Full wwPDB X-ray Structure Validation Report (i)

Feb 29, 2024 – 09:16 AM EST

PDB ID	:	5UW7
Title	:	PCY1 Y481F Variant in Complex with Follower Peptide
Authors	:	Chekan, J.R.; Nair, S.K.
Deposited on	:	2017-02-20
Resolution	:	2.37 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

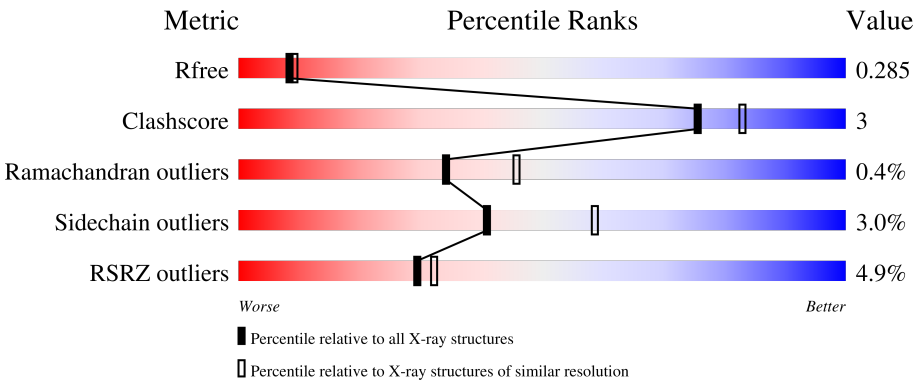
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.37 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}	130704	5509 (2.40-2.36)
Clashscore	141614	6082 (2.40-2.36)
Ramachandran outliers	138981	5973 (2.40-2.36)
Sidechain outliers	138945	5975 (2.40-2.36)
RSRZ outliers	127900	5397 (2.40-2.36)

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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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 <=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	750	4% 80% 8% • 11%
1	B	750	5% 78% 9% • 13%
2	C	19	32% 68%
2	D	19	32% 68%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 10789 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 Peptide cyclase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	666	5369	3433	910	999	27	0	2	0
1	B	656	5308	3405	901	976	26	0	3	0

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-25	MET	-	initiating methionine	UNP R4P353
A	-24	SER	-	expression tag	UNP R4P353
A	-23	TYR	-	expression tag	UNP R4P353
A	-22	TYR	-	expression tag	UNP R4P353
A	-21	HIS	-	expression tag	UNP R4P353
A	-20	HIS	-	expression tag	UNP R4P353
A	-19	HIS	-	expression tag	UNP R4P353
A	-18	HIS	-	expression tag	UNP R4P353
A	-17	HIS	-	expression tag	UNP R4P353
A	-16	HIS	-	expression tag	UNP R4P353
A	-15	LEU	-	expression tag	UNP R4P353
A	-14	GLU	-	expression tag	UNP R4P353
A	-13	SER	-	expression tag	UNP R4P353
A	-12	THR	-	expression tag	UNP R4P353
A	-11	SER	-	expression tag	UNP R4P353
A	-10	LEU	-	expression tag	UNP R4P353
A	-9	TYR	-	expression tag	UNP R4P353
A	-8	LYS	-	expression tag	UNP R4P353
A	-7	LYS	-	expression tag	UNP R4P353
A	-6	ALA	-	expression tag	UNP R4P353
A	-5	GLY	-	expression tag	UNP R4P353
A	-4	SER	-	expression tag	UNP R4P353
A	-3	GLU	-	expression tag	UNP R4P353
A	-2	PHE	-	expression tag	UNP R4P353
A	-1	ALA	-	expression tag	UNP R4P353

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Chain	Residue	Modelled	Actual	Comment	Reference
A	0	LEU	-	expression tag	UNP R4P353
A	481	PHE	TYR	conflict	UNP R4P353
B	-25	MET	-	initiating methionine	UNP R4P353
B	-24	SER	-	expression tag	UNP R4P353
B	-23	TYR	-	expression tag	UNP R4P353
B	-22	TYR	-	expression tag	UNP R4P353
B	-21	HIS	-	expression tag	UNP R4P353
B	-20	HIS	-	expression tag	UNP R4P353
B	-19	HIS	-	expression tag	UNP R4P353
B	-18	HIS	-	expression tag	UNP R4P353
B	-17	HIS	-	expression tag	UNP R4P353
B	-16	HIS	-	expression tag	UNP R4P353
B	-15	LEU	-	expression tag	UNP R4P353
B	-14	GLU	-	expression tag	UNP R4P353
B	-13	SER	-	expression tag	UNP R4P353
B	-12	THR	-	expression tag	UNP R4P353
B	-11	SER	-	expression tag	UNP R4P353
B	-10	LEU	-	expression tag	UNP R4P353
B	-9	TYR	-	expression tag	UNP R4P353
B	-8	LYS	-	expression tag	UNP R4P353
B	-7	LYS	-	expression tag	UNP R4P353
B	-6	ALA	-	expression tag	UNP R4P353
B	-5	GLY	-	expression tag	UNP R4P353
B	-4	SER	-	expression tag	UNP R4P353
B	-3	GLU	-	expression tag	UNP R4P353
B	-2	PHE	-	expression tag	UNP R4P353
B	-1	ALA	-	expression tag	UNP R4P353
B	0	LEU	-	expression tag	UNP R4P353
B	481	PHE	TYR	conflict	UNP R4P353

- Molecule 2 is a protein called Presegetalin A1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	C	6	38	23	7	8	0	0	0
			Total	C	N	O			
2	D	6	38	23	7	8	0	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
3	A	1	1	1	0	0

- Molecule 4 is water.

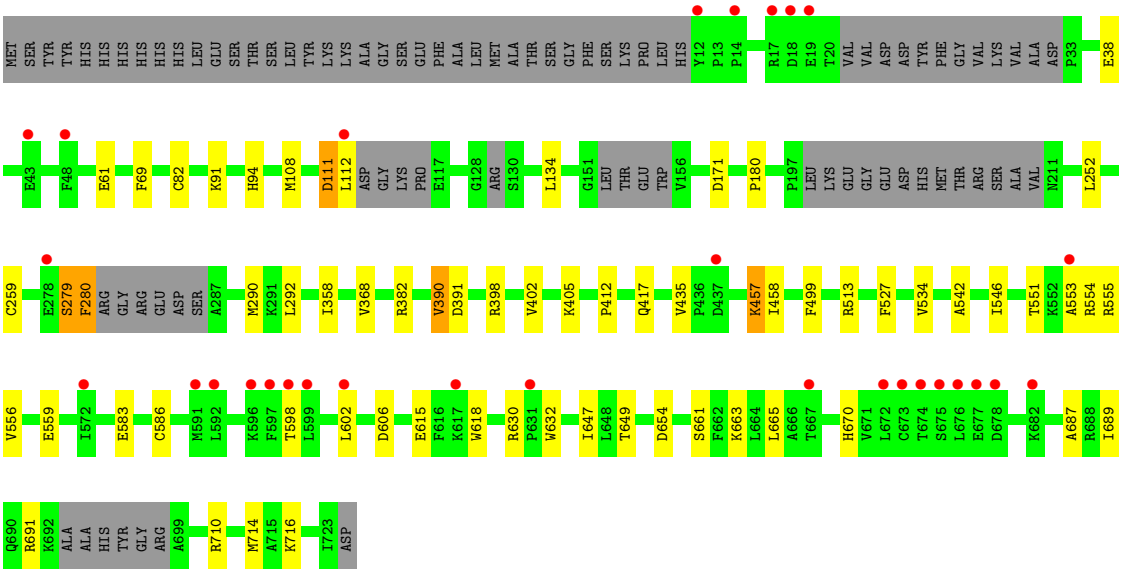
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	19	19	19	0	0
			Total	O		
4	B	16	16	16	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

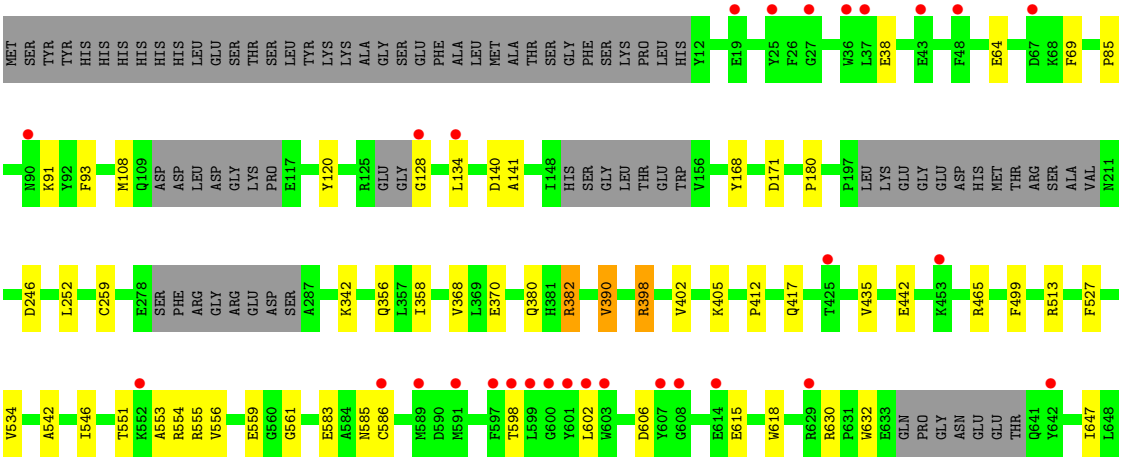
• Molecule 1: Peptide cyclase 1

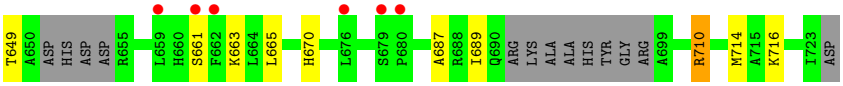
Chain A:



• Molecule 1: Peptide cyclase 1

Chain B:





- Molecule 2: Presegetalin A1

Chain C:

- Molecule 2: Presegetalin A1

Chain D:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	86.95Å 59.63Å 134.16Å 90.00° 93.12° 90.00°	Depositor
Resolution (Å)	86.80 – 2.37 86.82 – 2.37	Depositor EDS
% Data completeness (in resolution range)	99.2 (86.80-2.37) 99.2 (86.82-2.37)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$< I/\sigma(I) >$ [1]	2.37 (at 2.37Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.236 , 0.284 0.240 , 0.285	Depositor DCC
R_{free} test set	2744 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å^2)	42.4	Xtriage
Anisotropy	0.633	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 36.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	10789	wwPDB-VP
Average B, all atoms (Å^2)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.51% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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: MG

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	0.56	0/5501	0.69	0/7438
1	B	0.54	0/5437	0.68	0/7351
2	C	0.57	0/38	0.57	0/52
2	D	0.67	0/38	0.47	0/52
All	All	0.55	0/11014	0.69	0/14893

There are no bond length outliers.

There are no bond angle outliers.

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	5369	0	5222	32	0
1	B	5308	0	5195	34	0
2	C	38	0	36	0	0
2	D	38	0	36	0	0
3	A	1	0	0	0	0
4	A	19	0	0	0	0
4	B	16	0	0	1	0
All	All	10789	0	10489	65	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 3.

All (65) 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:457:LYS:HG2	1:A:457:LYS:O	1.89	0.70
1:A:457:LYS:O	1:A:458:ILE:HD13	1.91	0.70
1:B:134:LEU:CD1	1:B:180:PRO:HA	2.25	0.67
1:A:290[B]:MET:HE1	1:A:292:LEU:HA	1.77	0.66
1:B:390:VAL:HA	1:B:405:LYS:O	2.02	0.60
1:A:134:LEU:CD1	1:A:180:PRO:HA	2.33	0.59
1:B:368:VAL:CG1	1:B:382:ARG:HD3	2.33	0.58
1:A:390:VAL:HA	1:A:405:LYS:O	2.05	0.57
1:A:279:SER:O	1:A:280:PHE:CD1	2.60	0.55
1:A:111:ASP:CG	1:A:112:LEU:N	2.62	0.54
1:A:457:LYS:O	1:A:457:LYS:CG	2.51	0.52
1:B:134:LEU:HD13	1:B:180:PRO:HA	1.90	0.52
1:A:358:ILE:HD11	1:A:402:VAL:HG21	1.92	0.52
1:A:412:PRO:HG3	1:A:435:VAL:HG23	1.93	0.51
1:B:370:GLU:HG2	1:B:382:ARG:HG2	1.94	0.50
1:A:82[B]:CYS:SG	1:A:94:HIS:CD2	3.05	0.50
1:B:559:GLU:HA	1:B:583:GLU:O	2.12	0.49
1:B:412:PRO:HG3	1:B:435:VAL:HG23	1.93	0.49
1:B:665:LEU:HD22	1:B:687:ALA:HB2	1.95	0.48
1:A:38:GLU:OE2	1:A:663:LYS:NZ	2.44	0.48
1:A:358:ILE:CD1	1:A:402:VAL:HG11	2.44	0.48
1:B:442:GLU:OE1	1:B:465[B]:ARG:NH2	2.47	0.48
1:A:559:GLU:HA	1:A:583:GLU:O	2.14	0.47
1:B:128:GLY:HA2	4:B:803:HOH:O	2.14	0.47
1:B:513:ARG:O	1:B:534:VAL:HG22	2.14	0.47
1:B:358:ILE:HD11	1:B:402:VAL:HG21	1.96	0.47
1:B:91:LYS:HD3	1:B:108[A]:MET:CE	2.44	0.47
1:A:630:ARG:HB3	1:A:632:TRP:CE2	2.50	0.47
1:A:91:LYS:HD3	1:A:108:MET:CE	2.45	0.47
1:A:665:LEU:HD22	1:A:687:ALA:HB2	1.96	0.47
1:B:358:ILE:CD1	1:B:402:VAL:HG11	2.46	0.46
1:B:542:ALA:O	1:B:546:ILE:HG12	2.15	0.46
1:A:649:THR:O	1:A:689:ILE:HA	2.15	0.46
1:B:134:LEU:HD11	1:B:180:PRO:HA	1.95	0.46
1:B:615:GLU:HG2	1:B:618:TRP:CH2	2.51	0.46
1:A:551:THR:HG21	1:A:556:VAL:HG22	1.98	0.46
1:B:551:THR:HG21	1:B:556:VAL:HG22	1.98	0.46
1:B:38:GLU:OE2	1:B:663:LYS:NZ	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:513:ARG:O	1:A:534:VAL:HG22	2.16	0.45
1:B:630:ARG:HB3	1:B:632:TRP:CE2	2.50	0.45
1:A:290[B]:MET:HE2	1:A:292:LEU:N	2.32	0.45
1:A:499:PHE:CE1	1:A:714:MET:CE	3.01	0.44
1:A:615:GLU:HG2	1:A:618:TRP:CH2	2.52	0.44
1:A:542:ALA:O	1:A:546:ILE:HG12	2.18	0.44
1:B:120:TYR:HE1	1:B:168:TYR:HH	1.63	0.44
1:B:85:PRO:HA	1:B:93:PHE:O	2.17	0.43
1:A:290[B]:MET:CE	1:A:292:LEU:N	2.81	0.43
1:B:546:ILE:HD12	1:B:553:ALA:N	2.34	0.43
1:B:649:THR:O	1:B:689:ILE:HA	2.18	0.43
1:B:499:PHE:CE1	1:B:714:MET:CE	3.02	0.43
1:A:134:LEU:HD13	1:A:180:PRO:HA	2.00	0.43
1:B:140:ASP:O	1:B:141:ALA:HB3	2.19	0.43
1:A:553:ALA:O	1:A:554:ARG:HB2	2.19	0.42
1:B:356:GLN:NE2	1:B:380:GLN:OE1	2.48	0.42
1:B:553:ALA:O	1:B:554:ARG:HB2	2.19	0.42
1:B:647:ILE:CG2	1:B:661:SER:HB3	2.50	0.42
1:B:91:LYS:HD3	1:B:108[B]:MET:SD	2.59	0.41
1:B:710[B]:ARG:HE	1:B:710[B]:ARG:HB3	1.52	0.41
1:A:647:ILE:CG2	1:A:661:SER:HB3	2.50	0.41
1:B:246:ASP:OD1	1:B:398:ARG:NH2	2.51	0.41
1:A:391:ASP:C	1:A:391:ASP:OD1	2.58	0.40
1:A:546:ILE:HD12	1:A:553:ALA:N	2.36	0.40
1:A:61:GLU:HG3	1:B:64:GLU:OE2	2.22	0.40
1:B:561:GLY:HA2	1:B:585:ASN:O	2.22	0.40
1:A:368:VAL:HG11	1:A:382:ARG:CZ	2.52	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	652/750 (87%)	615 (94%)	34 (5%)	3 (0%)	29	39
1	B	641/750 (86%)	609 (95%)	30 (5%)	2 (0%)	41	53
2	C	4/19 (21%)	3 (75%)	1 (25%)	0	100	100
2	D	4/19 (21%)	3 (75%)	1 (25%)	0	100	100
All	All	1301/1538 (85%)	1230 (94%)	66 (5%)	5 (0%)	34	46

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	598	THR
1	B	598	THR
1	A	670	HIS
1	A	691	ARG
1	B	670	HIS

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	584/652 (90%)	565 (97%)	19 (3%)	38	55
1	B	576/652 (88%)	559 (97%)	17 (3%)	41	59
2	C	4/14 (29%)	4 (100%)	0	100	100
2	D	4/14 (29%)	4 (100%)	0	100	100
All	All	1168/1332 (88%)	1132 (97%)	36 (3%)	41	57

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	69	PHE
1	A	111	ASP
1	A	171	ASP
1	A	252	LEU
1	A	259	CYS
1	A	279	SER

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Mol	Chain	Res	Type
1	A	280	PHE
1	A	390	VAL
1	A	398	ARG
1	A	417	GLN
1	A	457	LYS
1	A	527	PHE
1	A	555	ARG
1	A	586	CYS
1	A	602	LEU
1	A	606	ASP
1	A	654	ASP
1	A	710	ARG
1	A	716	LYS
1	B	69	PHE
1	B	171	ASP
1	B	252	LEU
1	B	259	CYS
1	B	342	LYS
1	B	382	ARG
1	B	390	VAL
1	B	398	ARG
1	B	417	GLN
1	B	527	PHE
1	B	555	ARG
1	B	586	CYS
1	B	602	LEU
1	B	606	ASP
1	B	710[A]	ARG
1	B	710[B]	ARG
1	B	716	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	94	HIS
1	A	149	HIS
1	B	275	ASN
1	B	595	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

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.

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	666/750 (88%)	0.33	30 (4%)	33	36	21, 46, 88, 123	0
1	B	656/750 (87%)	0.37	35 (5%)	26	29	24, 48, 86, 111	0
2	C	6/19 (31%)	0.08	0	100	100	35, 41, 46, 46	0
2	D	6/19 (31%)	0.09	0	100	100	36, 40, 47, 52	0
All	All	1334/1538 (86%)	0.35	65 (4%)	29	32	21, 47, 87, 123	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	572	ILE	4.9
1	A	43	GLU	4.5
1	A	17	ARG	4.2
1	A	596	LYS	4.1
1	B	43	GLU	3.9
1	A	592	LEU	3.9
1	B	453	LYS	3.8
1	B	134	LEU	3.8
1	B	36	TRP	3.5
1	A	678	ASP	3.5
1	B	607	TYR	3.4
1	A	667	THR	3.3
1	A	677	GLU	3.3
1	B	602	LEU	3.3
1	A	682	LYS	3.2
1	A	591	MET	3.2
1	A	48	PHE	3.1
1	B	128	GLY	3.1
1	A	598	THR	3.1
1	B	680	PRO	3.1
1	B	597	PHE	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	19	GLU	2.9
1	B	598	THR	2.9
1	A	14	PRO	2.8
1	A	278	GLU	2.8
1	A	553	ALA	2.7
1	B	37	LEU	2.7
1	B	586	CYS	2.7
1	B	591	MET	2.7
1	B	589	MET	2.6
1	A	112	LEU	2.6
1	A	631	PRO	2.6
1	A	676	LEU	2.6
1	B	659	LEU	2.5
1	A	674	THR	2.4
1	B	629	ARG	2.4
1	B	676	LEU	2.4
1	B	599	LEU	2.4
1	A	19	GLU	2.4
1	B	25	TYR	2.4
1	B	614	GLU	2.4
1	B	48	PHE	2.4
1	B	603	TRP	2.3
1	A	672	LEU	2.3
1	B	27	GLY	2.3
1	A	12	TYR	2.3
1	B	67	ASP	2.3
1	B	552	LYS	2.3
1	B	679	SER	2.3
1	A	675	SER	2.3
1	A	599	LEU	2.2
1	A	602	LEU	2.2
1	A	597	PHE	2.2
1	A	437	ASP	2.2
1	B	642	TYR	2.2
1	A	673	CYS	2.2
1	B	601	TYR	2.1
1	A	18	ASP	2.1
1	B	661	SER	2.1
1	B	600	GLY	2.1
1	A	617	LYS	2.1
1	B	608	GLY	2.1
1	B	662	PHE	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	425	THR	2.0
1	B	90	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 monosaccharides 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. 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	B-factors(Å^2)	Q<0.9
3	MG	A	801	1/1	0.96	0.15	29,29,29,29	0

6.5 Other polymers (i)

There are no such residues in this entry.