tag	UNP O75317
A	0	HIS	-	expression tag	UNP O75317

- Molecule 2 is a protein called WD repeat-containing protein 48.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	512	4030	2543	709	756	22	0	0	0

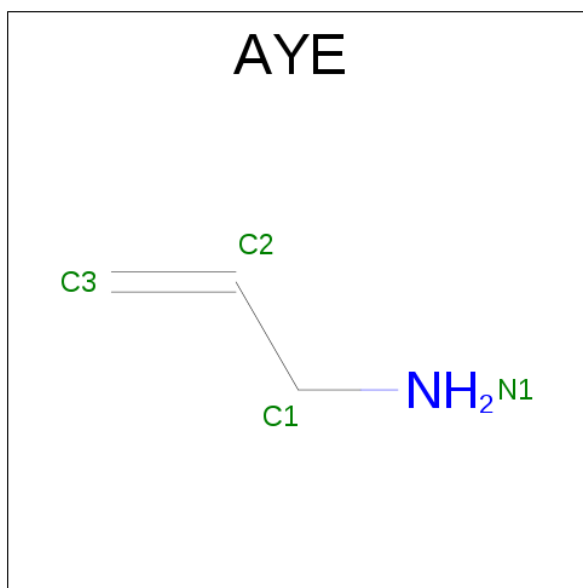
There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	TRP	-	expression tag	UNP Q8TAF3
B	2	SER	-	expression tag	UNP Q8TAF3
B	3	HIS	-	expression tag	UNP Q8TAF3
B	4	PRO	-	expression tag	UNP Q8TAF3
B	5	GLN	-	expression tag	UNP Q8TAF3
B	6	PHE	-	expression tag	UNP Q8TAF3
B	7	GLU	-	expression tag	UNP Q8TAF3
B	8	LYS	-	expression tag	UNP Q8TAF3
B	369	PHE	LEU	conflict	UNP Q8TAF3

- Molecule 3 is a protein called Polyubiquitin-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	75	597	376	104	116	1	0	0	0

- Molecule 4 is prop-2-en-1-amine (three-letter code: AYE) (formula: C₃H₇N).

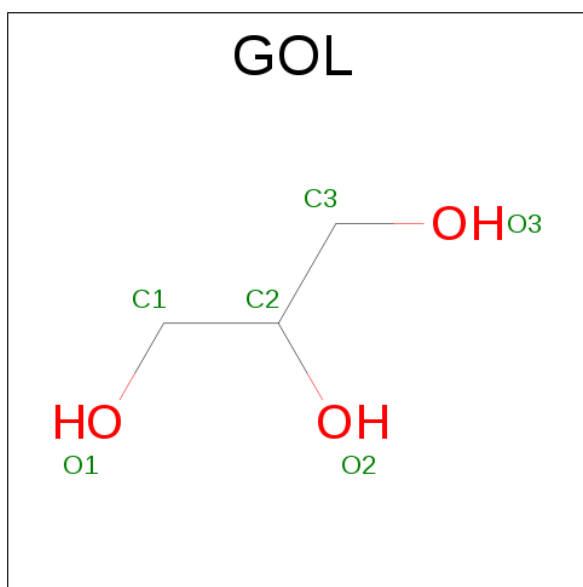


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	N		
4	A	1	4	3	1	0	0

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
5	A	1	1	1	0	0

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	C O	0	0
			6	3 3		

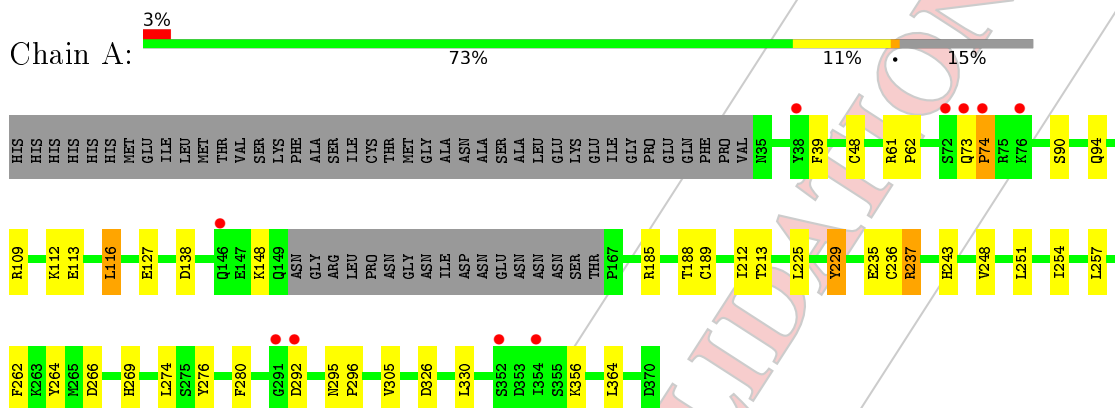
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	6	Total	O	0	0
			6	6		
7	B	9	Total	O	0	0
			9	9		
7	C	3	Total	O	0	0
			3	3		

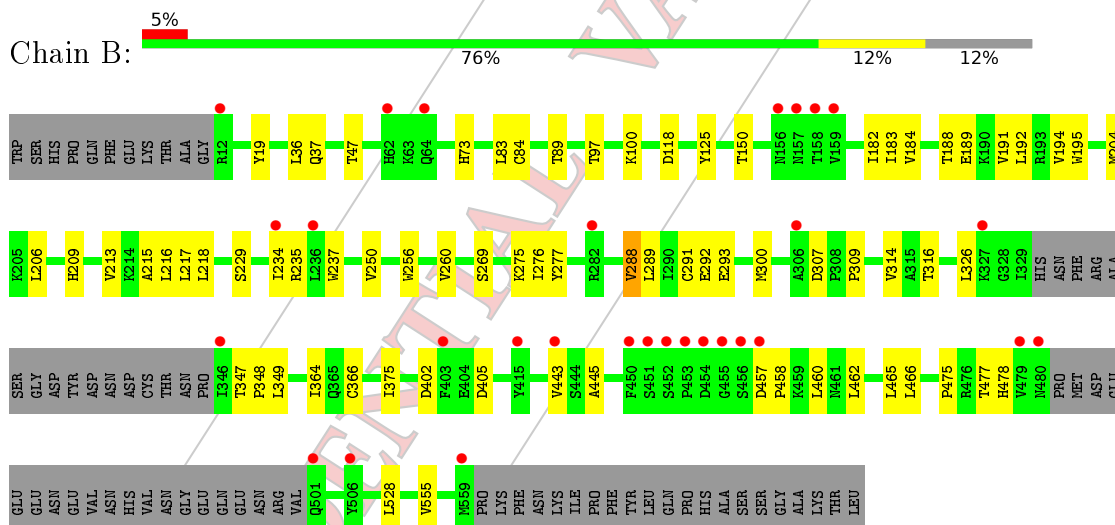
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

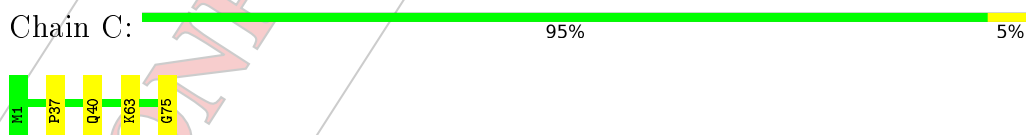
- Molecule 1: Ubiquitin carboxyl-terminal hydrolase 12



- Molecule 2: WD repeat-containing protein 48



- Molecule 3: Polyubiquitin-B



4 Data and refinement statistics i

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	103.68Å 152.82Å 182.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.40 – 2.79 47.41 – 2.79	Depositor EDS
% Data completeness (in resolution range)	99.2 (47.40-2.79) 99.2 (47.41-2.79)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.69 (at 2.81Å)	Xtrriage
Refinement program	REFMAC 5.8.0151	Depositor
R, R_{free}	0.208 , 0.259 0.211 , 0.258	Depositor DCC
R_{free} test set	1795 reflections (5.23%)	DCC
Wilson B-factor (Å ²)	62.2	Xtrriage
Anisotropy	0.438	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 38.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7287	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.56% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: AYE, GOL, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.93	1/2689 (0.0%)	0.95	7/3626 (0.2%)
2	B	0.54	0/4111	0.75	1/5579 (0.0%)
3	C	0.82	0/603	0.94	0/811
All	All	0.73	1/7403 (0.0%)	0.84	8/10016 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	90	SER	CB-OG	-5.17	1.35	1.42

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	188	THR	N-CA-CB	7.82	125.16	110.30
1	A	237	ARG	NE-CZ-NH1	6.63	123.62	120.30
1	A	237	ARG	NE-CZ-NH2	-6.41	117.10	120.30
1	A	116	LEU	CB-CG-CD1	6.10	121.36	111.00
1	A	109	ARG	NE-CZ-NH2	-5.59	117.51	120.30
1	A	138	ASP	CB-CG-OD1	5.31	123.08	118.30
2	B	235	ARG	NE-CZ-NH1	5.15	122.87	120.30
1	A	229	TYR	CA-CB-CG	-5.06	103.79	113.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2631	0	2583	28	0
2	B	4030	0	4033	47	0
3	C	597	0	626	5	0
4	A	4	0	7	10	0
5	A	1	0	0	0	0
6	A	6	0	8	0	0
7	A	6	0	0	0	0
7	B	9	0	0	0	0
7	C	3	0	0	0	0
All	All	7287	0	7257	78	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All (78) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:48:CYS:SG	4:A:401:AYE:C2	2.29	1.20
1:A:48:CYS:SG	4:A:401:AYE:C1	2.39	1.10
4:A:401:AYE:HN1A	3:C:75:GLY:C	1.57	1.07
1:A:48:CYS:SG	4:A:401:AYE:H1	1.97	1.05
4:A:401:AYE:N1	3:C:75:GLY:C	2.13	1.01
1:A:212:ILE:HD11	1:A:257:LEU:HD13	1.55	0.88
2:B:300:MET:HG2	2:B:314:VAL:HG22	1.64	0.80
2:B:184:VAL:HG23	2:B:216:LEU:HD13	1.66	0.77
1:A:48:CYS:SG	4:A:401:AYE:C3	2.87	0.61
1:A:305:VAL:HG13	1:A:364:LEU:HD23	1.81	0.61
2:B:250:VAL:HG12	2:B:277:TYR:CD2	2.36	0.61
2:B:204:MET:HE2	2:B:206:LEU:HD21	1.84	0.59
1:A:185:ARG:HB3	1:A:243:HIS:HB2	1.85	0.58
1:A:48:CYS:HG	4:A:401:AYE:C2	2.16	0.57
1:A:39:PHE:CZ	1:A:94:GLN:HG2	2.40	0.57
1:A:237:ARG:CZ	2:B:364:ILE:HG22	2.34	0.57
2:B:445:ALA:HB3	2:B:457:ASP:HB2	1.87	0.56
2:B:89:THR:HG21	2:B:150:THR:HG21	1.88	0.55
4:A:401:AYE:HN1A	3:C:75:GLY:CA	2.20	0.54
2:B:182:ILE:HD11	2:B:218:LEU:HD22	1.90	0.54
2:B:189:GLU:HG2	2:B:191:VAL:HG22	1.91	0.52
2:B:293:GLU:HG2	2:B:316:THR:HG21	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:347:THR:HB	2:B:348:PRO:HD2	1.92	0.51
1:A:237:ARG:NE	2:B:364:ILE:HG22	2.26	0.50
2:B:206:LEU:HB3	2:B:237:TRP:CZ3	2.46	0.50
1:A:212:ILE:HG22	1:A:280:PHE:HA	1.94	0.49
2:B:289:LEU:HD22	2:B:348:PRO:HA	1.94	0.48
2:B:97:THR:HG22	2:B:118:ASP:C	2.34	0.48
2:B:288:VAL:HG13	2:B:349:LEU:HD13	1.96	0.48
2:B:347:THR:HB	2:B:348:PRO:CD	2.44	0.48
1:A:113:GLU:HA	1:A:113:GLU:OE1	2.13	0.47
2:B:460:LEU:HB3	2:B:465:LEU:HD11	1.95	0.47
2:B:84:CYS:HB3	2:B:125:TYR:CZ	2.50	0.47
2:B:275:LYS:HD3	2:B:292:GLU:HG3	1.95	0.47
1:A:61:ARG:N	1:A:62:PRO:HD2	2.29	0.47
2:B:477:THR:HA	2:B:555:VAL:HG12	1.96	0.47
2:B:36:LEU:CD2	2:B:47:THR:HG22	2.45	0.47
1:A:235:GLU:OE2	1:A:235:GLU:HA	2.14	0.46
2:B:288:VAL:HG13	2:B:349:LEU:CD1	2.45	0.46
1:A:295:ASN:OD1	1:A:296:PRO:HD2	2.16	0.46
3:C:37:PRO:HD2	3:C:40:GLN:HE21	1.80	0.46
1:A:73:GLN:HB2	1:A:74:PRO:HD3	1.98	0.45
2:B:206:LEU:HD13	2:B:237:TRP:CE3	2.52	0.45
2:B:234:ILE:HD11	2:B:269:SER:CB	2.46	0.45
1:A:189:CYS:HB3	1:A:236:CYS:SG	2.57	0.44
2:B:276:ILE:HD12	2:B:291:CYS:SG	2.58	0.43
2:B:37:GLN:HE21	2:B:83:LEU:N	2.16	0.43
1:A:264:TYR:CE2	1:A:266:ASP:HA	2.54	0.43
2:B:402:ASP:OD2	2:B:405:ASP:CG	2.57	0.43
2:B:183:ILE:CG2	2:B:195:TRP:HB2	2.49	0.43
2:B:217:LEU:CD1	2:B:260:VAL:HG13	2.49	0.43
1:A:330:LEU:C	1:A:330:LEU:HD23	2.39	0.42
1:A:356:LYS:HA	1:A:356:LYS:HE2	2.01	0.42
4:A:401:AYE:C1	3:C:75:GLY:C	2.85	0.42
2:B:194:VAL:HG21	2:B:204:MET:HB2	2.02	0.42
2:B:182:ILE:C	2:B:182:ILE:HD12	2.40	0.42
2:B:19:TYR:HE1	2:B:466:LEU:HD21	1.85	0.42
2:B:475:PRO:HA	2:B:478:HIS:CE1	2.55	0.42
2:B:443:VAL:HB	2:B:462:LEU:HD11	2.02	0.42
2:B:209:HIS:CE1	2:B:229:SER:HB2	2.55	0.41
2:B:276:ILE:CD1	2:B:314:VAL:HG21	2.50	0.41
1:A:62:PRO:HG2	1:A:254:ILE:HD11	2.02	0.41
2:B:194:VAL:CG2	2:B:204:MET:HB2	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:309:PRO:O	2:B:326:LEU:HD12	2.21	0.41
2:B:307:ASP:O	2:B:309:PRO:HD3	2.21	0.41
1:A:48:CYS:SG	4:A:401:AYE:N1	2.91	0.41
2:B:366:CYS:SG	2:B:375:ILE:HG23	2.60	0.41
2:B:37:GLN:HE21	2:B:83:LEU:H	1.68	0.41
2:B:528:LEU:N	2:B:528:LEU:HD23	2.36	0.41
1:A:225:LEU:HB3	1:A:229:TYR:O	2.21	0.40
1:A:148:LYS:HD3	1:A:148:LYS:N	2.36	0.40
1:A:116:LEU:HD21	1:A:127:GLU:OE2	2.22	0.40
1:A:248:VAL:HG11	1:A:251:LEU:HD23	2.03	0.40
1:A:274:LEU:HD22	1:A:276:TYR:CZ	2.56	0.40
2:B:73:HIS:HD2	2:B:100:LYS:NZ	2.20	0.40
2:B:184:VAL:HG12	2:B:194:VAL:HG13	2.04	0.40
2:B:215:ALA:HB2	2:B:256:TRP:O	2.21	0.40
2:B:277:TYR:CD1	2:B:289:LEU:HA	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	315/376 (84%)	299 (95%)	14 (4%)	2 (1%)	30	65
2	B	506/580 (87%)	484 (96%)	21 (4%)	1 (0%)	52	84
3	C	73/75 (97%)	71 (97%)	2 (3%)	0	100	100
All	All	894/1031 (87%)	854 (96%)	37 (4%)	3 (0%)	46	79

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	458	PRO
1	A	292	ASP

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Mol	Chain	Res	Type
1	A	74	PRO

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	295/344 (86%)	290 (98%)	5 (2%)	68 92
2	B	448/508 (88%)	444 (99%)	4 (1%)	84 96
3	C	68/68 (100%)	67 (98%)	1 (2%)	72 93
All	All	811/920 (88%)	801 (99%)	10 (1%)	78 95

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	112	LYS
1	A	213	THR
1	A	262	PHE
1	A	269	HIS
1	A	326	ASP
2	B	188	THR
2	B	192	LEU
2	B	213	VAL
2	B	288	VAL
3	C	63	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	214	HIS
1	A	308	HIS
2	B	37	GLN
2	B	73	HIS
2	B	266	HIS
2	B	558	ASN

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Mol	Chain	Res	Type
3	C	40	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	AYE	A	401	-	3,3,3	0.66	0	1,2,2	0.07	0
6	GOL	A	403	-	5,5,5	0.29	0	5,5,5	0.23	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	AYE	A	401	-	-	0/1/1/1	0/0/0/0
6	GOL	A	403	-	-	0/4/4/4	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	401	AYE	10	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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6 Fit of model and data i

6.1 Protein, DNA and RNA chains i

In the following table, the column labelled '#RSRZ > 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q < 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2		OWAB(Å ²)	Q < 0.9
1	A	319/376 (84%)	0.07	10 (3%)	52 40	38, 56, 120, 150	0
2	B	512/580 (88%)	0.37	29 (5%)	27 17	44, 78, 120, 176	0
3	C	75/75 (100%)	-0.36	0	100 100	41, 52, 66, 78	0
All	All	906/1031 (87%)	0.21	39 (4%)	39 27	38, 69, 118, 176	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	62	HIS	5.3
1	A	73	GLN	4.8
2	B	158	THR	4.8
2	B	453	PRO	4.7
2	B	64	GLN	4.6
2	B	479	VAL	4.4
1	A	354	ILE	4.2
2	B	559	MET	4.1
2	B	452	SER	4.0
2	B	456	SER	3.9
2	B	157	ASN	3.9
2	B	451	SER	3.8
1	A	74	PRO	3.8
1	A	146	GLN	3.8
2	B	501	GLN	3.8
1	A	291	GLY	3.8
2	B	480	ASN	3.4
1	A	292	ASP	3.3
2	B	455	GLY	3.3
2	B	454	ASP	3.1
2	B	457	ASP	3.1
2	B	415	TYR	2.9
2	B	282	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
2	B	506	TYR	2.8
2	B	346	ILE	2.7
2	B	159	VAL	2.5
2	B	403	PHE	2.4
1	A	76	LYS	2.3
2	B	450	PHE	2.3
1	A	72	SER	2.3
2	B	236	LEU	2.3
2	B	306	ALA	2.1
2	B	234	ILE	2.1
2	B	327	LYS	2.1
2	B	12	ARG	2.1
2	B	443	VAL	2.0
1	A	38	TYR	2.0
1	A	352	SER	2.0
2	B	156	ASN	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	AYE	A	401	4/4	0.96	0.35	4.62	56,58,62,64	0
6	GOL	A	403	6/6	0.87	0.21	-0.09	92,105,107,109	0
5	ZN	A	402	1/1	1.00	0.16	-0.60	51,51,51,51	0

6.5 Other polymers [i](#)

There are no such residues in this entry.

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