



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:28 PM UTC

PDB ID : 5UW3 / pdb_00005uw3
Title : PCY1 in Complex with Follower Peptide
Authors : Chekan, J.R.; Nair, S.K.
Deposited on : 2017-02-20
Resolution : 1.96 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

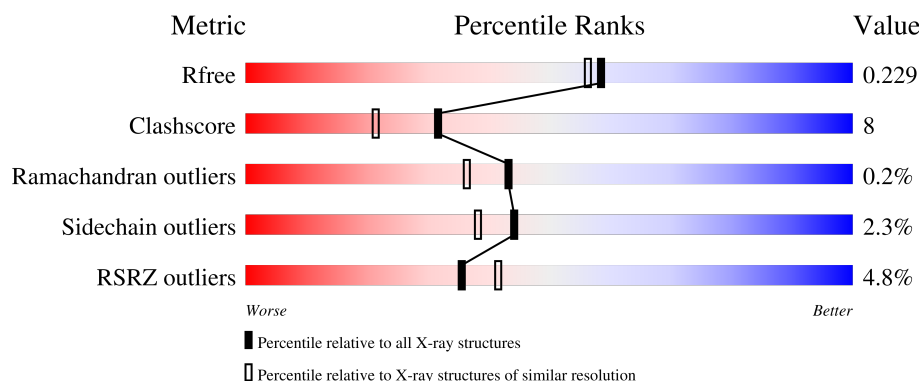
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.96 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}	180053	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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 $\leq 5\%$. 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	750	9% 80% 11% 8%
1	B	750	5% 82% 11% 6%
1	C	750	2% 81% 12% 6%
1	D	750	3% 82% 10% 7%
2	E	19	26% 5% 68%

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Mol	Chain	Length	Quality of chain
2	F	19	
2	G	19	
2	H	19	

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
3	CAC	C	801	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 24731 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
1	A	693	Total	C	N	O	S	0	0	0
			5573	3564	946	1038	25			
1	B	707	Total	C	N	O	S	0	0	0
			5669	3622	963	1058	26			
1	C	702	Total	C	N	O	S	0	0	0
			5646	3612	961	1048	25			
1	D	698	Total	C	N	O	S	0	0	0
			5608	3586	954	1043	25			

There are 104 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

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Chain	Residue	Modelled	Actual	Comment	Reference
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
A	0	LEU	-	expression tag	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
C	-25	MET	-	initiating methionine	UNP R4P353
C	-24	SER	-	expression tag	UNP R4P353
C	-23	TYR	-	expression tag	UNP R4P353
C	-22	TYR	-	expression tag	UNP R4P353
C	-21	HIS	-	expression tag	UNP R4P353
C	-20	HIS	-	expression tag	UNP R4P353
C	-19	HIS	-	expression tag	UNP R4P353
C	-18	HIS	-	expression tag	UNP R4P353
C	-17	HIS	-	expression tag	UNP R4P353
C	-16	HIS	-	expression tag	UNP R4P353
C	-15	LEU	-	expression tag	UNP R4P353

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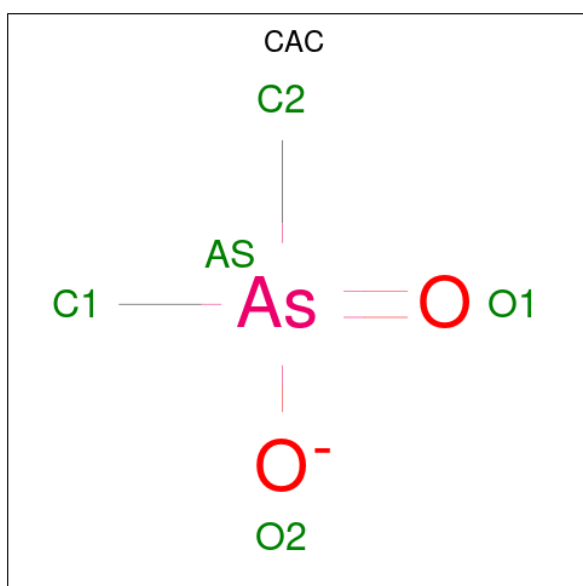
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Chain	Residue	Modelled	Actual	Comment	Reference
C	-14	GLU	-	expression tag	UNP R4P353
C	-13	SER	-	expression tag	UNP R4P353
C	-12	THR	-	expression tag	UNP R4P353
C	-11	SER	-	expression tag	UNP R4P353
C	-10	LEU	-	expression tag	UNP R4P353
C	-9	TYR	-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

- Molecule 2 is a protein called Presegetalin A1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	6	Total	C	N	O	0	0	0
			38	23	7	8			
2	F	6	Total	C	N	O	0	0	0
			39	23	7	9			
2	G	6	Total	C	N	O	0	0	0
			38	23	7	8			
2	H	6	Total	C	N	O	0	0	0
			39	23	7	9			

- Molecule 3 is CACODYLATE ION (CCD ID: CAC) (formula: $C_2H_6AsO_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	As	C	O	0	0
			5	1	2	2		
3	B	1	Total	As	C	O	0	0
			5	1	2	2		
3	C	1	Total	As	C	O	0	0
			5	1	2	2		
3	D	1	Total	As	C	O	0	0
			5	1	2	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	451	Total	O	0	0
			451	451		
4	E	6	Total	O	0	0
			6	6		

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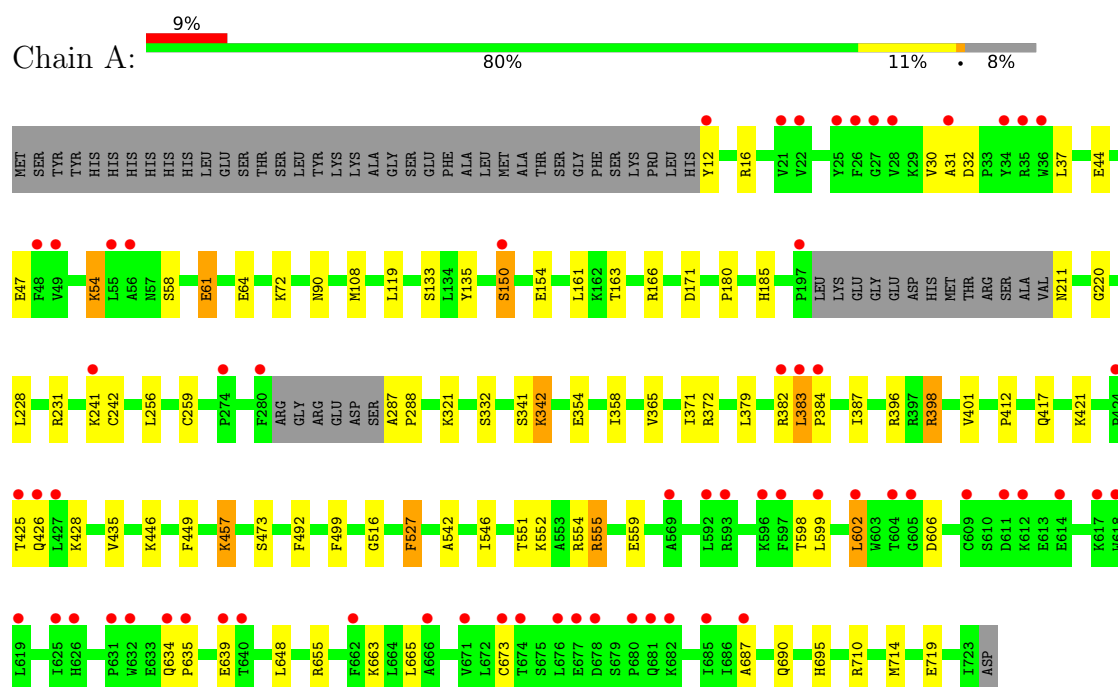
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	491	Total 491	O 491	0	0
4	F	5	Total 5	O 5	0	0
4	C	563	Total 563	O 563	0	0
4	G	5	Total 5	O 5	0	0
4	D	535	Total 535	O 535	0	0
4	H	5	Total 5	O 5	0	0

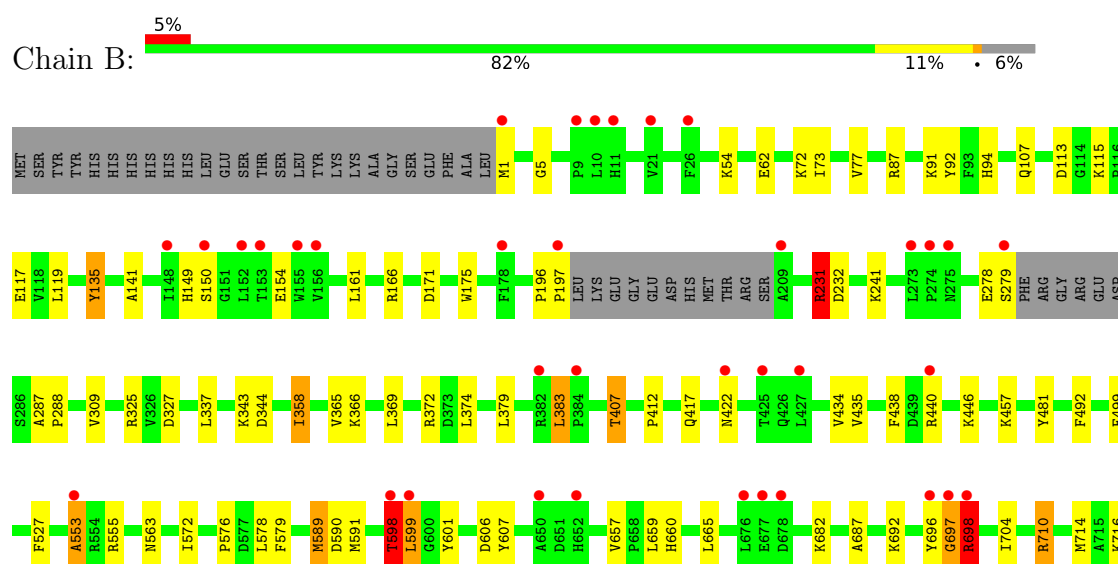
3 Residue-property plots [i](#)

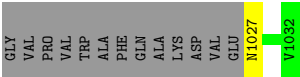
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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

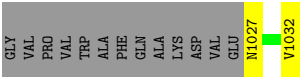


• Molecule 1: Peptide cyclase 1

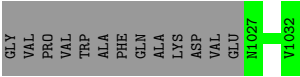




● Molecule 2: Presegetalin A1



● Molecule 2: Presegetalin A1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	65.50Å 85.59Å 137.72Å 87.41° 78.28° 89.33°	Depositor
Resolution (Å)	44.90 – 1.96 44.90 – 1.96	Depositor EDS
% Data completeness (in resolution range)	95.8 (44.90-1.96) 95.6 (44.90-1.96)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.16 (at 1.97Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.189 , 0.224 0.195 , 0.229	Depositor DCC
R_{free} test set	9945 reflections (4.73%)	wwPDB-VP
Wilson B-factor (Å ²)	16.5	Xtriage
Anisotropy	0.234	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 45.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.086 for h,-k,h-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	24731	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.14% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CAC

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	1.08	1/5717 (0.0%)	0.94	2/7743 (0.0%)
1	B	1.08	6/5815 (0.1%)	1.01	17/7876 (0.2%)
1	C	1.11	2/5793 (0.0%)	1.01	9/7845 (0.1%)
1	D	1.11	9/5753 (0.2%)	1.02	18/7791 (0.2%)
2	E	1.40	0/38	0.87	0/52
2	F	1.30	0/39	0.75	0/52
2	G	1.30	0/38	0.84	0/52
2	H	1.16	0/39	0.83	0/52
All	All	1.09	18/23232 (0.1%)	0.99	46/31463 (0.1%)

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	608	GLY	N-CA	11.70	1.62	1.45
1	C	608	GLY	N-CA	11.51	1.62	1.45
1	D	590	ASP	N-CA	8.99	1.57	1.46
1	D	496	ARG	CD-NE	-7.51	1.35	1.46
1	D	589	MET	C-N	-7.01	1.23	1.33
1	B	590	ASP	N-CA	6.89	1.55	1.46
1	D	698	ARG	CA-C	6.09	1.60	1.52
1	B	698	ARG	CA-C	6.08	1.60	1.52
1	B	589	MET	C-N	-5.89	1.25	1.33
1	B	232	ASP	N-CA	5.74	1.54	1.46
1	B	232	ASP	CA-C	5.71	1.59	1.53
1	D	607	TYR	C-N	-5.50	1.25	1.33
1	D	135	TYR	C-O	5.43	1.30	1.23
1	B	407	THR	CB-CG2	-5.41	1.34	1.52
1	A	516	GLY	C-O	-5.28	1.20	1.24
1	D	697	GLY	C-O	-5.22	1.16	1.23
1	D	698	ARG	N-CA	-5.12	1.39	1.46
1	C	607	TYR	C-N	-5.10	1.26	1.33

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	607	TYR	CA-C-N	-12.96	96.01	121.41
1	D	607	TYR	C-N-CA	-12.96	96.01	121.41
1	C	607	TYR	CA-C-N	-12.47	96.97	121.41
1	C	607	TYR	C-N-CA	-12.47	96.97	121.41
1	B	232	ASP	N-CA-C	11.80	125.78	111.02
1	C	232	ASP	N-CA-C	11.37	125.23	111.02
1	B	5	GLY	N-CA-C	-8.95	102.06	112.79
1	D	696	TYR	N-CA-C	8.70	123.15	110.28
1	D	589	MET	O-C-N	-8.62	112.30	123.16
1	D	607	TYR	O-C-N	-8.53	111.11	122.97
1	C	607	TYR	O-C-N	-8.53	111.12	122.97
1	D	589	MET	N-CA-C	-8.30	96.75	109.95
1	B	598	THR	CB-CA-C	-8.21	94.08	110.42
1	B	696	TYR	N-CA-C	7.99	122.82	110.20
1	D	590	ASP	N-CA-CB	7.75	123.59	110.49
1	B	589	MET	O-C-N	-7.72	113.43	123.16
1	C	231	ARG	N-CA-C	7.42	126.60	110.80
1	C	607	TYR	N-CA-C	-7.38	99.29	110.14
1	B	589	MET	N-CA-C	-7.06	98.72	109.95
1	D	496	ARG	NE-CZ-NH2	-6.83	113.05	119.20
1	B	231	ARG	N-CA-C	6.63	124.92	110.80
1	B	590	ASP	N-CA-CB	6.55	121.56	110.49
1	D	607	TYR	N-CA-C	-6.44	100.67	110.14
1	B	196	PRO	O-C-N	6.43	124.17	121.15
1	C	395	ALA	N-CA-C	6.21	119.24	110.23
1	B	710	ARG	CD-NE-CZ	6.04	132.86	124.40
1	D	698	ARG	CA-C-O	5.92	127.70	121.19
1	D	496	ARG	CD-NE-CZ	5.89	132.65	124.40
1	D	553	ALA	CA-C-N	-5.87	112.90	122.65
1	D	553	ALA	C-N-CA	-5.87	112.90	122.65
1	C	618	TRP	CB-CA-C	-5.84	101.68	110.90
1	C	135	TYR	N-CA-C	-5.76	98.11	108.48
1	B	553	ALA	CA-C-N	-5.66	113.25	122.65
1	B	553	ALA	C-N-CA	-5.66	113.25	122.65
1	D	589	MET	CA-C-N	-5.63	110.78	121.54
1	D	589	MET	C-N-CA	-5.63	110.78	121.54
1	A	135	TYR	N-CA-C	-5.51	98.57	108.48
1	B	698	ARG	CA-C-O	5.35	127.22	121.55
1	A	555	ARG	CG-CD-NE	-5.30	100.34	112.00
1	D	135	TYR	N-CA-C	-5.29	98.96	108.48
1	D	618	TRP	CB-CA-C	-5.21	102.66	110.90
1	B	598	THR	CA-C-N	-5.17	118.73	126.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	598	THR	C-N-CA	-5.17	118.73	126.86
1	B	135	TYR	CB-CA-C	-5.17	105.02	111.43
1	D	599	LEU	CB-CA-C	5.08	119.33	110.94
1	B	135	TYR	N-CA-C	5.01	115.71	107.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	5573	0	5417	115	1
1	B	5669	0	5515	79	0
1	C	5646	0	5494	74	0
1	D	5608	0	5457	94	1
2	E	38	0	36	1	0
2	F	39	0	36	1	0
2	G	38	0	36	2	0
2	H	39	0	36	0	0
3	A	5	0	0	0	0
3	B	5	0	0	3	0
3	C	5	0	0	4	0
3	D	5	0	0	1	0
4	A	451	0	0	60	0
4	B	491	0	0	43	0
4	C	563	0	0	29	0
4	D	535	0	0	46	0
4	E	6	0	0	1	0
4	F	5	0	0	1	0
4	G	5	0	0	1	0
4	H	5	0	0	0	0
All	All	24731	0	22027	362	1

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 8.

All (362) 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:321:LYS:HE3	4:A:905:HOH:O	1.31	1.30
1:C:422:ASN:CG	4:C:902:HOH:O	1.81	1.23
1:B:714:MET:SD	4:B:1318:HOH:O	1.99	1.18
1:D:714:MET:SD	4:D:1365:HOH:O	1.95	1.18
1:B:325:ARG:HB2	4:B:1294:HOH:O	1.46	1.12
1:B:161:LEU:HB3	4:B:1326:HOH:O	1.46	1.12
4:B:991:HOH:O	1:C:375:GLU:HG3	1.51	1.11
1:D:588:VAL:C	1:D:589:MET:HE2	1.76	1.11
1:D:297:ASP:HB3	4:D:1326:HOH:O	1.51	1.10
1:B:161:LEU:CB	4:B:1326:HOH:O	2.00	1.09
1:A:499:PHE:CE1	1:A:714:MET:HE1	1.87	1.09
1:B:499:PHE:CE1	1:B:714:MET:HE1	1.88	1.07
1:A:321:LYS:CE	4:A:905:HOH:O	1.89	1.07
1:D:499:PHE:CE1	1:D:714:MET:HE1	1.87	1.07
1:A:714:MET:SD	4:A:1291:HOH:O	2.09	1.06
1:D:588:VAL:O	1:D:589:MET:HE2	1.53	1.06
1:A:599:LEU:HD21	1:A:655:ARG:HA	1.36	1.05
1:D:161:LEU:HB3	4:D:1334:HOH:O	1.58	1.03
1:A:663:LYS:HG2	4:A:1227:HOH:O	1.63	0.99
1:B:576:PRO:HA	4:B:1282:HOH:O	1.63	0.99
1:A:673:CYS:SG	4:A:929:HOH:O	2.05	0.98
1:B:337:LEU:HB2	4:B:1294:HOH:O	1.66	0.96
1:D:135:TYR:C	4:D:908:HOH:O	2.06	0.96
1:A:663:LYS:CG	4:A:1227:HOH:O	2.14	0.96
1:C:723:ILE:C	4:C:1063:HOH:O	2.09	0.93
1:B:231:ARG:O	4:B:901:HOH:O	1.85	0.92
1:A:599:LEU:O	1:A:602:LEU:HD23	1.70	0.91
1:B:383:LEU:HD21	4:B:1312:HOH:O	1.70	0.91
1:B:438:PHE:CE2	1:B:440:ARG:HG2	2.04	0.91
1:C:246:ASP:OD1	4:C:901:HOH:O	1.89	0.90
1:D:588:VAL:C	1:D:589:MET:CE	2.45	0.89
1:C:320:ARG:NH1	1:C:341:SER:O	2.05	0.88
1:B:481:TYR:OH	3:B:801:CAC:C2	2.23	0.87
1:D:211:ASN:N	4:D:902:HOH:O	2.05	0.87
1:A:259:CYS:SG	1:A:602:LEU:HD12	2.14	0.86
1:D:572:ILE:HA	4:D:1240:HOH:O	1.74	0.85
1:C:434:VAL:HG23	4:C:1128:HOH:O	1.76	0.85
2:F:1027:ASN:N	4:F:1101:HOH:O	2.09	0.84
1:B:72:LYS:HD3	4:B:1303:HOH:O	1.77	0.84
1:B:589:MET:O	1:B:660:HIS:ND1	2.10	0.83
1:D:496:ARG:HD2	1:D:507:PHE:CG	2.12	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:599:LEU:HD23	1:A:599:LEU:H	1.44	0.83
4:A:1160:HOH:O	1:D:249:LYS:HD2	1.77	0.83
1:D:230:TRP:CD1	4:D:919:HOH:O	2.31	0.82
1:D:185:HIS:HE1	4:D:1345:HOH:O	1.62	0.82
1:D:589:MET:O	1:D:660:HIS:ND1	2.11	0.81
1:C:422:ASN:ND2	4:C:902:HOH:O	2.00	0.81
1:B:553:ALA:O	1:B:578:LEU:O	2.00	0.79
1:C:287:ALA:N	4:C:904:HOH:O	2.14	0.79
1:C:563:ASN:H	3:C:801:CAC:C1	1.96	0.79
1:C:142:LYS:HG2	1:C:164:GLU:OE2	1.83	0.78
1:A:398:ARG:HG2	4:A:925:HOH:O	1.82	0.78
1:D:587:GLY:C	1:D:589:MET:HE3	2.09	0.78
1:B:91:LYS:HG3	4:B:1109:HOH:O	1.82	0.77
1:D:211:ASN:N	4:D:904:HOH:O	2.17	0.77
1:C:409:ILE:HD12	1:C:496:ARG:NH1	2.00	0.76
1:D:588:VAL:N	1:D:589:MET:HE3	2.00	0.76
3:D:801:CAC:O2	4:D:901:HOH:O	2.04	0.76
1:A:648:LEU:HD21	4:A:1322:HOH:O	1.86	0.75
1:D:576:PRO:HA	4:D:1240:HOH:O	1.86	0.75
1:C:149:HIS:HD2	4:C:917:HOH:O	1.67	0.75
1:D:499:PHE:CD1	1:D:714:MET:HE1	2.22	0.75
1:B:499:PHE:CD1	1:B:714:MET:HE1	2.20	0.75
1:A:499:PHE:CE1	1:A:714:MET:CE	2.70	0.74
1:A:499:PHE:CD1	1:A:714:MET:HE1	2.22	0.74
1:A:16:ARG:HG2	4:A:1079:HOH:O	1.87	0.73
1:D:287:ALA:N	4:D:906:HOH:O	2.21	0.73
1:D:566:LEU:HA	1:D:589:MET:HE1	1.70	0.73
1:B:499:PHE:HE1	1:B:714:MET:HE1	1.54	0.73
1:D:297:ASP:CB	4:D:1326:HOH:O	2.18	0.73
1:B:598:THR:O	1:B:598:THR:OG1	2.00	0.73
1:A:710:ARG:HB3	4:A:1322:HOH:O	1.89	0.72
1:B:374:LEU:HD22	4:B:1014:HOH:O	1.89	0.71
1:D:579:PHE:HD2	4:D:1240:HOH:O	1.72	0.71
1:A:228:LEU:HD11	1:A:231:ARG:CG	2.21	0.71
1:B:438:PHE:CE2	1:B:440:ARG:CG	2.75	0.70
1:D:553:ALA:O	1:D:578:LEU:O	2.08	0.70
1:A:90:ASN:HB3	4:D:1328:HOH:O	1.90	0.70
1:C:481:TYR:OH	3:C:801:CAC:C1	2.40	0.69
1:D:473:SER:O	1:D:555:ARG:NH2	2.25	0.69
1:B:499:PHE:CE1	1:B:714:MET:CE	2.72	0.69
1:A:180:PRO:HG2	4:A:1284:HOH:O	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:343:LYS:HG2	1:B:344:ASP:OD1	1.93	0.69
1:C:290:MET:HB3	4:C:1407:HOH:O	1.93	0.69
1:D:499:PHE:HE1	1:D:714:MET:HE1	1.55	0.68
1:B:572:ILE:HA	4:B:1282:HOH:O	1.93	0.68
1:A:710:ARG:CB	4:A:1322:HOH:O	2.42	0.68
1:C:210:VAL:N	4:C:908:HOH:O	2.26	0.68
1:A:180:PRO:HD2	4:A:1284:HOH:O	1.93	0.68
1:D:588:VAL:O	1:D:589:MET:CE	2.36	0.68
1:A:37:LEU:HB2	4:A:1227:HOH:O	1.95	0.67
1:B:407:THR:CG2	1:B:492:PHE:H	2.07	0.67
1:A:30:VAL:O	4:A:903:HOH:O	2.12	0.67
1:A:719:GLU:OE1	4:A:904:HOH:O	2.13	0.67
1:B:117:GLU:HB3	1:B:166:ARG:HH21	1.59	0.67
1:A:256:LEU:HD13	4:A:1012:HOH:O	1.94	0.67
1:A:387:ILE:HG22	4:A:976:HOH:O	1.95	0.66
1:D:499:PHE:CE1	1:D:714:MET:CE	2.71	0.66
1:A:58:SER:O	1:A:61:GLU:OE1	2.14	0.66
1:D:136:SER:N	4:D:908:HOH:O	2.26	0.66
1:D:191:PHE:CE1	1:D:229:LEU:HD21	2.30	0.66
1:D:496:ARG:HD2	1:D:507:PHE:CD1	2.30	0.66
4:B:1130:HOH:O	1:C:421:LYS:HE2	1.96	0.66
1:A:47:GLU:HG3	4:A:1210:HOH:O	1.94	0.65
1:A:342:LYS:HB3	4:A:1308:HOH:O	1.96	0.65
1:A:599:LEU:HB2	1:A:602:LEU:CD2	2.27	0.65
1:A:599:LEU:CD2	1:A:655:ARG:HA	2.21	0.65
1:A:44:GLU:HA	1:A:47:GLU:HG2	1.79	0.65
1:D:191:PHE:HE1	1:D:229:LEU:HD21	1.62	0.64
1:D:195:TYR:OH	4:D:903:HOH:O	2.07	0.64
1:D:343:LYS:HG2	1:D:344:ASP:OD1	1.96	0.64
1:B:113:ASP:OD1	4:B:903:HOH:O	2.15	0.64
1:B:154:GLU:O	4:B:904:HOH:O	2.15	0.64
1:D:618:TRP:CZ2	4:D:949:HOH:O	2.50	0.64
1:C:136:SER:HB2	4:C:1359:HOH:O	1.97	0.64
1:A:64:GLU:OE2	4:A:906:HOH:O	2.15	0.64
1:A:354:GLU:HG2	4:A:1268:HOH:O	1.98	0.63
1:A:710:ARG:NE	4:A:901:HOH:O	1.96	0.63
1:B:117:GLU:HG2	4:B:1274:HOH:O	1.99	0.63
1:D:159:LYS:HE3	4:D:1054:HOH:O	1.98	0.62
1:A:332:SER:HB3	4:A:1279:HOH:O	2.00	0.62
1:A:90:ASN:HB3	4:D:932:HOH:O	1.98	0.62
1:D:161:LEU:HD23	4:D:1334:HOH:O	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:107:GLN:HB3	4:B:912:HOH:O	2.00	0.61
1:B:555:ARG:HD3	4:B:1201:HOH:O	1.99	0.61
1:B:563:ASN:H	3:B:801:CAC:C2	2.13	0.61
1:A:499:PHE:HE1	1:A:714:MET:HE1	1.54	0.61
1:D:496:ARG:HD2	1:D:507:PHE:CD2	2.35	0.61
1:D:423:ASP:OD2	1:D:426:GLN:NE2	2.34	0.61
1:D:698:ARG:HD2	4:D:1062:HOH:O	2.00	0.61
1:B:161:LEU:HD13	4:B:1326:HOH:O	2.00	0.60
1:A:358:ILE:HG12	1:A:371:ILE:CD1	2.31	0.60
1:B:698:ARG:HG2	4:B:1356:HOH:O	2.02	0.60
1:A:228:LEU:HD11	1:A:231:ARG:HG2	1.83	0.59
1:B:87:ARG:CZ	4:B:916:HOH:O	2.50	0.59
1:B:457:LYS:HG3	4:B:914:HOH:O	2.02	0.59
1:A:180:PRO:CG	4:A:1284:HOH:O	2.50	0.59
1:B:94:HIS:HD2	4:B:1029:HOH:O	1.85	0.59
1:D:614:GLU:C	4:D:949:HOH:O	2.46	0.59
1:D:90:ASN:HB2	4:D:1351:HOH:O	2.02	0.58
1:D:589:MET:HE2	1:D:589:MET:N	2.17	0.58
1:C:440:ARG:NH2	4:C:903:HOH:O	2.11	0.58
1:A:559:GLU:HG2	4:A:911:HOH:O	2.03	0.58
1:A:663:LYS:HG3	4:A:1227:HOH:O	1.95	0.58
1:C:451:PRO:HA	4:C:1328:HOH:O	2.02	0.58
1:C:546:ILE:HD13	1:C:551:THR:HG23	1.85	0.58
1:D:668:MET:HE2	1:D:685:ILE:HD12	1.86	0.57
1:D:698:ARG:HG2	4:D:1406:HOH:O	2.02	0.57
1:C:113:ASP:HB2	4:C:986:HOH:O	2.04	0.57
1:A:499:PHE:HE1	1:A:714:MET:CE	2.12	0.57
1:C:446:LYS:HE3	1:C:447:GLN:O	2.04	0.57
1:A:321:LYS:NZ	4:A:905:HOH:O	2.14	0.57
1:B:161:LEU:HB2	4:B:1326:HOH:O	1.88	0.57
1:A:710:ARG:CD	4:A:1322:HOH:O	2.53	0.56
1:C:290:MET:HE2	4:C:1407:HOH:O	2.05	0.56
1:B:499:PHE:HE1	1:B:714:MET:CE	2.15	0.56
1:A:166:ARG:NH1	4:A:922:HOH:O	2.39	0.56
1:A:449:PHE:HB2	4:C:1328:HOH:O	2.04	0.56
1:A:473:SER:O	1:A:555:ARG:NH1	2.38	0.56
1:A:32:ASP:N	4:A:903:HOH:O	2.38	0.56
1:A:384:PRO:HG2	1:C:342:LYS:HB2	1.86	0.56
1:A:546:ILE:HD13	1:A:551:THR:HG23	1.88	0.55
1:C:134:LEU:CD1	1:C:179:SER:O	2.55	0.55
1:C:553:ALA:O	1:C:578:LEU:O	2.24	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:249:LYS:NZ	4:D:912:HOH:O	2.36	0.55
1:A:382:ARG:HH22	1:C:382:ARG:NH2	2.04	0.55
1:B:598:THR:O	1:B:599:LEU:HG	2.06	0.55
1:C:438:PHE:HD1	4:C:1382:HOH:O	1.88	0.55
1:D:650:ALA:HB2	1:D:698:ARG:NH2	2.21	0.55
1:A:599:LEU:HD21	1:A:655:ARG:CA	2.23	0.55
1:B:279:SER:C	4:B:1041:HOH:O	2.49	0.55
1:A:31:ALA:C	4:A:903:HOH:O	2.50	0.55
1:C:546:ILE:CD1	1:C:551:THR:HG23	2.37	0.55
1:A:412:PRO:HG3	1:A:435:VAL:HG23	1.90	0.54
1:B:87:ARG:NE	4:B:916:HOH:O	2.40	0.54
1:C:703:GLN:HG3	2:G:1032:VAL:HG21	1.90	0.54
1:D:618:TRP:CE2	4:D:949:HOH:O	2.59	0.54
1:B:161:LEU:CD1	4:B:1326:HOH:O	2.51	0.54
1:D:520:GLU:HG3	1:D:524:LYS:HE2	1.89	0.54
1:D:499:PHE:HE1	1:D:714:MET:CE	2.15	0.54
1:C:87:ARG:HG3	1:C:88:ARG:N	2.22	0.54
1:C:191:PHE:CE2	1:C:244:ILE:HD11	2.42	0.54
1:B:309:VAL:HG13	4:B:1290:HOH:O	2.08	0.54
1:C:446:LYS:HD3	1:C:448:VAL:HG13	1.90	0.54
1:D:218:PHE:HE2	1:D:227:ILE:HD11	1.72	0.54
1:D:566:LEU:CA	1:D:589:MET:HE1	2.37	0.53
1:B:62:GLU:CG	1:B:716:LYS:NZ	2.70	0.53
1:B:412:PRO:HG3	1:B:435:VAL:HG23	1.89	0.53
1:B:422:ASN:OD1	1:C:330:ASN:ND2	2.31	0.53
1:B:682:LYS:HE2	4:B:930:HOH:O	2.09	0.53
1:A:398:ARG:NE	4:A:925:HOH:O	2.42	0.53
1:B:438:PHE:CZ	1:B:440:ARG:HG2	2.41	0.53
1:C:47:GLU:HG3	4:C:1277:HOH:O	2.07	0.53
1:D:166:ARG:HB2	4:D:1353:HOH:O	2.08	0.53
1:B:73:ILE:CG2	1:B:704:ILE:HD12	2.39	0.53
1:A:710:ARG:HD2	4:A:1322:HOH:O	2.10	0.52
1:D:412:PRO:HG3	1:D:435:VAL:HG23	1.91	0.52
1:A:401:VAL:HG13	1:A:401:VAL:O	2.09	0.52
1:D:316:LYS:HE3	4:D:1326:HOH:O	2.09	0.52
1:D:614:GLU:HG2	1:D:615:GLU:N	2.24	0.52
1:C:356:GLN:NE2	1:C:380:GLN:OE1	2.42	0.52
1:C:412:PRO:HG3	1:C:435:VAL:HG23	1.92	0.52
1:C:375:GLU:OE2	1:C:375:GLU:HA	2.09	0.52
1:D:230:TRP:NE1	4:D:919:HOH:O	2.41	0.52
1:A:54:LYS:HD2	1:A:54:LYS:O	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:473:SER:C	4:A:1096:HOH:O	2.52	0.52
1:A:673:CYS:N	4:A:929:HOH:O	2.42	0.52
1:A:710:ARG:NH2	4:A:901:HOH:O	2.42	0.52
1:C:197:PRO:HD2	4:C:1394:HOH:O	2.09	0.52
1:D:4:SER:O	4:D:905:HOH:O	2.18	0.52
1:A:12:TYR:HB3	4:A:1107:HOH:O	2.09	0.51
1:A:546:ILE:CD1	1:A:551:THR:HG23	2.40	0.51
1:A:90:ASN:CB	4:D:1328:HOH:O	2.54	0.51
1:B:92:TYR:OH	4:B:905:HOH:O	2.19	0.51
1:C:412:PRO:HA	1:C:492:PHE:CG	2.44	0.51
1:A:599:LEU:HD23	1:A:599:LEU:N	2.18	0.51
1:C:546:ILE:HD12	1:C:552:LYS:HA	1.92	0.51
1:D:697:GLY:HA3	4:D:1077:HOH:O	2.11	0.51
1:A:119:LEU:CD1	1:A:161:LEU:HD11	2.41	0.50
1:B:87:ARG:NH1	4:B:925:HOH:O	2.45	0.50
1:A:211:ASN:N	4:A:937:HOH:O	2.45	0.50
1:B:366:LYS:HG2	4:B:1003:HOH:O	2.10	0.50
1:A:119:LEU:HD11	1:A:161:LEU:HD11	1.94	0.50
1:A:341:SER:CB	4:A:907:HOH:O	2.58	0.50
1:C:136:SER:CB	4:C:1359:HOH:O	2.58	0.50
1:A:457:LYS:HE2	1:C:449:PHE:HB2	1.93	0.50
1:C:129:ARG:NH1	4:C:921:HOH:O	2.45	0.50
1:D:589:MET:HE2	1:D:589:MET:CA	2.42	0.50
1:D:166:ARG:HD3	4:D:1353:HOH:O	2.11	0.49
1:A:228:LEU:HD11	1:A:231:ARG:HG3	1.94	0.49
1:A:37:LEU:HD12	4:A:1227:HOH:O	2.11	0.49
1:C:191:PHE:HE2	1:C:244:ILE:HD11	1.76	0.49
1:A:185:HIS:HD2	4:D:962:HOH:O	1.96	0.49
1:B:54:LYS:HG3	4:B:1321:HOH:O	2.11	0.49
1:A:180:PRO:CD	4:A:1284:HOH:O	2.55	0.49
1:B:698:ARG:N	4:B:929:HOH:O	2.46	0.49
1:A:108:MET:HE1	1:A:163:THR:HB	1.95	0.49
1:B:710:ARG:NH2	4:B:902:HOH:O	2.45	0.49
1:B:149:HIS:HE1	4:B:904:HOH:O	1.96	0.48
1:B:358:ILE:HD11	1:B:369:LEU:HB3	1.96	0.48
1:A:166:ARG:HD3	4:A:922:HOH:O	2.14	0.48
1:D:161:LEU:CB	4:D:1334:HOH:O	2.32	0.48
1:C:8:LYS:HE3	1:C:62:GLU:CG	2.44	0.48
1:A:417:GLN:OE1	1:A:428:LYS:NZ	2.46	0.48
1:A:690:GLN:OE1	4:A:908:HOH:O	2.20	0.48
1:A:54:LYS:HD2	1:A:54:LYS:C	2.39	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:134:LEU:HD12	1:C:179:SER:O	2.14	0.48
1:C:409:ILE:HD12	1:C:496:ARG:HH11	1.77	0.47
1:A:412:PRO:HA	1:A:492:PHE:CG	2.48	0.47
1:D:412:PRO:HA	1:D:492:PHE:CG	2.50	0.47
1:A:401:VAL:HG11	4:A:1000:HOH:O	2.14	0.47
1:B:62:GLU:HG2	1:B:716:LYS:NZ	2.30	0.47
1:B:278:GLU:O	1:B:279:SER:C	2.58	0.47
1:B:412:PRO:HA	1:B:492:PHE:CG	2.50	0.47
1:C:8:LYS:HE3	1:C:62:GLU:CD	2.39	0.47
1:D:259:CYS:HB2	4:D:1148:HOH:O	2.14	0.47
1:D:554:ARG:CB	1:D:554:ARG:CZ	2.93	0.47
1:D:599:LEU:C	1:D:599:LEU:HD12	2.40	0.47
1:B:287:ALA:HB1	1:B:288:PRO:HD2	1.96	0.46
1:C:527:PHE:C	1:C:527:PHE:CD1	2.93	0.46
1:A:287:ALA:HB1	1:A:288:PRO:HD2	1.97	0.46
1:C:287:ALA:HB1	1:C:288:PRO:HD2	1.96	0.46
1:D:698:ARG:N	4:D:922:HOH:O	2.43	0.46
1:A:372:ARG:HG2	1:A:379:LEU:HA	1.97	0.46
1:C:446:LYS:CD	1:C:448:VAL:HG13	2.45	0.46
1:A:546:ILE:HD12	1:A:552:LYS:HA	1.97	0.46
1:C:383:LEU:HD23	4:C:955:HOH:O	2.15	0.46
1:C:423:ASP:OD2	1:C:426:GLN:HG3	2.15	0.45
1:B:327:ASP:HB2	4:B:1290:HOH:O	2.16	0.45
1:D:698:ARG:HB2	4:D:1062:HOH:O	2.15	0.45
1:D:161:LEU:HD11	1:D:168:TYR:CZ	2.51	0.45
1:A:259:CYS:SG	1:A:602:LEU:CD1	2.99	0.45
1:C:211:ASN:HB3	4:C:993:HOH:O	2.16	0.45
1:C:562:SER:CB	3:C:801:CAC:C1	2.95	0.45
1:C:562:SER:HB3	3:C:801:CAC:C1	2.47	0.45
1:D:161:LEU:CD1	1:D:168:TYR:CD2	3.00	0.45
1:D:614:GLU:CG	4:D:949:HOH:O	2.65	0.45
1:A:648:LEU:CD2	4:A:1322:HOH:O	2.52	0.45
2:G:1027:ASN:N	4:G:1101:HOH:O	2.49	0.45
1:A:220:GLY:HA2	4:A:1102:HOH:O	2.17	0.45
1:B:579:PHE:HD2	4:B:1282:HOH:O	2.00	0.45
1:C:372:ARG:HG2	1:C:379:LEU:HA	1.98	0.45
1:D:491:THR:O	1:D:496:ARG:NH2	2.50	0.44
1:B:135:TYR:CD2	1:B:135:TYR:O	2.70	0.44
1:B:73:ILE:HG21	1:B:704:ILE:HD12	1.99	0.44
1:A:665:LEU:HD22	1:A:687:ALA:HB2	1.98	0.44
1:A:154:GLU:CD	4:A:1020:HOH:O	2.60	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:401:VAL:O	1:A:401:VAL:CG1	2.65	0.44
1:A:527:PHE:CD1	1:A:527:PHE:C	2.94	0.44
1:D:287:ALA:HB1	1:D:288:PRO:HD2	2.00	0.44
1:D:135:TYR:HB2	4:D:908:HOH:O	2.17	0.44
1:D:161:LEU:HD11	1:D:168:TYR:CE2	2.53	0.44
1:A:446:LYS:CE	4:A:1048:HOH:O	2.65	0.44
1:A:44:GLU:CA	1:A:47:GLU:HG2	2.46	0.44
1:A:449:PHE:HB3	1:A:457:LYS:HG3	2.00	0.44
1:C:255:ILE:HB	1:C:264:LYS:HB2	2.00	0.44
1:D:604:THR:O	1:D:607:TYR:O	2.36	0.43
1:C:665:LEU:HD22	1:C:687:ALA:HB2	1.99	0.43
1:D:591:MET:HE1	1:D:607:TYR:CD2	2.54	0.43
1:D:372:ARG:HG2	1:D:379:LEU:HA	2.00	0.43
1:A:655:ARG:HD2	1:A:695:HIS:CD2	2.54	0.43
1:B:665:LEU:HD22	1:B:687:ALA:HB2	2.01	0.43
1:D:655:ARG:HD2	1:D:695:HIS:CD2	2.54	0.43
1:B:591:MET:HE1	1:B:607:TYR:CD2	2.54	0.43
1:B:62:GLU:HG3	1:B:716:LYS:NZ	2.33	0.43
1:D:554:ARG:NH1	1:D:554:ARG:HB3	2.34	0.43
1:A:166:ARG:CD	4:A:922:HOH:O	2.66	0.42
1:B:117:GLU:HB3	1:B:166:ARG:NH2	2.31	0.42
1:A:673:CYS:CB	4:A:929:HOH:O	2.53	0.42
1:B:115:LYS:HD3	4:B:986:HOH:O	2.18	0.42
1:C:696:TYR:CD1	1:C:696:TYR:C	2.97	0.42
1:D:614:GLU:HG2	1:D:615:GLU:HG3	2.01	0.42
1:B:141:ALA:HB1	4:B:1109:HOH:O	2.18	0.42
1:B:481:TYR:CZ	3:B:801:CAC:C2	3.01	0.42
1:C:47:GLU:HB2	4:C:1075:HOH:O	2.19	0.42
1:C:87:ARG:HE	1:C:90:ASN:HA	1.84	0.42
1:D:453:LYS:HG3	4:D:1037:HOH:O	2.19	0.42
1:D:698:ARG:CB	4:D:1062:HOH:O	2.67	0.42
1:A:341:SER:HB2	4:A:907:HOH:O	2.19	0.42
1:C:281:ARG:O	4:C:906:HOH:O	2.21	0.42
1:C:639:GLU:OE1	4:C:905:HOH:O	2.21	0.42
1:D:72:LYS:HD2	4:D:1301:HOH:O	2.20	0.42
1:A:37:LEU:CD1	4:A:1227:HOH:O	2.66	0.42
1:D:448:VAL:HG22	1:D:449:PHE:N	2.34	0.42
1:D:166:ARG:CG	4:D:1353:HOH:O	2.67	0.42
4:A:1160:HOH:O	1:D:307:GLY:HA2	2.19	0.41
1:B:372:ARG:HG2	1:B:379:LEU:HA	2.01	0.41
1:C:613:GLU:CD	4:C:907:HOH:O	2.62	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:546:ILE:HD12	1:C:552:LYS:CA	2.50	0.41
1:D:684:PRO:C	1:D:685:ILE:HG12	2.44	0.41
1:A:44:GLU:O	1:A:47:GLU:HG2	2.19	0.41
1:A:634:GLN:HA	1:A:635:PRO:HD3	1.97	0.41
1:B:161:LEU:CD2	1:B:166:ARG:O	2.68	0.41
1:D:589:MET:CE	1:D:589:MET:N	2.82	0.41
1:A:396:ARG:NE	4:A:915:HOH:O	2.34	0.41
1:B:710:ARG:NE	4:B:902:HOH:O	1.99	0.41
2:E:1027:ASN:N	4:E:1101:HOH:O	2.53	0.41
1:C:613:GLU:OE2	4:C:907:HOH:O	2.22	0.41
1:C:655:ARG:HD2	1:C:695:HIS:CD2	2.55	0.41
1:A:546:ILE:HD12	1:A:552:LYS:CA	2.50	0.41
1:B:175:TRP:CD1	1:B:197:PRO:HA	2.56	0.41
1:A:599:LEU:CD2	1:A:599:LEU:N	2.84	0.41
1:A:719:GLU:CD	4:A:904:HOH:O	2.62	0.41
1:C:129:ARG:NH2	1:C:151:GLY:O	2.54	0.41
1:C:542:ALA:O	1:C:546:ILE:HG12	2.21	0.41
1:A:44:GLU:O	1:A:47:GLU:CG	2.69	0.41
1:A:383:LEU:HA	4:A:1203:HOH:O	2.21	0.41
1:B:657:VAL:HG23	1:B:659:LEU:HG	2.03	0.41
1:B:697:GLY:HA3	4:B:1111:HOH:O	2.21	0.41
1:B:599:LEU:HA	1:B:601:TYR:CE2	2.56	0.41
1:D:161:LEU:CG	4:D:1334:HOH:O	2.65	0.41
1:A:150:SER:N	4:A:923:HOH:O	2.39	0.40
1:A:542:ALA:O	1:A:546:ILE:HG12	2.21	0.40
1:C:699:ALA:O	1:C:700:THR:C	2.63	0.40
1:C:553:ALA:HB3	4:C:950:HOH:O	2.19	0.40
1:D:161:LEU:CD1	1:D:168:TYR:CE2	3.04	0.40
1:C:134:LEU:HD23	4:C:1359:HOH:O	2.21	0.40
1:A:58:SER:HA	1:A:61:GLU:OE1	2.21	0.40
1:A:241:LYS:HG3	1:A:242:CYS:N	2.36	0.40
1:D:255:ILE:HB	1:D:264:LYS:HB2	2.03	0.40
1:A:72:LYS:HD2	4:A:974:HOH:O	2.21	0.40
1:D:588:VAL:C	1:D:589:MET:HE3	2.37	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:554:ARG:NH2	1:D:638:GLU:OE1[1_456]	2.12	0.08

5.3 Torsion angles

5.3.1 Protein backbone

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	687/750 (92%)	666 (97%)	20 (3%)	1 (0%)	48	41
1	B	701/750 (94%)	676 (96%)	23 (3%)	2 (0%)	36	28
1	C	696/750 (93%)	673 (97%)	21 (3%)	2 (0%)	36	28
1	D	692/750 (92%)	671 (97%)	20 (3%)	1 (0%)	48	41
2	E	4/19 (21%)	4 (100%)	0	0	100	100
2	F	4/19 (21%)	4 (100%)	0	0	100	100
2	G	4/19 (21%)	4 (100%)	0	0	100	100
2	H	4/19 (21%)	4 (100%)	0	0	100	100
All	All	2792/3076 (91%)	2702 (97%)	84 (3%)	6 (0%)	43	36

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	598	THR
1	C	279	SER
1	C	598	THR
1	A	598	THR
1	D	598	THR
1	B	697	GLY

5.3.2 Protein sidechains

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	603/652 (92%)	586 (97%)	17 (3%)	38	30
1	B	614/652 (94%)	596 (97%)	18 (3%)	37	29
1	C	611/652 (94%)	598 (98%)	13 (2%)	47	41
1	D	607/652 (93%)	598 (98%)	9 (2%)	57	54
2	E	4/14 (29%)	4 (100%)	0	100	100
2	F	4/14 (29%)	4 (100%)	0	100	100
2	G	4/14 (29%)	4 (100%)	0	100	100
2	H	4/14 (29%)	4 (100%)	0	100	100
All	All	2451/2664 (92%)	2394 (98%)	57 (2%)	44	38

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	54	LYS
1	A	61	GLU
1	A	133	SER
1	A	150	SER
1	A	171	ASP
1	A	342	LYS
1	A	365	VAL
1	A	383	LEU
1	A	398	ARG
1	A	421	LYS
1	A	425	THR
1	A	426	GLN
1	A	457	LYS
1	A	527	PHE
1	A	602	LEU
1	A	606	ASP
1	A	639	GLU
1	B	1	MET
1	B	77	VAL
1	B	119	LEU
1	B	150	SER
1	B	171	ASP
1	B	231	ARG
1	B	241	LYS
1	B	358	ILE
1	B	365	VAL
1	B	383	LEU

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Mol	Chain	Res	Type
1	B	417	GLN
1	B	434	VAL
1	B	446	LYS
1	B	527	PHE
1	B	599	LEU
1	B	606	ASP
1	B	692	LYS
1	B	698	ARG
1	C	62	GLU
1	C	171	ASP
1	C	231	ARG
1	C	234	GLU
1	C	365	VAL
1	C	383	LEU
1	C	417	GLN
1	C	425	THR
1	C	446	LYS
1	C	527	PHE
1	C	554	ARG
1	C	555	ARG
1	C	606	ASP
1	D	133	SER
1	D	161	LEU
1	D	171	ASP
1	D	290	MET
1	D	365	VAL
1	D	527	PHE
1	D	554	ARG
1	D	606	ASP
1	D	685	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	107	GLN
1	A	109	GLN
1	A	149	HIS
1	A	185	HIS
1	A	211	ASN
1	A	353	ASN
1	A	356	GLN
1	A	532	GLN

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Mol	Chain	Res	Type
1	A	574	GLN
1	A	595	HIS
1	A	670	HIS
1	B	94	HIS
1	B	275	ASN
1	B	417	GLN
1	C	107	GLN
1	C	149	HIS
1	C	670	HIS
1	D	107	GLN
1	D	185	HIS
1	D	353	ASN
1	D	356	GLN
1	D	381	HIS
1	D	417	GLN
1	D	479	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 ligands are modelled in this entry.

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
3	CAC	A	801	-	2,4,4	2.96	1 (50%)	4,6,6	1.93	2 (50%)
3	CAC	B	801	-	2,4,4	1.35	0	4,6,6	3.07	2 (50%)
3	CAC	D	801	-	2,4,4	2.37	2 (100%)	4,6,6	2.08	1 (25%)
3	CAC	C	801	-	2,4,4	2.29	1 (50%)	4,6,6	2.10	2 (50%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	801	CAC	AS-C2	3.81	1.99	1.90
3	C	801	CAC	AS-C2	3.19	1.97	1.90
3	D	801	CAC	AS-C1	2.52	1.96	1.90
3	D	801	CAC	AS-C2	2.22	1.95	1.90

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	801	CAC	O1-AS-C2	-4.89	105.42	111.50
3	B	801	CAC	O2-AS-C1	3.32	113.87	105.84
3	C	801	CAC	O1-AS-C1	3.18	115.46	111.50
3	D	801	CAC	O1-AS-C1	-3.05	107.71	111.50
3	A	801	CAC	O2-AS-C1	2.48	111.84	105.84
3	A	801	CAC	O1-AS-C1	-2.36	108.56	111.50
3	C	801	CAC	O2-AS-C2	2.17	111.11	105.84

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	801	CAC	3	0
3	D	801	CAC	1	0
3	C	801	CAC	4	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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	693/750 (92%)	0.58	64 (9%)	14	16	8, 20, 41, 58	0
1	B	707/750 (94%)	0.22	36 (5%)	33	39	8, 17, 39, 59	0
1	C	702/750 (93%)	0.12	16 (2%)	61	68	6, 15, 34, 63	0
1	D	698/750 (93%)	0.13	20 (2%)	53	60	7, 16, 34, 74	0
2	E	6/19 (31%)	-0.14	0	100	100	13, 14, 16, 18	0
2	F	6/19 (31%)	-0.32	0	100	100	12, 14, 17, 19	0
2	G	6/19 (31%)	0.28	0	100	100	15, 16, 20, 20	0
2	H	6/19 (31%)	-0.17	0	100	100	13, 14, 18, 19	0
All	All	2824/3076 (91%)	0.26	136 (4%)	35	41	6, 17, 37, 74	0

All (136) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	602	LEU	4.4
1	A	425	THR	4.3
1	B	599	LEU	3.9
1	B	274	PRO	3.8
1	B	153	THR	3.8
1	D	3	THR	3.7
1	C	112	LEU	3.6
1	A	26	PHE	3.5
1	D	697	GLY	3.5
1	B	652	HIS	3.4
1	B	440	ARG	3.4
1	D	425	THR	3.4
1	A	424	PRO	3.3
1	B	148	ILE	3.3
1	B	1	MET	3.3
1	A	676	LEU	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	12	TYR	3.2
1	A	597	PHE	3.2
1	C	8	LYS	3.2
1	C	210	VAL	3.2
1	B	696	TYR	3.2
1	B	178	PHE	3.2
1	D	274	PRO	3.1
1	A	631	PRO	3.1
1	A	599	LEU	3.1
1	D	423	ASP	3.1
1	D	424	PRO	3.0
1	A	625	ILE	3.0
1	A	48	PHE	3.0
1	A	27	GLY	3.0
1	A	682	LYS	2.9
1	C	9	PRO	2.9
1	B	155	TRP	2.9
1	C	677	GLU	2.9
1	B	427	LEU	2.9
1	A	612	LYS	2.9
1	C	10	LEU	2.9
1	A	609	CYS	2.9
1	B	275	ASN	2.8
1	A	384	PRO	2.8
1	A	427	LEU	2.8
1	D	652	HIS	2.8
1	A	632	TRP	2.8
1	A	49	VAL	2.7
1	A	22	VAL	2.7
1	A	662	PHE	2.7
1	A	383	LEU	2.7
1	A	680	PRO	2.7
1	B	10	LEU	2.7
1	A	56	ALA	2.6
1	A	241	LYS	2.6
1	B	676	LEU	2.6
1	B	11	HIS	2.6
1	A	687	ALA	2.6
1	A	274	PRO	2.6
1	B	9	PRO	2.6
1	A	678	ASP	2.6
1	A	639	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	678	ASP	2.6
1	A	21	VAL	2.6
1	B	156	VAL	2.6
1	B	650	ALA	2.5
1	A	28	VAL	2.5
1	D	554	ARG	2.5
1	A	197	PRO	2.5
1	A	55	LEU	2.5
1	D	275	ASN	2.5
1	C	652	HIS	2.5
1	B	425	THR	2.5
1	C	113	ASP	2.5
1	B	273	LEU	2.4
1	B	677	GLU	2.4
1	A	596	LYS	2.4
1	D	427	LEU	2.4
1	D	696	TYR	2.4
1	A	640	THR	2.4
1	A	635	PRO	2.4
1	A	618	TRP	2.4
1	A	605	GLY	2.4
1	A	626	HIS	2.4
1	C	5	GLY	2.4
1	D	418	CYS	2.4
1	B	553	ALA	2.4
1	A	681	GLN	2.4
1	B	197	PRO	2.4
1	D	421	LYS	2.4
1	A	611	ASP	2.3
1	C	676	LEU	2.3
1	A	604	THR	2.3
1	A	614	GLU	2.3
1	B	209	ALA	2.3
1	D	608	GLY	2.3
1	D	166	ARG	2.3
1	A	382	ARG	2.3
1	A	619	LEU	2.3
1	B	598	THR	2.3
1	C	134	LEU	2.3
1	B	697	GLY	2.2
1	C	696	TYR	2.2
1	D	260	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	35	ARG	2.2
1	B	382	ARG	2.2
1	A	36	TRP	2.2
1	C	383	LEU	2.2
1	A	150	SER	2.2
1	B	384	PRO	2.2
1	A	280	PHE	2.2
1	A	685	ILE	2.2
1	D	422	ASN	2.2
1	C	608	GLY	2.2
1	A	31	ALA	2.2
1	B	21	VAL	2.1
1	C	425	THR	2.1
1	D	257	ASP	2.1
1	A	593	ARG	2.1
1	A	617	LYS	2.1
1	B	698	ARG	2.1
1	A	666	ALA	2.1
1	A	671	VAL	2.1
1	D	9	PRO	2.1
1	A	25	TYR	2.1
1	A	677	GLU	2.1
1	A	634	GLN	2.1
1	A	673	CYS	2.1
1	D	178	PHE	2.0
1	B	279	SER	2.0
1	B	422	ASN	2.0
1	A	592	LEU	2.0
1	B	152	LEU	2.0
1	A	569	ALA	2.0
1	B	150	SER	2.0
1	B	26	PHE	2.0
1	C	280	PHE	2.0
1	A	426	GLN	2.0
1	A	674	THR	2.0
1	A	34	TYR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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($\text{\AA}^2$)	Q<0.9
3	CAC	A	801	5/5	0.98	0.08	24,25,28,28	0
3	CAC	B	801	5/5	0.98	0.10	17,21,25,25	0
3	CAC	C	801	5/5	0.99	0.07	14,17,18,20	0
3	CAC	D	801	5/5	1.00	0.05	15,16,17,17	0

6.5 Other polymers [i](#)

There are no such residues in this entry.