



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 12:59 PM UTC

PDB ID : 7CS9 / pdb_00007cs9
Title : AtPrR1 in apo form
Authors : Shao, K.; Zhang, P.
Deposited on : 2020-08-14
Resolution : 2.80 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
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

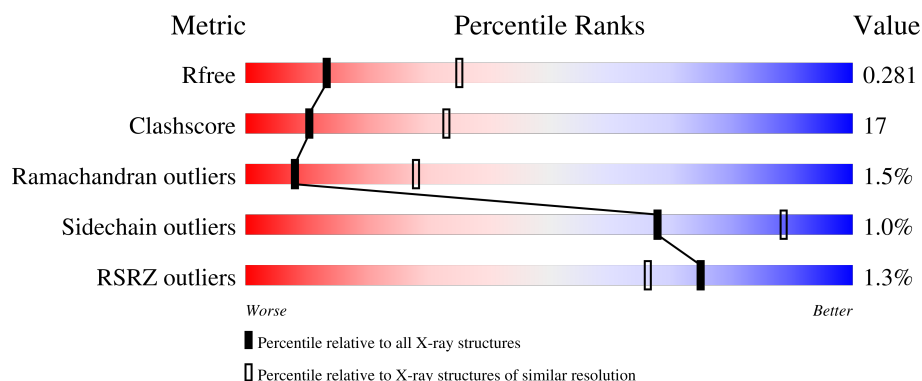
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (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 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	317	0% 70% 25% .
1	B	317	2% 74% 20% ..
1	C	317	3% 55% 39% ..
1	D	317	67% 27% ..

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 9564 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.

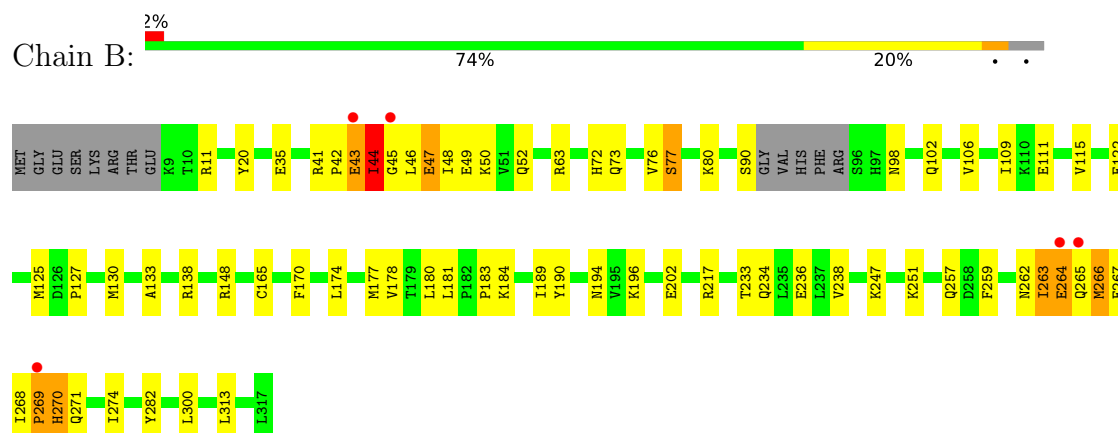
- Molecule 1 is a protein called Pinorexinol reductase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	304	Total	C	N	O	S	0	0	0
			2390	1528	404	447	11			
1	C	304	Total	C	N	O	S	0	0	0
			2395	1533	404	447	11			
1	A	303	Total	C	N	O	S	0	0	0
			2384	1525	403	445	11			
1	D	304	Total	C	N	O	S	0	0	0
			2395	1533	404	447	11			

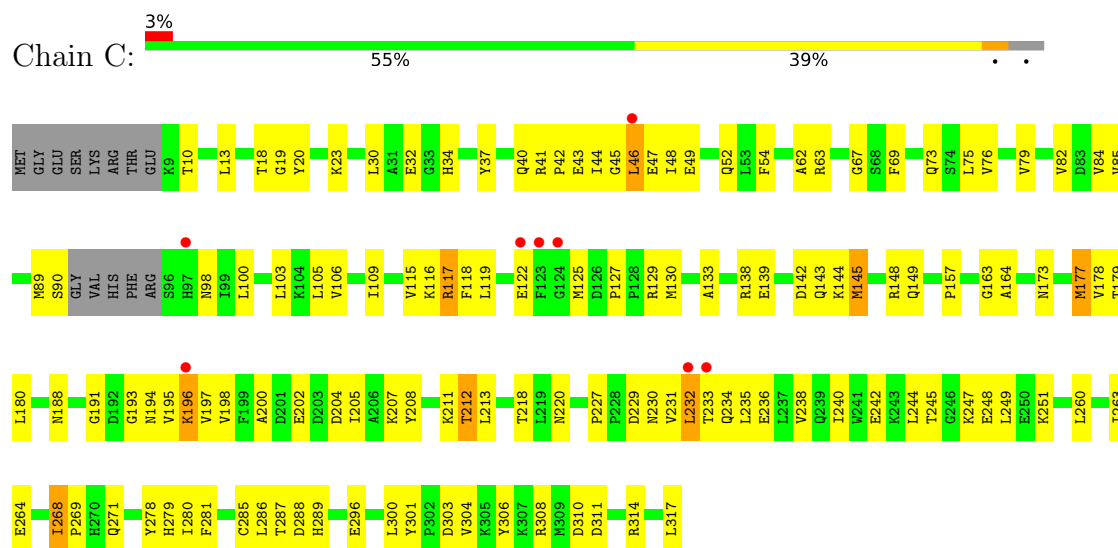
3 Residue-property plots [i](#)

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.

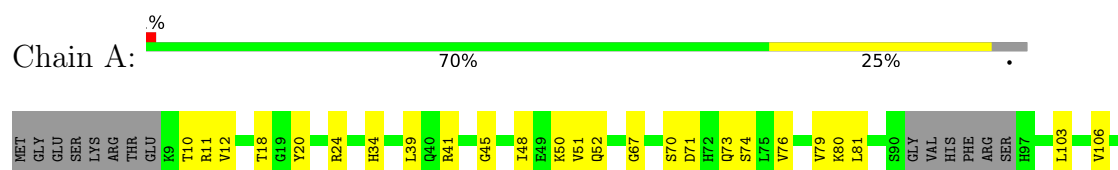
• Molecule 1: Pinorensinol reductase 1

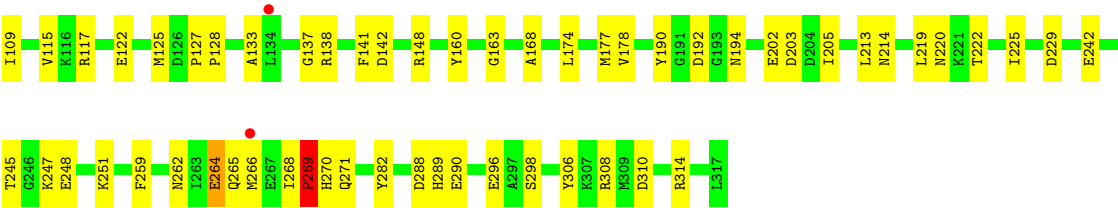


• Molecule 1: Pinorensinol reductase 1

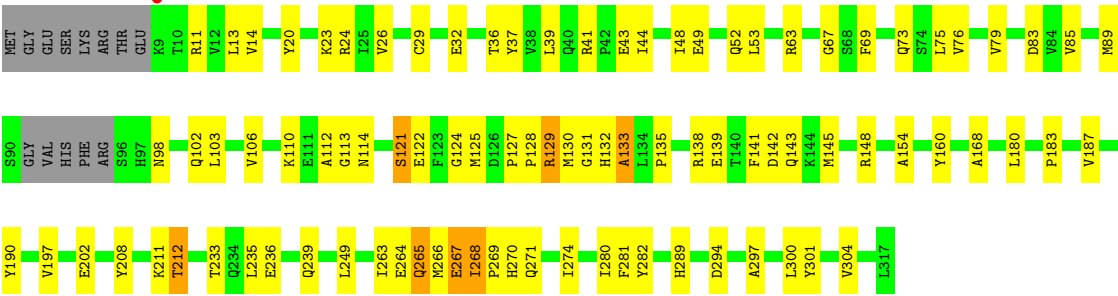


• Molecule 1: Pinorensinol reductase 1





● Molecule 1: Pinorensinol reductase 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	81.73Å 134.92Å 142.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.27 – 2.80 39.27 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (39.27-2.80) 91.8 (39.27-2.80)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.80 (at 2.81Å)	Xtriage
Refinement program	PHENIX 1.10_2155, PHENIX 1.10_2155	Depositor
R, R_{free}	0.221 , 0.280 0.223 , 0.281	Depositor DCC
R_{free} test set	2003 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	54.5	Xtriage
Anisotropy	0.623	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 34.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.022 for -h,l,k	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	9564	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.33% 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

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	1/2431 (0.0%)	0.73	1/3288 (0.0%)
1	B	0.52	1/2437 (0.0%)	0.78	5/3296 (0.2%)
1	C	0.60	4/2442 (0.2%)	0.82	2/3303 (0.1%)
1	D	0.44	0/2442	0.70	4/3303 (0.1%)
All	All	0.54	6/9752 (0.1%)	0.76	12/13190 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	5
1	D	0	1
All	All	0	8

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	269	PRO	N-CD	-17.04	1.23	1.47
1	C	117	ARG	NE-CZ	-8.87	1.23	1.33
1	C	196	LYS	CB-CG	6.24	1.71	1.52
1	C	117	ARG	CZ-NH1	-6.21	1.24	1.32
1	B	44	ILE	CA-CB	-5.24	1.47	1.54
1	C	117	ARG	CZ-NH2	-5.03	1.26	1.33

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	163	GLY	N-CA-C	8.88	123.08	113.58
1	B	270	HIS	N-CA-C	-8.17	103.31	113.28
1	B	45	GLY	N-CA-C	-7.41	95.62	113.18

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	196	LYS	CB-CG-CD	6.55	126.37	111.30
1	D	133	ALA	CA-C-N	-6.11	112.13	123.55
1	D	133	ALA	C-N-CA	-6.11	112.13	123.55
1	C	232	LEU	CB-CG-CD1	-6.00	92.70	110.70
1	B	122	GLU	CA-C-N	-5.61	110.94	121.81
1	B	122	GLU	C-N-CA	-5.61	110.94	121.81
1	D	129	ARG	NE-CZ-NH1	-5.49	116.01	121.50
1	D	135	PRO	O-C-N	5.24	123.72	121.31
1	B	77	SER	N-CA-C	5.18	116.74	111.14

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	264	GLU	Peptide
1	A	269	PRO	Peptide
1	B	263	ILE	Peptide
1	B	264	GLU	Peptide
1	B	269	PRO	Peptide
1	B	43	GLU	Peptide
1	B	44	ILE	Peptide
1	D	265	GLN	Peptide

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	2384	0	2390	68	0
1	B	2390	0	2395	48	0
1	C	2395	0	2409	140	0
1	D	2395	0	2411	78	0
All	All	9564	0	9605	324	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 17.

All (324) 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:C:196:LYS:HZ3	1:C:233:THR:HG22	1.07	1.11
1:C:84:VAL:HG11	1:C:213:LEU:HD21	1.47	0.97
1:D:130:MET:O	1:D:138:ARG:NH2	2.02	0.93
1:D:208:TYR:HE2	1:D:304:VAL:HG11	1.32	0.93
1:C:242:GLU:HA	1:C:245:THR:HG22	1.51	0.92
1:B:184:LYS:O	1:B:247:LYS:NZ	2.03	0.91
1:C:196:LYS:NZ	1:C:233:THR:HG22	1.85	0.90
1:A:242:GLU:OE2	1:A:251:LYS:NZ	2.04	0.89
1:C:196:LYS:HZ1	1:C:236:GLU:HG2	1.36	0.89
1:B:35:GLU:OE1	1:B:63:ARG:NH2	2.06	0.88
1:D:127:PRO:HB2	1:D:145:MET:HE3	1.56	0.86
1:D:208:TYR:CE2	1:D:304:VAL:HG11	2.11	0.86
1:C:145:MET:HG3	1:C:148:ARG:HD3	1.56	0.85
1:D:110:LYS:HG3	1:D:154:ALA:HB1	1.58	0.84
1:B:77:SER:HA	1:B:80:LYS:HD2	1.59	0.84
1:C:32:GLU:HG2	1:C:34:HIS:HE1	1.42	0.84
1:A:34:HIS:CE1	1:A:213:LEU:HD21	2.13	0.83
1:C:69:PHE:HA	1:C:75:LEU:HD11	1.62	0.82
1:B:73:GLN:NE2	1:B:111:GLU:OE2	2.12	0.82
1:A:117:ARG:HH21	1:A:219:LEU:HB2	1.45	0.82
1:C:127:PRO:HB2	1:C:145:MET:HE2	1.62	0.80
1:C:163:GLY:O	1:C:198:VAL:HG21	1.81	0.79
1:C:229:ASP:HB2	1:C:308:ARG:HD2	1.64	0.78
1:C:204:ASP:OD2	1:C:207:LYS:NZ	2.17	0.78
1:D:133:ALA:O	1:D:138:ARG:NH1	2.17	0.78
1:C:196:LYS:HD2	1:C:233:THR:CB	2.14	0.78
1:C:48:ILE:HD12	1:C:49:GLU:H	1.49	0.77
1:C:245:THR:HG23	1:C:247:LYS:H	1.48	0.76
1:C:117:ARG:NH2	1:C:213:LEU:O	2.20	0.75
1:C:268:ILE:HA	1:C:271:GLN:HG3	1.67	0.75
1:A:229:ASP:OD2	1:A:308:ARG:NH1	2.20	0.75
1:C:263:ILE:O	1:C:271:GLN:NE2	2.20	0.74
1:C:48:ILE:HD12	1:C:49:GLU:N	2.02	0.74
1:C:48:ILE:CD1	1:C:49:GLU:HG2	2.17	0.73
1:A:109:ILE:HG23	1:A:115:VAL:HG21	1.70	0.73
1:A:18:THR:HG21	1:A:50:LYS:HD3	1.71	0.73
1:A:52:GLN:HE22	1:D:24:ARG:HH22	1.35	0.72
1:A:73:GLN:HA	1:A:76:VAL:HG22	1.72	0.71
1:A:268:ILE:O	1:A:270:HIS:N	2.23	0.71
1:C:233:THR:HG23	1:C:235:LEU:H	1.55	0.70
1:C:227:PRO:HB2	1:C:230:ASN:HB2	1.73	0.70
1:B:194:ASN:O	1:B:194:ASN:ND2	2.24	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:129:ARG:HH12	1:C:289:HIS:CG	2.11	0.69
1:C:249:LEU:O	1:C:251:LYS:NZ	2.26	0.69
1:C:138:ARG:NH2	1:C:142:ASP:OD1	2.26	0.68
1:D:129:ARG:HH12	1:D:289:HIS:CG	2.11	0.68
1:A:245:THR:HG21	1:A:247:LYS:HE2	1.74	0.68
1:C:79:VAL:HG22	1:C:85:VAL:HG11	1.76	0.67
1:C:90:SER:O	1:C:98:ASN:ND2	2.28	0.67
1:C:196:LYS:HD2	1:C:233:THR:N	2.09	0.67
1:C:264:GLU:HA	1:C:271:GLN:HE22	1.60	0.67
1:A:117:ARG:NH1	1:A:213:LEU:O	2.28	0.66
1:D:11:ARG:NH2	1:D:83:ASP:OD2	2.28	0.66
1:D:139:GLU:O	1:D:143:GLN:HG3	1.94	0.66
1:B:268:ILE:O	1:B:270:HIS:N	2.20	0.66
1:C:196:LYS:HD2	1:C:233:THR:HB	1.76	0.66
1:B:52:GLN:NE2	1:C:20:TYR:OH	2.29	0.65
1:D:29:CYS:HB3	1:D:36:THR:HG21	1.76	0.65
1:A:177:MET:HE1	1:A:259:PHE:CZ	2.32	0.65
1:C:196:LYS:HD2	1:C:233:THR:H	1.62	0.65
1:C:196:LYS:HZ1	1:C:236:GLU:CG	2.09	0.65
1:D:20:TYR:HE2	1:D:202:GLU:HG2	1.62	0.64
1:C:32:GLU:HG2	1:C:34:HIS:CE1	2.30	0.64
1:D:20:TYR:CE2	1:D:202:GLU:HG2	2.33	0.64
1:B:44:ILE:HA	1:B:47:GLU:H	1.62	0.64
1:C:196:LYS:HD2	1:C:233:THR:HG22	1.79	0.63
1:A:265:GLN:HE21	1:A:271:GLN:HE22	1.46	0.63
1:A:103:LEU:O	1:A:106:VAL:HG12	1.99	0.63
1:C:69:PHE:HZ	1:C:89:MET:HE1	1.64	0.62
1:A:122:GLU:OE1	1:A:148:ARG:NH2	2.23	0.62
1:C:139:GLU:O	1:C:143:GLN:HG3	1.99	0.62
1:C:232:LEU:HD11	1:C:236:GLU:HB2	1.82	0.61
1:C:311:ASP:OD1	1:C:314:ARG:NH2	2.33	0.61
1:C:84:VAL:HG11	1:C:213:LEU:CD2	2.27	0.61
1:C:196:LYS:HD2	1:C:233:THR:CG2	2.30	0.61
1:C:200:ALA:HB3	1:C:205:ILE:HD11	1.81	0.61
1:A:20:TYR:CE2	1:A:202:GLU:HG2	2.36	0.61
1:C:85:VAL:HG23	1:C:118:PHE:CD1	2.36	0.60
1:A:20:TYR:HE2	1:A:202:GLU:HG2	1.66	0.60
1:B:234:GLN:O	1:B:238:VAL:HG23	2.01	0.60
1:A:34:HIS:HE1	1:A:213:LEU:HD21	1.64	0.60
1:C:164:ALA:HA	1:C:198:VAL:CG2	2.30	0.60
1:C:244:LEU:HD11	1:C:310:ASP:OD2	2.01	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:41:ARG:HG3	1:C:42:PRO:HD2	1.81	0.60
1:C:40:GLN:HG3	1:C:44:ILE:CD1	2.31	0.60
1:C:164:ALA:HA	1:C:198:VAL:HG23	1.84	0.60
1:C:188:ASN:O	1:C:234:GLN:NE2	2.34	0.60
1:D:102:GLN:O	1:D:106:VAL:HG13	2.02	0.59
1:D:129:ARG:NH1	1:D:289:HIS:CG	2.71	0.59
1:A:177:MET:HE1	1:A:259:PHE:HZ	1.67	0.59
1:A:168:ALA:HB1	1:D:48:ILE:HD11	1.85	0.58
1:A:11:ARG:NH2	1:A:81:LEU:O	2.32	0.58
1:D:14:VAL:HG11	1:D:26:VAL:HG23	1.83	0.58
1:B:189:ILE:HD11	1:B:251:LYS:HB3	1.86	0.58
1:A:268:ILE:HG22	1:A:269:PRO:HD2	1.85	0.58
1:C:103:LEU:O	1:C:106:VAL:HG22	2.05	0.57
1:A:52:GLN:NE2	1:D:24:ARG:HH22	2.02	0.57
1:B:133:ALA:HB3	1:B:138:ARG:HG3	1.86	0.57
1:C:37:TYR:CZ	1:C:63:ARG:HD3	2.40	0.57
1:C:260:LEU:HD11	1:C:278:TYR:CE1	2.39	0.57
1:C:13:LEU:HB3	1:C:85:VAL:HG12	1.86	0.56
1:C:40:GLN:HG3	1:C:44:ILE:HD11	1.86	0.56
1:A:268:ILE:C	1:A:270:HIS:H	2.13	0.56
1:C:13:LEU:N	1:C:82:VAL:HG21	2.20	0.56
1:C:303:ASP:OD1	1:C:303:ASP:N	2.38	0.56
1:C:13:LEU:H	1:C:82:VAL:HG21	1.70	0.56
1:C:84:VAL:CG1	1:C:213:LEU:HD21	2.30	0.56
1:B:233:THR:OG1	1:B:236:GLU:HG3	2.05	0.56
1:C:208:TYR:OH	1:C:304:VAL:HG21	2.06	0.56
1:D:235:LEU:O	1:D:239:GLN:HG3	2.05	0.56
1:B:165:CYS:HB3	1:B:170:PHE:CD1	2.40	0.56
1:C:37:TYR:CE2	1:C:63:ARG:HD3	2.41	0.55
1:C:105:LEU:O	1:C:109:ILE:HG13	2.06	0.55
1:C:196:LYS:CD	1:C:233:THR:H	2.18	0.55
1:A:205:ILE:HG23	1:A:225:ILE:CD1	2.35	0.55
1:C:195:VAL:O	1:C:233:THR:OG1	2.17	0.55
1:C:194:ASN:HA	1:C:233:THR:HG21	1.88	0.55
1:B:41:ARG:O	1:B:43:GLU:HG3	2.05	0.55
1:C:100:LEU:HD21	1:C:143:GLN:HB3	1.89	0.55
1:D:138:ARG:HG2	1:D:142:ASP:OD2	2.07	0.55
1:D:263:ILE:HA	1:D:266:MET:HG3	1.89	0.54
1:B:262:ASN:O	1:B:266:MET:HB2	2.07	0.54
1:C:45:GLY:C	1:C:46:LEU:HD12	2.32	0.54
1:C:85:VAL:HG23	1:C:118:PHE:HD1	1.72	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:242:GLU:OE2	1:C:248:GLU:HA	2.07	0.54
1:D:41:ARG:HH21	1:D:43:GLU:CD	2.15	0.54
1:C:44:ILE:C	1:C:46:LEU:H	2.15	0.54
1:C:300:LEU:HB2	1:C:301:TYR:CE2	2.43	0.54
1:C:127:PRO:HD2	1:C:148:ARG:NH1	2.22	0.54
1:C:19:GLY:O	1:C:23:LYS:HG3	2.07	0.54
1:B:20:TYR:HE2	1:B:202:GLU:HG2	1.72	0.54
1:D:103:LEU:O	1:D:106:VAL:HG22	2.08	0.54
1:A:262:ASN:HA	1:A:264:GLU:OE1	2.08	0.53
1:C:127:PRO:HD2	1:C:148:ARG:HH12	1.73	0.53
1:D:73:GLN:HA	1:D:76:VAL:HG22	1.90	0.53
1:A:219:LEU:HD23	1:A:220:ASN:OD1	2.08	0.53
1:A:290:GLU:OE1	1:A:290:GLU:N	2.41	0.53
1:C:48:ILE:HD13	1:C:49:GLU:HG2	1.88	0.53
1:A:265:GLN:NE2	1:A:271:GLN:OE1	2.42	0.53
1:A:117:ARG:NH1	1:A:213:LEU:C	2.67	0.53
1:A:270:HIS:HD2	1:A:270:HIS:O	1.91	0.53
1:C:227:PRO:HB3	1:C:306:TYR:CE2	2.44	0.53
1:B:41:ARG:O	1:B:43:GLU:N	2.43	0.52
1:C:196:LYS:HG3	1:C:232:LEU:HA	1.90	0.52
1:C:306:TYR:CE1	1:C:308:ARG:NH2	2.67	0.52
1:A:202:GLU:CD	1:A:202:GLU:H	2.18	0.52
1:A:242:GLU:HG2	1:A:248:GLU:HA	1.91	0.52
1:C:208:TYR:CE1	1:C:304:VAL:HG21	2.44	0.52
1:A:160:TYR:HB2	1:A:222:THR:HG23	1.91	0.52
1:D:110:LYS:HE2	1:D:154:ALA:HA	1.91	0.52
1:A:192:ASP:HB2	1:A:194:ASN:ND2	2.25	0.52
1:C:129:ARG:HH22	1:C:289:HIS:CG	2.28	0.51
1:A:39:LEU:HD11	1:A:67:GLY:HA3	1.91	0.51
1:B:102:GLN:O	1:B:106:VAL:HG23	2.09	0.51
1:C:173:ASN:HB3	1:C:180:LEU:HA	1.92	0.51
1:D:48:ILE:O	1:D:52:GLN:HG3	2.11	0.51
1:C:145:MET:O	1:C:149:GLN:HG3	2.09	0.51
1:B:265:GLN:NE2	1:B:271:GLN:HE22	2.09	0.51
1:D:270:HIS:CD2	1:D:274:ILE:HG13	2.45	0.51
1:C:196:LYS:CD	1:C:233:THR:N	2.74	0.51
1:D:127:PRO:HD2	1:D:148:ARG:NH2	2.26	0.51
1:B:271:GLN:O	1:B:274:ILE:HG22	2.11	0.51
1:B:127:PRO:HD2	1:B:148:ARG:NH2	2.26	0.51
1:C:212:THR:HG23	1:C:218:THR:OG1	2.11	0.50
1:C:125:MET:SD	1:C:280:ILE:HD11	2.51	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:128:PRO:HG3	1:D:145:MET:HE1	1.93	0.50
1:D:29:CYS:HB3	1:D:36:THR:CG2	2.41	0.50
1:D:212:THR:HA	1:D:301:TYR:OH	2.12	0.50
1:A:268:ILE:CG2	1:A:269:PRO:HD2	2.41	0.50
1:D:32:GLU:OE1	1:D:211:LYS:HE3	2.11	0.50
1:B:44:ILE:C	1:B:46:LEU:H	2.19	0.50
1:C:177:MET:O	1:C:179:THR:N	2.45	0.49
1:D:69:PHE:HA	1:D:75:LEU:HD11	1.94	0.49
1:C:208:TYR:CZ	1:C:304:VAL:HG21	2.47	0.49
1:D:148:ARG:HD3	1:D:160:TYR:CE1	2.47	0.49
1:B:267:GLU:HB3	1:D:266:MET:HE2	1.93	0.49
1:D:183:PRO:HG3	1:D:187:VAL:HG22	1.95	0.49
1:C:82:VAL:HG22	1:C:84:VAL:H	1.77	0.49
1:C:129:ARG:HH22	1:C:289:HIS:CB	2.26	0.49
1:C:157:PRO:HA	1:C:220:ASN:HD21	1.77	0.49
1:C:196:LYS:HG3	1:C:232:LEU:C	2.38	0.49
1:A:265:GLN:HE21	1:A:271:GLN:NE2	2.08	0.49
1:D:122:GLU:O	1:D:124:GLY:N	2.46	0.49
1:C:314:ARG:O	1:C:317:LEU:HD12	2.13	0.48
1:C:287:THR:C	1:C:289:HIS:H	2.20	0.48
1:A:190:TYR:HB3	1:A:282:TYR:CZ	2.48	0.48
1:B:76:VAL:HG12	1:B:80:LYS:HZ2	1.78	0.48
1:B:20:TYR:CE2	1:B:202:GLU:HG2	2.48	0.48
1:B:44:ILE:CB	1:B:47:GLU:H	2.26	0.48
1:B:44:ILE:C	1:B:46:LEU:N	2.71	0.48
1:B:47:GLU:OE2	1:B:50:LYS:NZ	2.46	0.48
1:C:144:LYS:O	1:C:148:ARG:HG3	2.13	0.48
1:D:131:GLY:C	1:D:138:ARG:HH22	2.20	0.48
1:C:79:VAL:HG11	1:C:109:ILE:HA	1.96	0.47
1:C:133:ALA:HB2	1:C:279:HIS:CE1	2.50	0.47
1:C:118:PHE:C	1:C:119:LEU:HD12	2.40	0.47
1:B:73:GLN:HA	1:B:76:VAL:HG23	1.95	0.47
1:C:238:VAL:O	1:C:242:GLU:HG2	2.14	0.47
1:B:266:MET:HE3	1:D:270:HIS:CE1	2.50	0.47
1:C:212:THR:OG1	1:C:301:TYR:OH	2.30	0.47
1:A:20:TYR:O	1:A:24:ARG:HD2	2.14	0.47
1:A:133:ALA:O	1:A:138:ARG:NH2	2.47	0.47
1:C:227:PRO:HB3	1:C:306:TYR:CZ	2.50	0.47
1:A:12:VAL:HG21	1:A:213:LEU:HD11	1.96	0.47
1:A:20:TYR:HE1	1:D:52:GLN:NE2	2.13	0.47
1:A:48:ILE:HD11	1:D:168:ALA:HB1	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:13:LEU:HA	1:D:37:TYR:O	2.15	0.47
1:C:20:TYR:HE2	1:C:202:GLU:HG2	1.80	0.47
1:C:122:GLU:OE2	1:C:148:ARG:HD2	2.15	0.47
1:C:193:GLY:O	1:C:233:THR:HG21	2.15	0.47
1:D:37:TYR:CD2	1:D:63:ARG:HB2	2.50	0.47
1:C:40:GLN:HB2	1:C:54:PHE:CE2	2.50	0.47
1:C:240:ILE:O	1:C:244:LEU:HD13	2.15	0.47
1:D:112:ALA:C	1:D:114:ASN:H	2.23	0.46
1:C:10:THR:HB	1:C:34:HIS:HD2	1.80	0.46
1:C:196:LYS:O	1:C:287:THR:OG1	2.27	0.46
1:A:125:MET:HE3	1:A:141:PHE:CZ	2.50	0.46
1:D:145:MET:CE	1:D:148:ARG:HD2	2.45	0.46
1:C:43:GLU:O	1:C:46:LEU:HD13	2.16	0.46
1:C:287:THR:O	1:C:289:HIS:N	2.40	0.46
1:B:196:LYS:HG2	1:B:233:THR:HG22	1.97	0.46
1:B:72:HIS:O	1:B:76:VAL:HG23	2.16	0.46
1:D:270:HIS:HD2	1:D:274:ILE:HG13	1.81	0.46
1:C:40:GLN:HB2	1:C:54:PHE:HE2	1.80	0.46
1:C:301:TYR:O	1:C:304:VAL:HG22	2.15	0.45
1:C:296:GLU:O	1:C:300:LEU:HD12	2.16	0.45
1:D:44:ILE:HD12	1:D:44:ILE:H	1.82	0.45
1:D:294:ASP:OD2	1:D:294:ASP:N	2.44	0.45
1:C:196:LYS:HG3	1:C:232:LEU:CA	2.47	0.45
1:A:41:ARG:HA	1:A:67:GLY:O	2.17	0.45
1:D:145:MET:HE2	1:D:148:ARG:HD2	1.99	0.45
1:C:69:PHE:CZ	1:C:89:MET:HE1	2.47	0.45
1:A:71:ASP:OD2	1:A:74:SER:HB3	2.17	0.45
1:C:130:MET:HE1	1:C:285:CYS:HB3	1.98	0.45
1:A:127:PRO:N	1:A:128:PRO:HD2	2.32	0.45
1:A:310:ASP:O	1:A:314:ARG:HG3	2.17	0.45
1:D:190:TYR:HB3	1:D:282:TYR:CE1	2.52	0.45
1:A:10:THR:HG21	1:A:214:ASN:HB3	1.99	0.45
1:B:177:MET:HE1	1:B:259:PHE:HE1	1.82	0.45
1:D:266:MET:HB2	1:D:271:GLN:HG2	1.99	0.45
1:B:48:ILE:HG23	1:B:49:GLU:N	2.32	0.45
1:A:270:HIS:O	1:A:270:HIS:CD2	2.70	0.45
1:B:266:MET:HE2	1:B:266:MET:HB3	1.61	0.44
1:C:198:VAL:HG22	1:C:286:LEU:HD13	1.99	0.44
1:C:211:LYS:HB2	1:C:211:LYS:HE2	1.73	0.44
1:D:89:MET:N	1:D:121:SER:OG	2.44	0.44
1:C:116:LYS:O	1:C:157:PRO:HG2	2.17	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:132:HIS:N	1:D:138:ARG:HH22	2.16	0.44
1:C:314:ARG:HA	1:C:317:LEU:CD1	2.47	0.44
1:D:268:ILE:HB	1:D:269:PRO:HD3	1.99	0.44
1:A:142:ASP:OD2	1:A:142:ASP:N	2.50	0.44
1:D:264:GLU:HG3	1:D:265:GLN:OE1	2.18	0.44
1:B:257:GLN:N	1:B:257:GLN:CD	2.75	0.44
1:D:39:LEU:HD11	1:D:67:GLY:HA3	1.98	0.44
1:D:301:TYR:O	1:D:304:VAL:HG12	2.17	0.44
1:B:189:ILE:CD1	1:B:251:LYS:HB3	2.47	0.44
1:D:98:ASN:N	1:D:98:ASN:OD1	2.51	0.44
1:B:174:LEU:HD12	1:B:183:PRO:HD2	2.00	0.44
1:A:229:ASP:CG	1:A:308:ARG:HH11	2.22	0.44
1:D:79:VAL:HG22	1:D:85:VAL:HG21	1.99	0.44
1:B:44:ILE:CA	1:B:47:GLU:H	2.28	0.43
1:C:196:LYS:HD2	1:C:233:THR:CA	2.49	0.43
1:A:127:PRO:HD2	1:A:148:ARG:NH2	2.33	0.43
1:A:296:GLU:CD	1:A:298:SER:H	2.25	0.43
1:C:145:MET:HE3	1:C:145:MET:HB2	1.69	0.43
1:D:187:VAL:HG21	1:D:249:LEU:HD13	1.99	0.43
1:D:197:VAL:HG21	1:D:281:PHE:CE2	2.53	0.43
1:C:48:ILE:HD12	1:C:49:GLU:HG2	1.97	0.43
1:C:191:GLY:C	1:C:193:GLY:H	2.25	0.43
1:A:117:ARG:HH11	1:A:213:LEU:C	2.22	0.43
1:C:198:VAL:HG12	1:C:231:VAL:HG22	2.01	0.43
1:C:202:GLU:HA	1:C:205:ILE:HD12	2.01	0.43
1:A:264:GLU:HG2	1:A:265:GLN:H	1.83	0.43
1:B:313:LEU:HD23	1:B:313:LEU:HA	1.81	0.43
1:D:297:ALA:O	1:D:301:TYR:HD1	2.02	0.43
1:A:73:GLN:HA	1:A:76:VAL:CG2	2.46	0.43
1:C:234:GLN:HB2	1:C:281:PHE:HE1	1.83	0.43
1:D:304:VAL:O	1:D:304:VAL:HG13	2.18	0.43
1:A:79:VAL:HG11	1:A:109:ILE:HA	2.02	0.42
1:D:114:ASN:O	1:D:114:ASN:ND2	2.45	0.42
1:B:190:TYR:HB3	1:B:282:TYR:CE2	2.54	0.42
1:D:23:LYS:HD3	1:D:53:LEU:HD22	2.01	0.42
1:D:233:THR:HG23	1:D:236:GLU:OE1	2.19	0.42
1:A:125:MET:O	1:A:127:PRO:HD3	2.20	0.42
1:D:266:MET:O	1:D:267:GLU:HB2	2.18	0.42
1:B:11:ARG:HA	1:B:35:GLU:HB2	2.01	0.42
1:B:263:ILE:HG13	1:B:271:GLN:HG2	2.01	0.42
1:C:98:ASN:OD1	1:C:98:ASN:N	2.52	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:129:ARG:NH2	1:C:289:HIS:ND1	2.67	0.42
1:B:217:ARG:NH1	1:B:300:LEU:HD22	2.35	0.42
1:C:89:MET:HB3	1:C:98:ASN:HB2	2.01	0.42
1:A:52:GLN:HE22	1:D:24:ARG:NH2	2.10	0.42
1:C:73:GLN:O	1:C:76:VAL:HB	2.19	0.42
1:C:234:GLN:O	1:C:238:VAL:HG23	2.20	0.42
1:C:232:LEU:HA	1:C:232:LEU:HD12	1.62	0.42
1:B:125:MET:HE2	1:B:130:MET:HE2	2.02	0.42
1:D:187:VAL:CG2	1:D:249:LEU:HD13	2.50	0.42
1:D:168:ALA:O	1:D:180:LEU:HD12	2.20	0.41
1:B:90:SER:O	1:B:98:ASN:ND2	2.53	0.41
1:C:196:LYS:HA	1:C:233:THR:HA	2.02	0.41
1:C:79:VAL:HG13	1:C:115:VAL:HG21	2.02	0.41
1:C:30:LEU:HD11	1:C:62:ALA:HB2	2.02	0.41
1:A:24:ARG:HG2	1:A:203:ASP:OD1	2.19	0.41
1:D:73:GLN:CA	1:D:76:VAL:HG22	2.51	0.41
1:A:45:GLY:HA2	1:A:51:VAL:CG2	2.50	0.41
1:A:266:MET:O	1:A:266:MET:HG2	2.20	0.41
1:D:125:MET:HE2	1:D:280:ILE:HD11	2.02	0.41
1:C:197:VAL:HG11	1:C:280:ILE:HG22	2.01	0.41
1:A:168:ALA:CB	1:D:48:ILE:HD11	2.50	0.41
1:A:288:ASP:OD1	1:A:289:HIS:ND1	2.33	0.41
1:D:266:MET:HE2	1:D:266:MET:HA	2.02	0.41
1:C:196:LYS:NZ	1:C:236:GLU:HG2	2.21	0.41
1:C:196:LYS:HE3	1:C:232:LEU:HD12	2.03	0.41
1:D:13:LEU:HD12	1:D:37:TYR:HB2	2.03	0.40
1:D:300:LEU:HB2	1:D:301:TYR:CE1	2.56	0.40
1:C:304:VAL:O	1:C:304:VAL:HG23	2.21	0.40
1:A:306:TYR:CZ	1:A:308:ARG:NH1	2.89	0.40
1:B:180:LEU:O	1:B:181:LEU:HD23	2.22	0.40
1:C:41:ARG:HA	1:C:67:GLY:O	2.21	0.40
1:D:49:GLU:H	1:D:49:GLU:CD	2.30	0.40
1:C:202:GLU:H	1:C:202:GLU:CD	2.29	0.40
1:A:80:LYS:HE2	1:A:80:LYS:HB2	1.81	0.40
1:B:109:ILE:HG23	1:B:115:VAL:HG21	2.03	0.40
1:D:130:MET:HG3	1:D:141:PHE:CE1	2.57	0.40

There are no symmetry-related clashes.

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	299/317 (94%)	279 (93%)	16 (5%)	4 (1%)	9	31
1	B	300/317 (95%)	286 (95%)	9 (3%)	5 (2%)	7	25
1	C	300/317 (95%)	283 (94%)	11 (4%)	6 (2%)	6	21
1	D	300/317 (95%)	283 (94%)	14 (5%)	3 (1%)	12	38
All	All	1199/1268 (95%)	1131 (94%)	50 (4%)	18 (2%)	8	28

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	44	ILE
1	B	178	VAL
1	C	178	VAL
1	C	288	ASP
1	A	178	VAL
1	D	267	GLU
1	B	264	GLU
1	B	269	PRO
1	C	47	GLU
1	A	174	LEU
1	A	269	PRO
1	B	42	PRO
1	C	177	MET
1	C	268	ILE
1	A	137	GLY
1	D	113	GLY
1	C	269	PRO
1	D	268	ILE

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	256/270 (95%)	255 (100%)	1 (0%)	84	94
1	B	257/270 (95%)	255 (99%)	2 (1%)	73	90
1	C	259/270 (96%)	254 (98%)	5 (2%)	50	81
1	D	259/270 (96%)	257 (99%)	2 (1%)	73	90
All	All	1031/1080 (96%)	1021 (99%)	10 (1%)	68	88

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

Mol	Chain	Res	Type
1	B	47	GLU
1	B	266	MET
1	C	18	THR
1	C	46	LEU
1	C	52	GLN
1	C	145	MET
1	C	212	THR
1	A	70	SER
1	D	121	SER
1	D	212	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	52	GLN
1	B	265	GLN
1	C	34	HIS
1	C	271	GLN
1	A	34	HIS
1	A	52	GLN
1	A	98	ASN
1	A	143	GLN
1	A	224	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	265	GLN
1	A	270	HIS
1	D	52	GLN
1	D	72	HIS
1	D	270	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](#)

There are no ligands in this entry.

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	303/317 (95%)	-0.08	2 (0%) 84 77	42, 60, 86, 110	0
1	B	304/317 (95%)	-0.21	5 (1%) 70 61	30, 54, 81, 122	0
1	C	304/317 (95%)	0.43	8 (2%) 57 47	53, 82, 106, 143	0
1	D	304/317 (95%)	-0.10	1 (0%) 90 86	38, 60, 83, 136	0
All	All	1215/1268 (95%)	0.01	16 (1%) 75 66	30, 64, 96, 143	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	45	GLY	3.9
1	A	134	LEU	2.9
1	C	232	LEU	2.9
1	C	196	LYS	2.6
1	B	265	GLN	2.4
1	C	46	LEU	2.4
1	C	97	HIS	2.4
1	B	43	GLU	2.3
1	B	269	PRO	2.3
1	B	264	GLU	2.1
1	C	123	PHE	2.1
1	C	233	THR	2.1
1	D	9	LYS	2.0
1	C	124	GLY	2.0
1	C	122	GLU	2.0
1	A	266	MET	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.