



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 04:05 PM UTC

PDB ID : 2HQG / pdb_00002hqq
Title : Conformation of the AcrB Multidrug Efflux Pump in Mutants of the Putative Proton Relay Pathway
Authors : Su, C.-C.; Li, M.; Gu, R.; Takatsuka, Y.; McDermott, G.; Nikaido, H.; Yu, E.W.
Deposited on : 2006-07-18
Resolution : 3.38 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

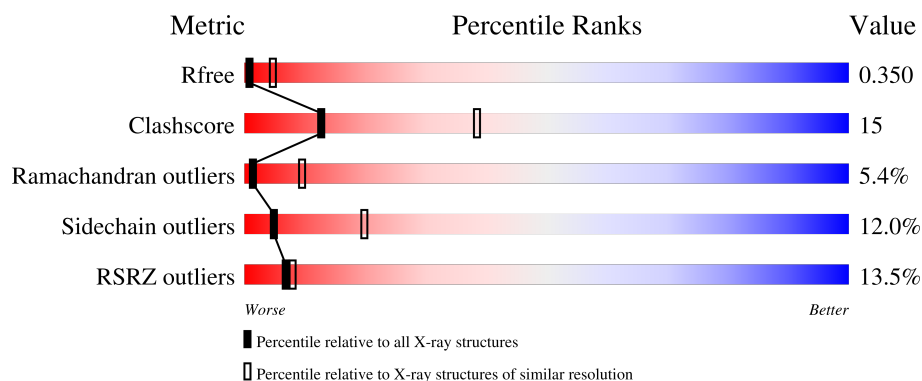
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.38 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	1047 (3.42-3.34)
Clashscore	190562	1067 (3.42-3.34)
Ramachandran outliers	187476	1056 (3.42-3.34)
Sidechain outliers	187428	1056 (3.42-3.34)
RSRZ outliers	180081	1047 (3.42-3.34)

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	1053	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 7719 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 Acriflavine resistance protein B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	1016	7719	4964	1276	1436	43	0	0	0

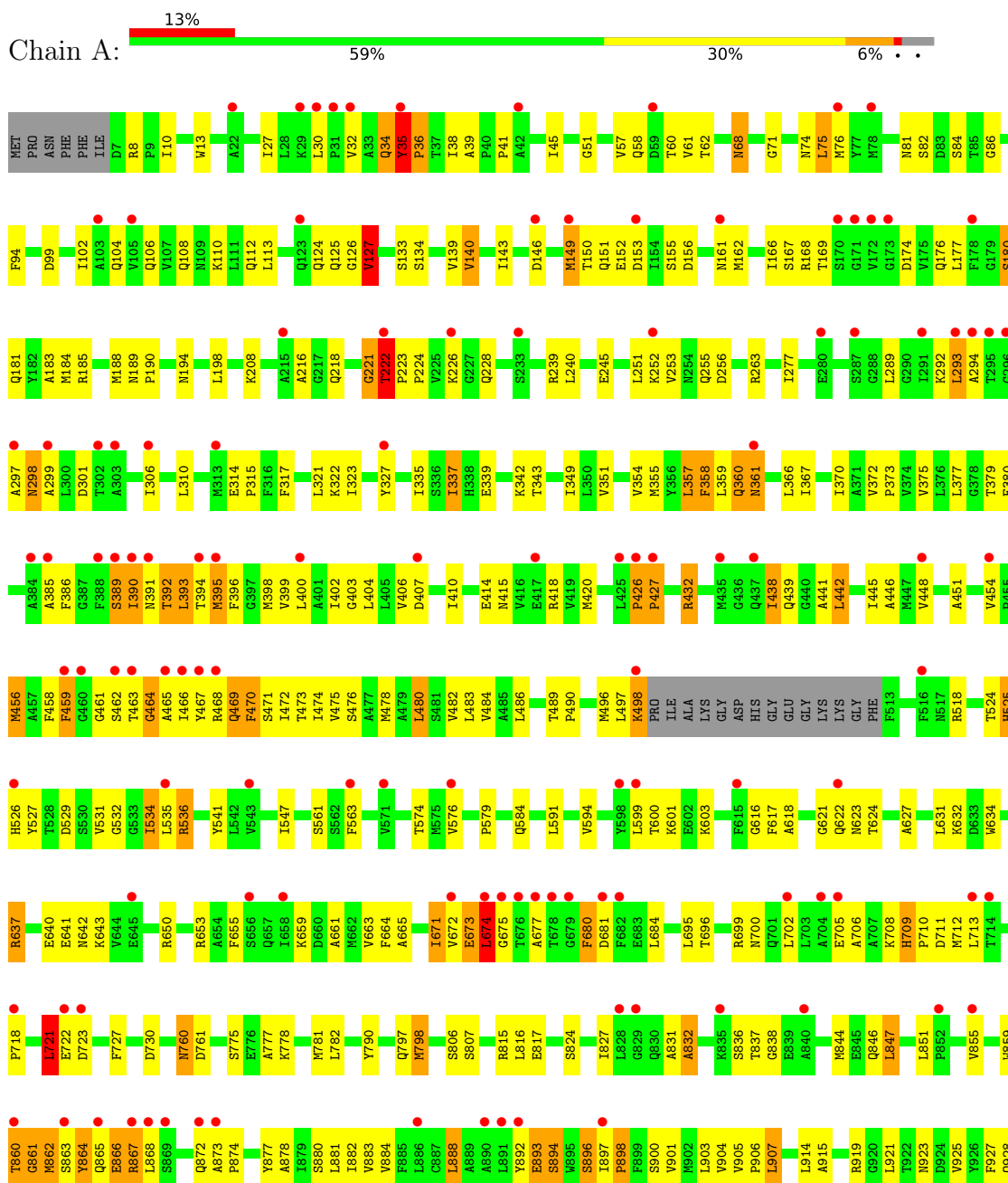
There are 5 discrepancies between the modelled and reference sequences:

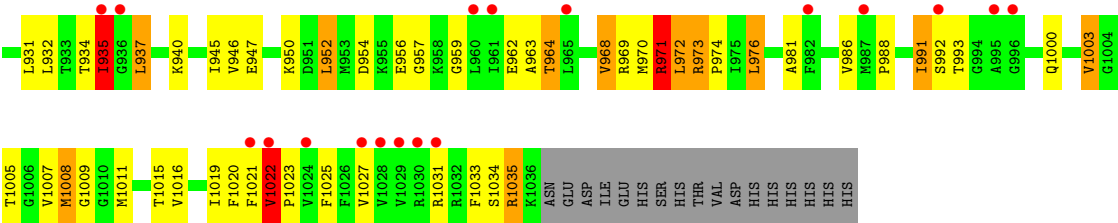
Chain	Residue	Modelled	Actual	Comment	Reference
A	978	ALA	THR	engineered mutation	UNP P31224
A	1050	HIS	-	cloning artifact	UNP P31224
A	1051	HIS	-	cloning artifact	UNP P31224
A	1052	HIS	-	cloning artifact	UNP P31224
A	1053	HIS	-	cloning artifact	UNP P31224

3 Residue-property plots

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: Acriflavine resistance protein B





4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	144.90Å 144.90Å 518.63Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 3.38 20.00 – 3.38	Depositor EDS
% Data completeness (in resolution range)	96.5 (20.00-3.38) 95.9 (20.00-3.38)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.07 (at 3.01Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.254 , 0.275 0.339 , 0.350	Depositor DCC
R_{free} test set	1968 reflections (4.66%)	wwPDB-VP
Wilson B-factor (Å ²)	101.3	Xtriage
Anisotropy	0.052	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 46.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.54$, $\langle L^2 \rangle = 0.38$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	7719	wwPDB-VP
Average B, all atoms (Å ²)	94.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.82% 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	0.77	12/7862 (0.2%)	0.93	8/10677 (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

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1035	ARG	CZ-NH1	17.82	1.57	1.32
1	A	815	ARG	CZ-NH1	8.72	1.45	1.32
1	A	395	MET	C-O	-8.40	1.13	1.24
1	A	964	THR	CB-OG1	8.17	1.56	1.43
1	A	395	MET	C-N	7.93	1.44	1.33
1	A	536	ARG	CZ-NH1	7.61	1.43	1.32
1	A	1035	ARG	NE-CZ	6.81	1.40	1.33
1	A	1008	MET	SD-CE	6.54	1.96	1.79
1	A	496	MET	C-O	6.06	1.31	1.24
1	A	367	ILE	CA-CB	5.97	1.57	1.54
1	A	653	ARG	CZ-NH1	5.55	1.40	1.32
1	A	124	GLN	CD-NE2	5.11	1.44	1.33

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	35	TYR	CA-C-N	19.58	144.31	119.84
1	A	35	TYR	C-N-CA	19.58	144.31	119.84
1	A	426	PRO	N-CA-C	8.20	120.70	110.70
1	A	1035	ARG	NE-CZ-NH2	-7.05	112.85	119.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	456	MET	N-CA-C	-5.64	106.07	114.64
1	A	680	PHE	N-CA-C	5.46	117.48	109.24
1	A	896	SER	CA-C-N	5.07	123.44	120.24
1	A	896	SER	C-N-CA	5.07	123.44	120.24

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	35	TYR	Peptide
1	A	469	GLN	Peptide

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	7719	0	7875	237	10
All	All	7719	0	7875	237	10

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 15.

All (237) 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:680:PHE:HA	1:A:862:MET:HG3	1.44	1.00
1:A:864:TYR:HB3	1:A:867:ARG:HG2	1.47	0.96
1:A:861:GLY:HA3	1:A:862:MET:HB3	1.44	0.96
1:A:867:ARG:HG3	1:A:868:LEU:H	1.37	0.89
1:A:861:GLY:H	1:A:862:MET:HE2	1.41	0.82
1:A:934:THR:O	1:A:935:ILE:HB	1.81	0.80
1:A:864:TYR:HB2	1:A:865:GLN:C	2.06	0.79
1:A:525:HIS:HA	1:A:529:ASP:HB2	1.63	0.79
1:A:166:ILE:HG22	1:A:167:SER:H	1.48	0.79
1:A:465:ALA:HB1	1:A:468:ARG:HB3	1.65	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:867:ARG:HG3	1:A:868:LEU:N	2.00	0.76
1:A:426:PRO:HD2	1:A:427:PRO:HD3	1.65	0.76
1:A:637:ARG:HB2	1:A:642:ASN:HB3	1.67	0.75
1:A:861:GLY:HA3	1:A:862:MET:CB	2.16	0.75
1:A:472:ILE:O	1:A:476:SER:N	2.17	0.75
1:A:861:GLY:CA	1:A:862:MET:HB3	2.17	0.74
1:A:684:LEU:HD11	1:A:855:VAL:HG13	1.69	0.72
1:A:968:VAL:HG21	1:A:1025:PHE:CZ	2.24	0.72
1:A:462:SER:HB2	1:A:867:ARG:HD3	1.73	0.71
1:A:864:TYR:HB2	1:A:866:GLU:N	2.05	0.71
1:A:466:ILE:HA	1:A:469:GLN:HG2	1.74	0.70
1:A:462:SER:C	1:A:464:GLY:H	2.00	0.68
1:A:973:ARG:HB3	1:A:974:PRO:HD3	1.75	0.67
1:A:372:VAL:HG12	1:A:406:VAL:HG22	1.76	0.67
1:A:392:THR:C	1:A:394:THR:H	2.04	0.66
1:A:790:TYR:HB3	1:A:798:MET:HG3	1.78	0.65
1:A:923:ASN:HD22	1:A:927:PHE:HD2	1.45	0.65
1:A:188:MET:N	1:A:775:SER:HA	2.11	0.65
1:A:1022:VAL:HG23	1:A:1023:PRO:HD3	1.79	0.65
1:A:355:MET:HE1	1:A:410:ILE:HG12	1.77	0.65
1:A:451:ALA:HB1	1:A:883:VAL:HG13	1.77	0.65
1:A:426:PRO:CD	1:A:427:PRO:HD3	2.27	0.64
1:A:156:ASP:HA	1:A:181:GLN:HA	1.79	0.63
1:A:357:LEU:O	1:A:358:PHE:HB2	1.97	0.63
1:A:407:ASP:HA	1:A:410:ILE:HD12	1.81	0.63
1:A:959:GLY:HA3	1:A:963:ALA:HB2	1.80	0.62
1:A:861:GLY:H	1:A:862:MET:CE	2.12	0.62
1:A:1025:PHE:H	1:A:1027:VAL:HG22	1.64	0.62
1:A:684:LEU:CD1	1:A:855:VAL:HG13	2.29	0.62
1:A:584:GLN:H	1:A:622:GLN:HE21	1.46	0.61
1:A:681:ASP:N	1:A:862:MET:SD	2.66	0.61
1:A:574:THR:HA	1:A:665:ALA:HA	1.81	0.61
1:A:39:ALA:HB2	1:A:672:VAL:HG21	1.82	0.61
1:A:475:VAL:HA	1:A:478:MET:HB3	1.82	0.61
1:A:915:ALA:O	1:A:919:ARG:HB2	2.00	0.61
1:A:393:LEU:HA	1:A:396:PHE:HB3	1.83	0.61
1:A:860:THR:H	1:A:862:MET:CE	2.14	0.61
1:A:379:THR:HB	1:A:398:MET:HE1	1.82	0.61
1:A:884:VAL:O	1:A:888:LEU:HB2	2.02	0.60
1:A:673:GLU:HG3	1:A:674:LEU:H	1.65	0.60
1:A:859:TRP:HB3	1:A:863:SER:HB2	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1025:PHE:N	1:A:1027:VAL:HG22	2.17	0.60
1:A:675:GLY:HA3	1:A:867:ARG:NH2	2.17	0.59
1:A:473:THR:HA	1:A:476:SER:HB2	1.83	0.59
1:A:343:THR:HG23	1:A:988:PRO:HB2	1.85	0.58
1:A:864:TYR:HB2	1:A:865:GLN:CA	2.33	0.58
1:A:298:ASN:HB2	1:A:301:ASP:HB2	1.85	0.58
1:A:705:GLU:HG3	1:A:847:LEU:HD13	1.84	0.58
1:A:448:VAL:HA	1:A:451:ALA:HB3	1.86	0.57
1:A:462:SER:HB2	1:A:867:ARG:CD	2.34	0.57
1:A:1015:THR:O	1:A:1019:ILE:HB	2.05	0.57
1:A:718:PRO:HG2	1:A:721:LEU:HD13	1.86	0.57
1:A:81:ASN:O	1:A:816:LEU:O	2.23	0.56
1:A:351:VAL:HG22	1:A:981:ALA:HB1	1.86	0.56
1:A:372:VAL:HG23	1:A:373:PRO:HD3	1.87	0.56
1:A:864:TYR:HD2	1:A:865:GLN:HA	1.69	0.56
1:A:867:ARG:CG	1:A:868:LEU:N	2.65	0.56
1:A:166:ILE:HG22	1:A:167:SER:N	2.17	0.56
1:A:680:PHE:HA	1:A:862:MET:CG	2.29	0.56
1:A:1023:PRO:O	1:A:1027:VAL:HG13	2.05	0.56
1:A:34:GLN:HG3	1:A:35:TYR:H	1.71	0.56
1:A:74:ASN:O	1:A:75:LEU:HB3	2.06	0.56
1:A:466:ILE:HG22	1:A:925:VAL:HG11	1.88	0.55
1:A:991:ILE:C	1:A:993:THR:H	2.14	0.55
1:A:968:VAL:HG22	1:A:968:VAL:O	2.07	0.55
1:A:106:GLN:O	1:A:110:LYS:HG2	2.07	0.55
1:A:392:THR:HG22	1:A:393:LEU:H	1.71	0.55
1:A:99:ASP:HB3	1:A:102:ILE:HG22	1.89	0.55
1:A:134:SER:H	1:A:292:LYS:HZ2	1.55	0.55
1:A:41:PRO:HG2	1:A:94:PHE:HB2	1.89	0.55
1:A:188:MET:H	1:A:775:SER:HA	1.72	0.55
1:A:149:MET:HB3	1:A:153:ASP:HB3	1.88	0.55
1:A:641:GLU:O	1:A:650:ARG:NH2	2.39	0.54
1:A:60:THR:HG23	1:A:61:VAL:HG23	1.90	0.54
1:A:532:GLY:O	1:A:536:ARG:HB2	2.08	0.54
1:A:973:ARG:HB3	1:A:974:PRO:CD	2.36	0.54
1:A:438:ILE:HG22	1:A:442:LEU:HD23	1.89	0.54
1:A:901:VAL:O	1:A:904:VAL:HG22	2.08	0.54
1:A:470:PHE:CD1	1:A:473:THR:N	2.69	0.53
1:A:1033:PHE:C	1:A:1035:ARG:H	2.14	0.53
1:A:377:LEU:HA	1:A:380:PHE:CD1	2.44	0.53
1:A:465:ALA:O	1:A:469:GLN:N	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:390:ILE:HG22	1:A:390:ILE:O	2.09	0.53
1:A:76:MET:HE2	1:A:865:GLN:HB2	1.91	0.52
1:A:659:LYS:HG3	1:A:661:ALA:H	1.74	0.52
1:A:240:LEU:HD22	1:A:245:GLU:HB3	1.91	0.52
1:A:392:THR:C	1:A:394:THR:N	2.67	0.52
1:A:134:SER:H	1:A:292:LYS:NZ	2.07	0.52
1:A:293:LEU:HD13	1:A:294:ALA:O	2.10	0.52
1:A:721:LEU:O	1:A:723:ASP:N	2.43	0.52
1:A:462:SER:C	1:A:464:GLY:N	2.68	0.51
1:A:864:TYR:CD2	1:A:865:GLN:HA	2.45	0.51
1:A:986:VAL:HG11	1:A:1007:VAL:HG23	1.92	0.51
1:A:474:ILE:O	1:A:478:MET:HB2	2.10	0.51
1:A:634:TRP:HA	1:A:637:ARG:HE	1.75	0.51
1:A:389:SER:O	1:A:390:ILE:HB	2.11	0.51
1:A:1020:PHE:HA	1:A:1025:PHE:CE1	2.46	0.51
1:A:372:VAL:CG1	1:A:406:VAL:HG22	2.41	0.51
1:A:166:ILE:C	1:A:168:ARG:H	2.19	0.51
1:A:454:VAL:HA	1:A:471:SER:HB3	1.92	0.51
1:A:621:GLY:C	1:A:623:ASN:H	2.19	0.51
1:A:194:ASN:HD22	1:A:798:MET:HG2	1.75	0.50
1:A:541:TYR:HB3	1:A:1022:VAL:HG12	1.93	0.50
1:A:456:MET:HG2	1:A:467:TYR:HB3	1.94	0.50
1:A:139:VAL:HB	1:A:327:TYR:HB3	1.94	0.50
1:A:438:ILE:HA	1:A:441:ALA:HB3	1.93	0.50
1:A:360:GLN:O	1:A:361:ASN:HB2	2.11	0.50
1:A:919:ARG:HD2	1:A:921:LEU:HD13	1.94	0.49
1:A:937:LEU:HD11	1:A:1011:MET:SD	2.52	0.49
1:A:1020:PHE:HA	1:A:1025:PHE:HE1	1.75	0.49
1:A:709:HIS:N	1:A:710:PRO:HD3	2.28	0.49
1:A:674:LEU:O	1:A:674:LEU:HD22	2.12	0.49
1:A:140:VAL:HG23	1:A:289:LEU:HB2	1.94	0.49
1:A:1022:VAL:CG2	1:A:1023:PRO:HD3	2.42	0.49
1:A:400:LEU:HD13	1:A:1003:VAL:HG13	1.95	0.49
1:A:222:THR:O	1:A:224:PRO:HD3	2.13	0.48
1:A:459:PHE:HE1	1:A:468:ARG:HD2	1.78	0.48
1:A:126:GLY:O	1:A:127:VAL:HG22	2.13	0.48
1:A:446:ALA:HB2	1:A:482:VAL:HG21	1.94	0.48
1:A:617:PHE:O	1:A:618:ALA:HB3	2.14	0.48
1:A:57:VAL:HG11	1:A:86:GLY:HA2	1.95	0.48
1:A:873:ALA:N	1:A:874:PRO:HD2	2.29	0.48
1:A:637:ARG:O	1:A:637:ARG:HG2	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:727:PHE:CZ	1:A:807:SER:HB3	2.49	0.47
1:A:730:ASP:HB3	1:A:806:SER:HB3	1.96	0.47
1:A:239:ARG:NE	1:A:761:ASP:O	2.48	0.47
1:A:489:THR:HB	1:A:490:PRO:HD3	1.95	0.47
1:A:574:THR:HG21	1:A:594:VAL:HG11	1.95	0.47
1:A:892:TYR:CD2	1:A:897:ILE:HG21	2.49	0.47
1:A:441:ALA:HB2	1:A:947:GLU:HG2	1.95	0.47
1:A:68:ASN:HD21	1:A:113:LEU:HB2	1.79	0.47
1:A:531:VAL:HA	1:A:534:ILE:HD13	1.96	0.47
1:A:675:GLY:HA3	1:A:867:ARG:HH22	1.78	0.47
1:A:470:PHE:CD1	1:A:472:ILE:HB	2.50	0.47
1:A:817:GLU:HB2	1:A:824:SER:O	2.15	0.47
1:A:877:TYR:O	1:A:881:LEU:HB2	2.14	0.47
1:A:972:LEU:O	1:A:976:LEU:HB2	2.15	0.47
1:A:35:TYR:HB3	1:A:36:PRO:O	2.15	0.46
1:A:971:ARG:HH22	1:A:972:LEU:HB3	1.80	0.46
1:A:184:MET:HE3	1:A:184:MET:HA	1.97	0.46
1:A:380:PHE:HE2	1:A:395:MET:SD	2.38	0.46
1:A:484:VAL:C	1:A:486:LEU:H	2.24	0.46
1:A:527:TYR:HE1	1:A:1020:PHE:HB3	1.79	0.46
1:A:314:GLU:N	1:A:315:PRO:CD	2.79	0.46
1:A:426:PRO:N	1:A:427:PRO:HD3	2.31	0.46
1:A:915:ALA:HB1	1:A:1005:THR:HG22	1.97	0.46
1:A:862:MET:HG2	1:A:863:SER:H	1.80	0.46
1:A:36:PRO:CD	1:A:391:ASN:HB3	2.46	0.45
1:A:377:LEU:HA	1:A:380:PHE:HD1	1.80	0.45
1:A:393:LEU:HD21	1:A:469:GLN:HG3	1.97	0.45
1:A:860:THR:H	1:A:862:MET:HE1	1.82	0.45
1:A:166:ILE:CG2	1:A:167:SER:H	2.23	0.45
1:A:335:ILE:C	1:A:337:ILE:H	2.24	0.45
1:A:366:LEU:O	1:A:370:ILE:HG12	2.16	0.45
1:A:155:SER:HB3	1:A:180:SER:H	1.81	0.45
1:A:702:LEU:HB2	1:A:851:LEU:HD11	1.99	0.45
1:A:859:TRP:HB3	1:A:863:SER:CB	2.46	0.45
1:A:524:THR:O	1:A:526:HIS:N	2.47	0.45
1:A:877:TYR:HA	1:A:880:SER:HB2	1.99	0.45
1:A:420:MET:HE2	1:A:498:LYS:HB3	1.99	0.44
1:A:664:PHE:O	1:A:665:ALA:HB3	2.17	0.44
1:A:58:GLN:HA	1:A:62:THR:HB	1.99	0.44
1:A:706:ALA:HB2	1:A:844:MET:HE1	2.00	0.44
1:A:458:PHE:O	1:A:459:PHE:O	2.36	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:198:LEU:HD13	1:A:251:LEU:HD13	2.00	0.44
1:A:907:LEU:HD21	1:A:1023:PRO:HD2	2.00	0.44
1:A:420:MET:HE2	1:A:498:LYS:CB	2.48	0.43
1:A:463:THR:HG22	1:A:867:ARG:HB2	2.01	0.43
1:A:900:SER:HB3	1:A:1027:VAL:HB	2.00	0.43
1:A:952:LEU:O	1:A:956:GLU:HB3	2.18	0.43
1:A:862:MET:HG2	1:A:863:SER:N	2.33	0.43
1:A:959:GLY:HA3	1:A:963:ALA:CB	2.47	0.43
1:A:174:ASP:O	1:A:292:LYS:HB3	2.18	0.43
1:A:454:VAL:C	1:A:456:MET:H	2.27	0.43
1:A:414:GLU:CD	1:A:974:PRO:HG3	2.43	0.43
1:A:760:ASN:HD22	1:A:760:ASN:C	2.26	0.43
1:A:859:TRP:HE3	1:A:862:MET:SD	2.42	0.43
1:A:956:GLU:HG2	1:A:957:GLY:H	1.83	0.43
1:A:470:PHE:CE1	1:A:472:ILE:HB	2.54	0.43
1:A:897:ILE:HG23	1:A:946:VAL:HG11	2.00	0.43
1:A:399:VAL:HA	1:A:402:ILE:HB	2.00	0.43
1:A:699:ARG:HH21	1:A:700:ASN:HD21	1.65	0.43
1:A:705:GLU:HG3	1:A:847:LEU:CD1	2.48	0.43
1:A:468:ARG:C	1:A:470:PHE:N	2.76	0.42
1:A:711:ASP:O	1:A:712:MET:HB2	2.19	0.42
1:A:991:ILE:O	1:A:993:THR:N	2.43	0.42
1:A:905:VAL:HG12	1:A:935:ILE:HG13	2.01	0.42
1:A:905:VAL:CG2	1:A:906:PRO:HD3	2.49	0.42
1:A:1023:PRO:HA	1:A:1031:ARG:NH1	2.35	0.42
1:A:574:THR:HG22	1:A:627:ALA:HB3	2.00	0.42
1:A:616:GLY:HA3	1:A:624:THR:HB	2.01	0.42
1:A:339:GLU:HB3	1:A:1000:GLN:HE22	1.83	0.42
1:A:631:LEU:HD13	1:A:637:ARG:HH12	1.85	0.42
1:A:1016:VAL:O	1:A:1019:ILE:HG22	2.19	0.42
1:A:183:ALA:HB3	1:A:185:ARG:HD3	2.00	0.42
1:A:314:GLU:N	1:A:315:PRO:HD3	2.34	0.42
1:A:894:SER:C	1:A:896:SER:H	2.27	0.42
1:A:655:PHE:O	1:A:659:LYS:HB2	2.20	0.42
1:A:699:ARG:HH21	1:A:700:ASN:ND2	2.17	0.42
1:A:392:THR:O	1:A:394:THR:HG23	2.20	0.41
1:A:863:SER:C	1:A:864:TYR:CD2	2.98	0.41
1:A:897:ILE:N	1:A:898:PRO:CD	2.83	0.41
1:A:836:SER:O	1:A:838:GLY:N	2.54	0.41
1:A:1022:VAL:CB	1:A:1023:PRO:HD3	2.50	0.41
1:A:150:THR:HG22	1:A:151:GLN:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:903:LEU:HD13	1:A:1031:ARG:HE	1.85	0.41
1:A:1019:ILE:HG23	1:A:1020:PHE:CD2	2.55	0.41
1:A:576:VAL:HG13	1:A:663:VAL:HG22	2.02	0.41
1:A:945:ILE:HG22	1:A:971:ARG:HD2	2.02	0.41
1:A:354:VAL:O	1:A:354:VAL:HG12	2.21	0.41
1:A:317:PHE:HE2	1:A:323:ILE:HD11	1.85	0.41
1:A:897:ILE:N	1:A:898:PRO:HD2	2.36	0.41
1:A:1008:MET:HG3	1:A:1009:GLY:N	2.36	0.41
1:A:403:GLY:O	1:A:406:VAL:N	2.53	0.41
1:A:133:SER:H	1:A:292:LYS:HZ1	1.67	0.41
1:A:699:ARG:HG2	1:A:827:ILE:HD11	2.03	0.41
1:A:218:GLN:HG3	1:A:221:GLY:HA2	2.04	0.40
1:A:372:VAL:CG2	1:A:373:PRO:HD3	2.50	0.40
1:A:375:VAL:HA	1:A:480:LEU:HD12	2.02	0.40
1:A:777:ALA:O	1:A:781:MET:HG2	2.22	0.40
1:A:878:ALA:O	1:A:882:ILE:HG12	2.22	0.40
1:A:964:THR:O	1:A:968:VAL:HG12	2.21	0.40
1:A:897:ILE:H	1:A:897:ILE:HD12	1.86	0.40
1:A:36:PRO:HD3	1:A:391:ASN:CG	2.47	0.40
1:A:189:ASN:HA	1:A:190:PRO:HD3	1.95	0.40
1:A:476:SER:O	1:A:480:LEU:HB2	2.21	0.40
1:A:831:ALA:O	1:A:832:ALA:HB2	2.20	0.40

All (10) 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:599:LEU:O	1:A:778:LYS:NZ[6_555]	1.74	0.46
1:A:10:ILE:CG2	1:A:893:GLU:OE1[2_545]	1.79	0.41
1:A:113:LEU:CD2	1:A:127:VAL:O[3_655]	1.79	0.41
1:A:51:GLY:O	1:A:216:ALA:O[3_655]	1.88	0.32
1:A:112:GLN:NE2	1:A:112:GLN:NE2[2_545]	1.88	0.32
1:A:228:GLN:OE1	1:A:781:MET:CE[2_545]	1.88	0.32
1:A:536:ARG:NE	1:A:962:GLU:OE2[16_544]	1.89	0.31
1:A:600:THR:CG2	1:A:782:LEU:CD1[6_555]	1.98	0.22
1:A:71:GLY:N	1:A:167:SER:O[3_655]	2.05	0.15
1:A:603:LYS:NZ	1:A:778:LYS:O[6_555]	2.15	0.05

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	1012/1053 (96%)	838 (83%)	119 (12%)	55 (5%)	1 9

All (55) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	34	GLN
1	A	36	PRO
1	A	221	GLY
1	A	385	ALA
1	A	404	LEU
1	A	432	ARG
1	A	459	PHE
1	A	470	PHE
1	A	722	GLU
1	A	894	SER
1	A	935	ILE
1	A	82	SER
1	A	127	VAL
1	A	146	ASP
1	A	255	GLN
1	A	256	ASP
1	A	361	ASN
1	A	390	ILE
1	A	461	GLY
1	A	464	GLY
1	A	525	HIS
1	A	671	ILE
1	A	673	GLU
1	A	674	LEU
1	A	954	ASP
1	A	971	ARG
1	A	991	ILE
1	A	1021	PHE

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Mol	Chain	Res	Type
1	A	75	LEU
1	A	169	THR
1	A	299	ALA
1	A	358	PHE
1	A	389	SER
1	A	677	ALA
1	A	721	LEU
1	A	837	THR
1	A	149	MET
1	A	386	PHE
1	A	497	LEU
1	A	561	SER
1	A	579	PRO
1	A	861	GLY
1	A	867	ARG
1	A	893	GLU
1	A	898	PRO
1	A	222	THR
1	A	297	ALA
1	A	427	PRO
1	A	832	ALA
1	A	866	GLU
1	A	1022	VAL
1	A	1034	SER
1	A	992	SER
1	A	968	VAL
1	A	223	PRO

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	826/858 (96%)	727 (88%)	99 (12%)	5 20

All (99) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	ARG
1	A	13	TRP
1	A	27	ILE
1	A	30	LEU
1	A	32	VAL
1	A	38	ILE
1	A	45	ILE
1	A	68	ASN
1	A	84	SER
1	A	104	GLN
1	A	108	GLN
1	A	125	GLN
1	A	127	VAL
1	A	140	VAL
1	A	143	ILE
1	A	152	GLU
1	A	161	ASN
1	A	162	MET
1	A	176	GLN
1	A	177	LEU
1	A	180	SER
1	A	208	LYS
1	A	222	THR
1	A	226	LYS
1	A	252	LYS
1	A	253	VAL
1	A	263	ARG
1	A	277	ILE
1	A	293	LEU
1	A	298	ASN
1	A	306	ILE
1	A	310	LEU
1	A	321	LEU
1	A	322	LYS
1	A	337	ILE
1	A	342	LYS
1	A	349	ILE
1	A	357	LEU
1	A	359	LEU
1	A	360	GLN
1	A	392	THR
1	A	393	LEU
1	A	415	ASN

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Mol	Chain	Res	Type
1	A	418	ARG
1	A	432	ARG
1	A	438	ILE
1	A	439	GLN
1	A	442	LEU
1	A	445	ILE
1	A	480	LEU
1	A	483	LEU
1	A	498	LYS
1	A	518	ARG
1	A	534	ILE
1	A	535	LEU
1	A	547	ILE
1	A	563	PHE
1	A	591	LEU
1	A	601	LYS
1	A	632	LYS
1	A	637	ARG
1	A	640	GLU
1	A	643	LYS
1	A	671	ILE
1	A	674	LEU
1	A	695	LEU
1	A	696	THR
1	A	708	LYS
1	A	709	HIS
1	A	713	LEU
1	A	721	LEU
1	A	760	ASN
1	A	797	GLN
1	A	798	MET
1	A	846	GLN
1	A	847	LEU
1	A	860	THR
1	A	862	MET
1	A	864	TYR
1	A	872	GLN
1	A	888	LEU
1	A	907	LEU
1	A	914	LEU
1	A	928	GLN
1	A	931	LEU

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Mol	Chain	Res	Type
1	A	932	LEU
1	A	935	ILE
1	A	937	LEU
1	A	940	LYS
1	A	950	LYS
1	A	952	LEU
1	A	969	ARG
1	A	970	MET
1	A	971	ARG
1	A	972	LEU
1	A	973	ARG
1	A	976	LEU
1	A	1003	VAL
1	A	1022	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	68	ASN
1	A	108	GLN
1	A	112	GLN
1	A	124	GLN
1	A	176	GLN
1	A	189	ASN
1	A	194	ASN
1	A	197	GLN
1	A	213	GLN
1	A	218	GLN
1	A	284	GLN
1	A	360	GLN
1	A	361	ASN
1	A	437	GLN
1	A	517	ASN
1	A	525	HIS
1	A	604	ASN
1	A	605	ASN
1	A	622	GLN
1	A	687	GLN
1	A	700	ASN
1	A	760	ASN
1	A	820	ASN
1	A	872	GLN

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Mol	Chain	Res	Type
1	A	923	ASN
1	A	1000	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 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

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	1016/1053 (96%)	1.07	137 (13%) 7 8	31, 91, 152, 190	0

All (137) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	296	GLY	7.6
1	A	303	ALA	6.2
1	A	295	THR	5.7
1	A	1021	PHE	5.7
1	A	674	LEU	5.1
1	A	59	ASP	4.7
1	A	892	TYR	4.6
1	A	299	ALA	4.6
1	A	714	THR	4.6
1	A	960	LEU	4.5
1	A	297	ALA	4.4
1	A	713	LEU	4.4
1	A	1024	VAL	4.4
1	A	678	THR	4.3
1	A	149	MET	4.3
1	A	868	LEU	4.2
1	A	1030	ARG	4.1
1	A	829	GLY	4.1
1	A	992	SER	4.0
1	A	886	LEU	4.0
1	A	435	MET	3.8
1	A	395	MET	3.8
1	A	459	PHE	3.7
1	A	852	PRO	3.6
1	A	294	ALA	3.6
1	A	891	LEU	3.6
1	A	170	SER	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	681	ASP	3.6
1	A	105	VAL	3.6
1	A	936	GLY	3.5
1	A	390	ILE	3.5
1	A	306	ILE	3.5
1	A	705	GLU	3.5
1	A	722	GLU	3.5
1	A	389	SER	3.5
1	A	1028	VAL	3.5
1	A	171	GLY	3.4
1	A	863	SER	3.4
1	A	869	SER	3.3
1	A	407	ASP	3.3
1	A	872	GLN	3.3
1	A	222	THR	3.2
1	A	996	GLY	3.2
1	A	32	VAL	3.2
1	A	723	ASP	3.2
1	A	215	ALA	3.2
1	A	1022	VAL	3.1
1	A	1031	ARG	3.1
1	A	840	ALA	3.1
1	A	462	SER	3.1
1	A	543	VAL	3.1
1	A	302	THR	3.0
1	A	676	THR	3.0
1	A	865	GLN	3.0
1	A	394	THR	3.0
1	A	995	ALA	3.0
1	A	103	ALA	2.9
1	A	233	SER	2.9
1	A	855	VAL	2.9
1	A	385	ALA	2.8
1	A	468	ARG	2.8
1	A	30	LEU	2.8
1	A	388	PHE	2.8
1	A	293	LEU	2.8
1	A	526	HIS	2.7
1	A	658	ILE	2.7
1	A	327	TYR	2.7
1	A	599	LEU	2.7
1	A	897	ILE	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	645	GLU	2.7
1	A	987	MET	2.7
1	A	31	PRO	2.7
1	A	961	ILE	2.7
1	A	1029	VAL	2.7
1	A	437	GLN	2.6
1	A	718	PRO	2.6
1	A	35	TYR	2.6
1	A	426	PRO	2.6
1	A	677	ALA	2.6
1	A	466	ILE	2.5
1	A	78	MET	2.5
1	A	313	MET	2.5
1	A	467	TYR	2.5
1	A	400	LEU	2.5
1	A	598	TYR	2.5
1	A	675	GLY	2.5
1	A	361	ASN	2.5
1	A	835	LYS	2.5
1	A	226	LYS	2.4
1	A	454	VAL	2.4
1	A	22	ALA	2.4
1	A	498	LYS	2.4
1	A	287	SER	2.4
1	A	172	VAL	2.4
1	A	873	ALA	2.4
1	A	982	PHE	2.4
1	A	417	GLU	2.4
1	A	965	LEU	2.4
1	A	576	VAL	2.4
1	A	622	GLN	2.3
1	A	1027	VAL	2.3
1	A	161	ASN	2.3
1	A	867	ARG	2.3
1	A	291	ILE	2.3
1	A	448	VAL	2.3
1	A	252	LYS	2.3
1	A	828	LEU	2.2
1	A	280	GLU	2.2
1	A	76	MET	2.2
1	A	704	ALA	2.2
1	A	890	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	516	PHE	2.2
1	A	563	PHE	2.2
1	A	672	VAL	2.2
1	A	391	ASN	2.2
1	A	146	ASP	2.2
1	A	42	ALA	2.2
1	A	935	ILE	2.2
1	A	535	LEU	2.2
1	A	123	GLN	2.1
1	A	702	LEU	2.1
1	A	384	ALA	2.1
1	A	571	VAL	2.1
1	A	679	GLY	2.1
1	A	153	ASP	2.1
1	A	460	GLY	2.1
1	A	656	SER	2.1
1	A	178	PHE	2.1
1	A	463	THR	2.0
1	A	173	GLY	2.0
1	A	427	PRO	2.0
1	A	615	PHE	2.0
1	A	465	ALA	2.0
1	A	860	THR	2.0
1	A	682	PHE	2.0
1	A	29	LYS	2.0
1	A	425	LEU	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 ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.