



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2018 – 04:05 am GMT

PDB ID : 2HQD
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 : 3.65 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : trunk30967
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk30967

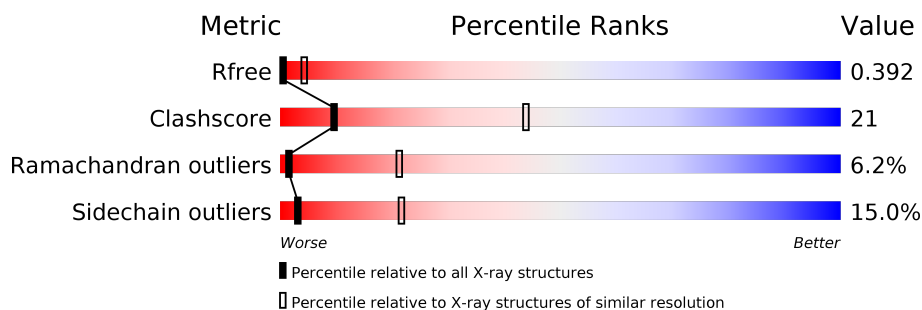
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.65 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}	111664	1290 (3.82-3.50)
Clashscore	122126	1394 (3.82-3.50)
Ramachandran outliers	120053	1346 (3.82-3.50)
Sidechain outliers	120020	1345 (3.82-3.50)

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

Mol	Chain	Length	Quality of chain
1	A	1053	<div> <div style="width: 52%; background-color: green;"></div> <div style="width: 34%; background-color: yellow;"></div> <div style="width: 8%; background-color: orange;"></div> <div style="width: 8%; background-color: red;"></div> <div style="width: 2%; background-color: grey;"></div> </div> <div>52% 34% 8% . .</div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 7718 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
1	A	1016	Total	C	N	O	S	0	0	0
			7718	4964	1276	1435	43			

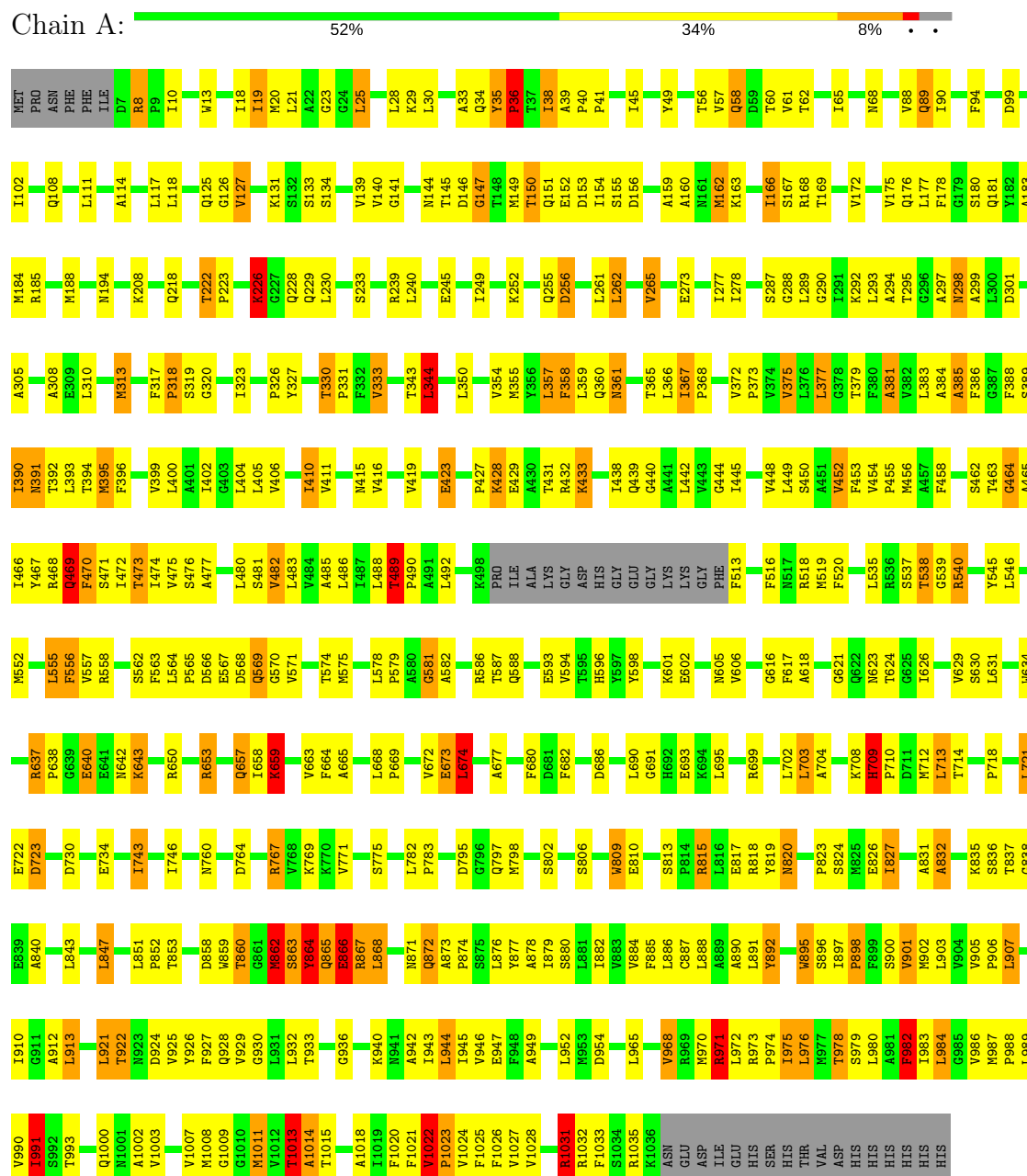
There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	408	ALA	ASP	ENGINEERED	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 and DNA 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. 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. 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	145.03Å 145.03Å 513.67Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 3.65 46.68 – 3.65	Depositor EDS
% Data completeness (in resolution range)	90.0 (20.00-3.65) 89.7 (46.68-3.65)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.76 (at 3.66Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.261 , 0.303 0.369 , 0.392	Depositor DCC
R_{free} test set	1101 reflections (5.19%)	wwPDB-VP
Wilson B-factor (Å ²)	101.4	Xtriage
Anisotropy	0.063	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.22 , 55.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.55$, $\langle L^2 \rangle = 0.40$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.80	EDS
Total number of atoms	7718	wwPDB-VP
Average B, all atoms (Å ²)	100.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.02% 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	0.83	23/7861 (0.3%)	0.74	10/10676 (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 (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	433	LYS	CD-CE	15.58	1.90	1.51
1	A	1031	ARG	NE-CZ	15.31	1.52	1.33
1	A	1035	ARG	CZ-NH1	14.66	1.52	1.33
1	A	1031	ARG	CZ-NH1	13.14	1.50	1.33
1	A	256	ASP	C-O	12.44	1.47	1.23
1	A	444	GLY	N-CA	9.46	1.60	1.46
1	A	593	GLU	CB-CG	8.38	1.68	1.52
1	A	640	GLU	CD-OE2	8.33	1.34	1.25
1	A	35	TYR	CG-CD2	8.22	1.49	1.39
1	A	734	GLU	CD-OE2	7.40	1.33	1.25
1	A	892	TYR	C-O	7.39	1.37	1.23
1	A	35	TYR	CE2-CZ	6.85	1.47	1.38
1	A	333	VAL	CB-CG1	6.24	1.66	1.52
1	A	1035	ARG	NE-CZ	6.21	1.41	1.33
1	A	29	LYS	CE-NZ	6.11	1.64	1.49
1	A	35	TYR	CE1-CZ	5.96	1.46	1.38
1	A	866	GLU	CG-CD	5.66	1.60	1.51
1	A	89	GLN	CD-NE2	5.41	1.46	1.32
1	A	653	ARG	CZ-NH1	5.35	1.40	1.33
1	A	593	GLU	CD-OE1	5.19	1.31	1.25

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	947	GLU	CD-OE1	5.10	1.31	1.25
1	A	428	LYS	CE-NZ	5.08	1.61	1.49
1	A	433	LYS	CB-CG	5.07	1.66	1.52

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1031	ARG	NE-CZ-NH2	-24.13	108.24	120.30
1	A	35	TYR	C-N-CD	-16.10	85.18	120.60
1	A	1035	ARG	NE-CZ-NH2	-13.84	113.38	120.30
1	A	35	TYR	C-N-CA	10.04	164.15	122.00
1	A	1031	ARG	NE-CZ-NH1	7.26	123.93	120.30
1	A	1035	ARG	NH1-CZ-NH2	6.30	126.33	119.40
1	A	333	VAL	CA-CB-CG2	-6.11	101.74	110.90
1	A	1031	ARG	CD-NE-CZ	-5.62	115.73	123.60
1	A	653	ARG	NE-CZ-NH2	-5.62	117.49	120.30
1	A	36	PRO	CA-N-CD	-5.12	104.33	111.50

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1031	ARG	Sidechain
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	7718	0	7878	325	0
All	All	7718	0	7878	325	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 21.

All (325) 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:433:LYS:CD	1:A:433:LYS:CE	1.90	1.46
1:A:1022:VAL:HB	1:A:1023:PRO:HD3	1.11	1.08
1:A:926:TYR:HB3	1:A:1003:VAL:HG23	1.31	1.07
1:A:1022:VAL:HB	1:A:1023:PRO:CD	1.83	1.07
1:A:653:ARG:O	1:A:657:GLN:HB2	1.61	0.99
1:A:58:GLN:HE22	1:A:818:ARG:HD2	1.27	0.98
1:A:680:PHE:HA	1:A:862:MET:HG3	1.45	0.98
1:A:709:HIS:H	1:A:710:PRO:HD3	1.30	0.92
1:A:456:MET:HG3	1:A:467:TYR:HB3	1.55	0.88
1:A:709:HIS:N	1:A:710:PRO:HD3	1.91	0.85
1:A:888:LEU:HD21	1:A:901:VAL:HG23	1.57	0.85
1:A:815:ARG:HH11	1:A:815:ARG:HG3	1.43	0.82
1:A:298:ASN:HB2	1:A:301:ASP:HB3	1.60	0.82
1:A:942:ALA:O	1:A:945:ILE:HG13	1.80	0.82
1:A:456:MET:CG	1:A:467:TYR:HB3	2.10	0.81
1:A:20:MET:HA	1:A:377:LEU:HD13	1.60	0.81
1:A:973:ARG:HB3	1:A:974:PRO:HD3	1.63	0.80
1:A:929:VAL:HA	1:A:932:LEU:HG	1.65	0.79
1:A:877:TYR:HA	1:A:880:SER:HB2	1.67	0.77
1:A:343:THR:O	1:A:344:LEU:HB3	1.85	0.77
1:A:637:ARG:HB2	1:A:642:ASN:HB3	1.69	0.74
1:A:1022:VAL:CB	1:A:1023:PRO:CD	2.65	0.74
1:A:901:VAL:HG22	1:A:943:ILE:HD13	1.71	0.72
1:A:450:SER:HA	1:A:453:PHE:HB2	1.72	0.72
1:A:399:VAL:HA	1:A:402:ILE:HD12	1.72	0.71
1:A:686:ASP:HB2	1:A:695:LEU:HD12	1.71	0.71
1:A:39:ALA:HB2	1:A:672:VAL:HG11	1.72	0.70
1:A:416:VAL:HG22	1:A:431:THR:HG21	1.72	0.70
1:A:699:ARG:HG2	1:A:827:ILE:HD11	1.73	0.70
1:A:188:MET:H	1:A:775:SER:HA	1.57	0.69
1:A:864:TYR:HB3	1:A:867:ARG:HG2	1.75	0.69
1:A:574:THR:HA	1:A:665:ALA:HA	1.73	0.68
1:A:357:LEU:O	1:A:358:PHE:HB2	1.91	0.68
1:A:730:ASP:HB3	1:A:806:SER:HB3	1.75	0.68
1:A:433:LYS:CG	1:A:433:LYS:CE	2.71	0.68
1:A:867:ARG:HG3	1:A:868:LEU:H	1.59	0.68
1:A:162:MET:HB3	1:A:313:MET:HG2	1.75	0.67
1:A:188:MET:N	1:A:775:SER:HA	2.09	0.67
1:A:470:PHE:CD2	1:A:473:THR:HB	2.29	0.67
1:A:392:THR:HG22	1:A:393:LEU:H	1.58	0.66
1:A:58:GLN:NE2	1:A:818:ARG:HD2	2.06	0.66
1:A:864:TYR:HA	1:A:867:ARG:HE	1.59	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:454:VAL:HG23	1:A:455:PRO:HD3	1.77	0.66
1:A:863:SER:C	1:A:864:TYR:CD2	2.69	0.66
1:A:901:VAL:C	1:A:903:LEU:H	1.99	0.66
1:A:470:PHE:CG	1:A:473:THR:HB	2.31	0.65
1:A:56:THR:O	1:A:60:THR:HG22	1.97	0.65
1:A:709:HIS:N	1:A:710:PRO:CD	2.59	0.65
1:A:672:VAL:HG22	1:A:673:GLU:HG2	1.78	0.64
1:A:166:ILE:O	1:A:168:ARG:N	2.30	0.64
1:A:888:LEU:HD21	1:A:901:VAL:CG2	2.27	0.64
1:A:578:LEU:HG	1:A:587:THR:HG22	1.80	0.63
1:A:886:LEU:O	1:A:887:CYS:HB2	1.97	0.63
1:A:470:PHE:O	1:A:471:SER:HB2	1.97	0.63
1:A:673:GLU:HG3	1:A:674:LEU:HD13	1.78	0.63
1:A:926:TYR:HB3	1:A:1003:VAL:CG2	2.20	0.63
1:A:900:SER:HB3	1:A:946:VAL:HG21	1.79	0.63
1:A:134:SER:H	1:A:292:LYS:HE3	1.62	0.63
1:A:965:LEU:HA	1:A:968:VAL:HG12	1.79	0.63
1:A:34:GLN:HB3	1:A:333:VAL:CG2	2.29	0.62
1:A:885:PHE:HA	1:A:888:LEU:HD22	1.81	0.62
1:A:481:SER:O	1:A:485:ALA:HB3	2.01	0.61
1:A:389:SER:HB3	1:A:391:ASN:HD21	1.65	0.61
1:A:907:LEU:O	1:A:910:ILE:HG22	2.01	0.61
1:A:982:PHE:O	1:A:984:LEU:N	2.34	0.61
1:A:968:VAL:HG21	1:A:1025:PHE:CZ	2.36	0.60
1:A:815:ARG:HG3	1:A:815:ARG:NH1	2.15	0.60
1:A:433:LYS:HB3	1:A:433:LYS:HE2	1.84	0.60
1:A:863:SER:O	1:A:864:TYR:HD2	1.84	0.60
1:A:34:GLN:HB3	1:A:333:VAL:HG21	1.84	0.60
1:A:1023:PRO:HA	1:A:1026:PHE:HB2	1.84	0.59
1:A:180:SER:OG	1:A:273:GLU:HG2	2.03	0.59
1:A:463:THR:H	1:A:867:ARG:HD2	1.67	0.59
1:A:477:ALA:O	1:A:481:SER:HB2	2.02	0.59
1:A:155:SER:HB3	1:A:180:SER:H	1.68	0.59
1:A:973:ARG:HB3	1:A:974:PRO:CD	2.33	0.59
1:A:471:SER:H	1:A:474:ILE:HD12	1.67	0.58
1:A:658:ILE:O	1:A:659:LYS:HB3	2.03	0.58
1:A:456:MET:SD	1:A:876:LEU:HG	2.42	0.58
1:A:159:ALA:HA	1:A:163:LYS:HB2	1.84	0.58
1:A:682:PHE:HB3	1:A:827:ILE:CG2	2.34	0.58
1:A:470:PHE:C	1:A:472:ILE:H	2.06	0.58
1:A:710:PRO:HA	1:A:713:LEU:HA	1.85	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:640:GLU:HA	1:A:643:LYS:HZ2	1.68	0.58
1:A:864:TYR:CB	1:A:867:ARG:HG2	2.33	0.58
1:A:159:ALA:HA	1:A:163:LYS:CB	2.34	0.58
1:A:355:MET:CE	1:A:359:LEU:HD11	2.34	0.58
1:A:140:VAL:HG23	1:A:289:LEU:HB2	1.85	0.57
1:A:394:THR:HB	1:A:470:PHE:CE2	2.39	0.57
1:A:867:ARG:HG3	1:A:868:LEU:N	2.20	0.57
1:A:556:PHE:C	1:A:558:ARG:H	2.09	0.57
1:A:702:LEU:HB2	1:A:851:LEU:HD11	1.87	0.57
1:A:156:ASP:HA	1:A:181:GLN:HA	1.86	0.56
1:A:482:VAL:O	1:A:486:LEU:HB2	2.05	0.56
1:A:8:ARG:HE	1:A:8:ARG:H	1.53	0.56
1:A:449:LEU:HD13	1:A:936:GLY:HA3	1.88	0.56
1:A:400:LEU:HD21	1:A:1003:VAL:HG21	1.87	0.56
1:A:545:TYR:HB2	1:A:1022:VAL:HG11	1.87	0.56
1:A:971:ARG:O	1:A:974:PRO:HD2	2.05	0.56
1:A:262:LEU:HA	1:A:265:VAL:HG12	1.86	0.56
1:A:569:GLN:HG3	1:A:668:LEU:HB2	1.88	0.56
1:A:1013:THR:HG23	1:A:1014:ALA:H	1.71	0.56
1:A:991:ILE:C	1:A:993:THR:H	2.09	0.55
1:A:389:SER:HB3	1:A:391:ASN:ND2	2.21	0.55
1:A:571:VAL:HG22	1:A:630:SER:HA	1.88	0.55
1:A:367:ILE:HG12	1:A:492:LEU:O	2.06	0.55
1:A:384:ALA:HB2	1:A:390:ILE:HD11	1.89	0.55
1:A:888:LEU:HD23	1:A:898:PRO:HA	1.89	0.55
1:A:722:GLU:O	1:A:723:ASP:HB2	2.05	0.54
1:A:978:THR:C	1:A:980:LEU:H	2.09	0.54
1:A:367:ILE:H	1:A:368:PRO:HD2	1.72	0.54
1:A:41:PRO:HG2	1:A:94:PHE:HB2	1.90	0.54
1:A:864:TYR:CD2	1:A:865:GLN:HA	2.43	0.54
1:A:350:LEU:HD11	1:A:984:LEU:HB2	1.88	0.54
1:A:392:THR:HG23	1:A:395:MET:HB2	1.90	0.54
1:A:562:SER:HB3	1:A:924:ASP:HB3	1.90	0.54
1:A:488:LEU:O	1:A:490:PRO:HD2	2.07	0.54
1:A:831:ALA:HA	1:A:840:ALA:HB1	1.89	0.54
1:A:890:ALA:O	1:A:891:LEU:HB2	2.08	0.54
1:A:864:TYR:HD2	1:A:865:GLN:HA	1.73	0.54
1:A:872:GLN:O	1:A:876:LEU:HB2	2.08	0.54
1:A:45:ILE:HD12	1:A:90:ILE:HB	1.89	0.54
1:A:555:LEU:HB3	1:A:913:LEU:HD22	1.90	0.53
1:A:396:PHE:O	1:A:399:VAL:HG22	2.08	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:540:ARG:O	1:A:540:ARG:HG2	2.07	0.53
1:A:400:LEU:HD11	1:A:1003:VAL:HG22	1.91	0.53
1:A:563:PHE:HE1	1:A:868:LEU:HD23	1.74	0.53
1:A:23:GLY:HA2	1:A:381:ALA:HB2	1.90	0.52
1:A:445:ILE:O	1:A:449:LEU:HD23	2.10	0.52
1:A:901:VAL:O	1:A:903:LEU:N	2.39	0.52
1:A:986:VAL:HG11	1:A:1007:VAL:HB	1.90	0.52
1:A:34:GLN:HG3	1:A:35:TYR:H	1.75	0.52
1:A:836:SER:O	1:A:838:GLY:N	2.43	0.52
1:A:979:SER:OG	1:A:1015:THR:HG23	2.10	0.52
1:A:820:ASN:HD22	1:A:820:ASN:N	2.07	0.52
1:A:149:MET:HB3	1:A:153:ASP:HB3	1.92	0.52
1:A:862:MET:C	1:A:864:TYR:H	2.11	0.52
1:A:45:ILE:O	1:A:89:GLN:HA	2.09	0.52
1:A:390:ILE:HG22	1:A:390:ILE:O	2.10	0.52
1:A:154:ILE:HG22	1:A:287:SER:HB3	1.92	0.52
1:A:40:PRO:HD2	1:A:674:LEU:HD21	1.92	0.52
1:A:831:ALA:O	1:A:832:ALA:HB2	2.09	0.52
1:A:452:VAL:HG12	1:A:932:LEU:HD22	1.92	0.51
1:A:1000:GLN:HA	1:A:1003:VAL:HG12	1.93	0.51
1:A:375:VAL:HG21	1:A:405:LEU:HB2	1.92	0.51
1:A:682:PHE:HB3	1:A:827:ILE:HG22	1.93	0.51
1:A:450:SER:HB3	1:A:454:VAL:HG22	1.92	0.51
1:A:782:LEU:HB2	1:A:783:PRO:HD2	1.93	0.51
1:A:126:GLY:O	1:A:127:VAL:HG22	2.11	0.50
1:A:851:LEU:HB3	1:A:852:PRO:HD2	1.92	0.50
1:A:897:ILE:N	1:A:898:PRO:CD	2.73	0.50
1:A:1027:VAL:HG23	1:A:1028:VAL:HG23	1.93	0.50
1:A:984:LEU:HA	1:A:987:MET:HB2	1.92	0.50
1:A:1008:MET:HA	1:A:1011:MET:HB2	1.93	0.50
1:A:974:PRO:C	1:A:976:LEU:H	2.15	0.50
1:A:562:SER:HB2	1:A:922:THR:HG23	1.93	0.50
1:A:640:GLU:HA	1:A:643:LYS:NZ	2.25	0.50
1:A:722:GLU:O	1:A:723:ASP:CB	2.59	0.50
1:A:99:ASP:HB3	1:A:102:ILE:HG22	1.93	0.50
1:A:463:THR:OG1	1:A:867:ARG:HB2	2.12	0.50
1:A:973:ARG:CB	1:A:974:PRO:HD3	2.36	0.50
1:A:21:LEU:O	1:A:25:LEU:HB2	2.11	0.49
1:A:454:VAL:HG13	1:A:475:VAL:HG21	1.94	0.49
1:A:1022:VAL:O	1:A:1024:VAL:N	2.41	0.49
1:A:718:PRO:HA	1:A:827:ILE:H	1.75	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:468:ARG:HG3	1:A:472:ILE:HD13	1.93	0.49
1:A:712:MET:HG3	1:A:835:LYS:HD3	1.94	0.49
1:A:990:VAL:HG23	1:A:991:ILE:HG13	1.93	0.49
1:A:172:VAL:HG11	1:A:175:VAL:HG23	1.94	0.49
1:A:594:VAL:C	1:A:596:HIS:H	2.15	0.49
1:A:686:ASP:HB3	1:A:823:PRO:HG2	1.94	0.49
1:A:355:MET:HB3	1:A:365:THR:HG22	1.94	0.49
1:A:410:ILE:HG13	1:A:411:VAL:N	2.27	0.48
1:A:166:ILE:O	1:A:169:THR:N	2.37	0.48
1:A:38:ILE:H	1:A:38:ILE:HD13	1.79	0.48
1:A:144:ASN:OD1	1:A:146:ASP:O	2.31	0.48
1:A:360:GLN:O	1:A:361:ASN:HB2	2.12	0.48
1:A:465:ALA:O	1:A:469:GLN:N	2.46	0.48
1:A:472:ILE:O	1:A:476:SER:N	2.40	0.48
1:A:973:ARG:CB	1:A:974:PRO:CD	2.91	0.48
1:A:617:PHE:O	1:A:618:ALA:HB3	2.13	0.48
1:A:896:SER:HB2	1:A:1032:ARG:HG3	1.95	0.48
1:A:885:PHE:HD1	1:A:898:PRO:HB3	1.78	0.48
1:A:924:ASP:O	1:A:928:GLN:HB2	2.14	0.48
1:A:149:MET:O	1:A:150:THR:CB	2.61	0.48
1:A:383:LEU:HB3	1:A:390:ILE:HG13	1.96	0.48
1:A:970:MET:O	1:A:971:ARG:HB3	2.13	0.47
1:A:249:ILE:HB	1:A:262:LEU:CD2	2.44	0.47
1:A:809:TRP:O	1:A:810:GLU:HB3	2.13	0.47
1:A:222:THR:OG1	1:A:223:PRO:HD3	2.15	0.47
1:A:456:MET:HG2	1:A:467:TYR:HB3	1.95	0.47
1:A:925:VAL:O	1:A:925:VAL:HG12	2.14	0.47
1:A:146:ASP:O	1:A:147:GLY:C	2.53	0.47
1:A:682:PHE:HD1	1:A:859:TRP:CH2	2.33	0.47
1:A:912:ALA:HB1	1:A:927:PHE:HE1	1.80	0.47
1:A:160:ALA:HA	1:A:767:ARG:NH1	2.30	0.47
1:A:23:GLY:HA3	1:A:377:LEU:O	2.15	0.47
1:A:864:TYR:HD1	1:A:868:LEU:HD11	1.79	0.47
1:A:355:MET:HE1	1:A:359:LEU:HD11	1.98	0.46
1:A:682:PHE:HB3	1:A:827:ILE:HG21	1.97	0.46
1:A:921:LEU:HD11	1:A:1002:ALA:HA	1.96	0.46
1:A:139:VAL:HG22	1:A:290:GLY:HA2	1.96	0.46
1:A:975:ILE:HD12	1:A:975:ILE:H	1.81	0.46
1:A:249:ILE:HB	1:A:262:LEU:HD23	1.97	0.46
1:A:975:ILE:O	1:A:975:ILE:HG22	2.14	0.46
1:A:18:ILE:HG22	1:A:19:ILE:H	1.81	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:463:THR:HA	1:A:466:ILE:HD12	1.98	0.46
1:A:60:THR:HG23	1:A:61:VAL:HG23	1.98	0.46
1:A:901:VAL:C	1:A:903:LEU:N	2.68	0.46
1:A:456:MET:HG3	1:A:467:TYR:CB	2.36	0.46
1:A:873:ALA:N	1:A:874:PRO:CD	2.79	0.46
1:A:330:THR:N	1:A:331:PRO:CD	2.79	0.46
1:A:1013:THR:O	1:A:1015:THR:N	2.49	0.46
1:A:462:SER:C	1:A:464:GLY:H	2.20	0.46
1:A:131:LYS:HD2	1:A:295:THR:HB	1.98	0.45
1:A:488:LEU:HG	1:A:489:THR:H	1.80	0.45
1:A:851:LEU:HB3	1:A:852:PRO:CD	2.45	0.45
1:A:139:VAL:O	1:A:326:PRO:HD2	2.16	0.45
1:A:151:GLN:HG2	1:A:278:ILE:HG22	1.98	0.45
1:A:570:GLY:HA2	1:A:637:ARG:HH22	1.81	0.45
1:A:831:ALA:O	1:A:832:ALA:CB	2.65	0.45
1:A:831:ALA:HA	1:A:840:ALA:CB	2.46	0.45
1:A:354:VAL:O	1:A:354:VAL:HG12	2.17	0.45
1:A:442:LEU:O	1:A:482:VAL:HG21	2.16	0.45
1:A:895:TRP:HA	1:A:898:PRO:HG2	1.98	0.45
1:A:968:VAL:HA	1:A:971:ARG:NH2	2.32	0.45
1:A:372:VAL:HG11	1:A:406:VAL:HG22	1.98	0.45
1:A:419:VAL:HA	1:A:423:GLU:HG2	1.99	0.45
1:A:581:GLY:CA	1:A:582:ALA:HB3	2.47	0.45
1:A:859:TRP:HB2	1:A:863:SER:OG	2.17	0.45
1:A:616:GLY:HA3	1:A:624:THR:HB	1.98	0.45
1:A:1007:VAL:O	1:A:1011:MET:HB2	2.17	0.45
1:A:392:THR:C	1:A:394:THR:H	2.20	0.45
1:A:355:MET:HE3	1:A:359:LEU:HD11	1.98	0.45
1:A:704:ALA:O	1:A:708:LYS:HG2	2.17	0.45
1:A:65:ILE:HD12	1:A:111:LEU:HD12	1.99	0.45
1:A:819:TYR:HE1	1:A:860:THR:HG23	1.81	0.45
1:A:141:GLY:HA2	1:A:288:GLY:HA2	1.99	0.45
1:A:34:GLN:HB3	1:A:333:VAL:HG22	1.98	0.45
1:A:379:THR:HG21	1:A:473:THR:HG23	1.99	0.45
1:A:878:ALA:O	1:A:882:ILE:HG12	2.17	0.44
1:A:452:VAL:CG1	1:A:932:LEU:HD22	2.47	0.44
1:A:664:PHE:O	1:A:665:ALA:HB3	2.17	0.44
1:A:448:VAL:HG11	1:A:888:LEU:HD13	1.99	0.44
1:A:228:GLN:HE21	1:A:229:GLN:H	1.64	0.44
1:A:668:LEU:HA	1:A:669:PRO:HD3	1.87	0.44
1:A:1020:PHE:HE1	1:A:1021:PHE:CE1	2.35	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:36:PRO:HG3	1:A:469:GLN:CD	2.38	0.44
1:A:702:LEU:HD11	1:A:847:LEU:HB3	2.00	0.44
1:A:438:ILE:HG22	1:A:944:LEU:HD21	2.00	0.44
1:A:819:TYR:HE1	1:A:860:THR:CG2	2.30	0.44
1:A:897:ILE:N	1:A:898:PRO:HD2	2.33	0.44
1:A:149:MET:O	1:A:150:THR:HB	2.18	0.44
1:A:392:THR:C	1:A:394:THR:N	2.71	0.44
1:A:489:THR:OG1	1:A:490:PRO:HD2	2.18	0.43
1:A:723:ASP:HA	1:A:813:SER:HA	2.00	0.43
1:A:1014:ALA:O	1:A:1018:ALA:HB3	2.18	0.43
1:A:905:VAL:CG2	1:A:906:PRO:HD3	2.48	0.43
1:A:575:MET:HA	1:A:626:ILE:HG22	2.00	0.43
1:A:184:MET:HB3	1:A:771:VAL:HG13	2.00	0.43
1:A:360:GLN:O	1:A:361:ASN:CB	2.65	0.43
1:A:826:GLU:HB3	1:A:827:ILE:O	2.18	0.43
1:A:33:ALA:HB1	1:A:299:ALA:HB3	2.00	0.43
1:A:598:TYR:HB3	1:A:606:VAL:HG21	2.00	0.43
1:A:721:LEU:HD23	1:A:722:GLU:N	2.33	0.43
1:A:162:MET:O	1:A:166:ILE:HG12	2.19	0.43
1:A:949:ALA:HB3	1:A:1028:VAL:HG21	2.01	0.43
1:A:556:PHE:CD1	1:A:913:LEU:HD23	2.54	0.43
1:A:864:TYR:CD1	1:A:868:LEU:HD11	2.54	0.43
1:A:372:VAL:N	1:A:373:PRO:HD2	2.34	0.43
1:A:394:THR:HB	1:A:470:PHE:HE2	1.83	0.43
1:A:240:LEU:HD22	1:A:245:GLU:HB3	2.01	0.42
1:A:317:PHE:HE2	1:A:323:ILE:HD11	1.84	0.42
1:A:466:ILE:HA	1:A:469:GLN:HB2	2.00	0.42
1:A:892:TYR:O	1:A:897:ILE:HD13	2.19	0.42
1:A:897:ILE:HG23	1:A:943:ILE:HD11	2.00	0.42
1:A:926:TYR:O	1:A:930:GLY:N	2.53	0.42
1:A:114:ALA:HA	1:A:117:LEU:HD13	2.01	0.42
1:A:537:SER:O	1:A:538:THR:C	2.57	0.42
1:A:39:ALA:HA	1:A:40:PRO:HD2	1.91	0.42
1:A:62:THR:HG23	1:A:88:VAL:HG21	2.00	0.42
1:A:912:ALA:HB1	1:A:927:PHE:CE1	2.54	0.42
1:A:318:PRO:HB2	1:A:319:SER:H	1.66	0.42
1:A:470:PHE:C	1:A:472:ILE:N	2.72	0.42
1:A:987:MET:N	1:A:988:PRO:CD	2.82	0.42
1:A:139:VAL:HB	1:A:327:TYR:HB3	2.01	0.42
1:A:310:LEU:HD21	1:A:323:ILE:HD13	2.02	0.42
1:A:819:TYR:CE1	1:A:860:THR:HG23	2.54	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:879:ILE:O	1:A:879:ILE:HG22	2.20	0.42
1:A:1008:MET:HG3	1:A:1009:GLY:N	2.35	0.42
1:A:65:ILE:HD11	1:A:118:LEU:HD11	2.02	0.42
1:A:56:THR:HG23	1:A:57:VAL:N	2.35	0.42
1:A:690:LEU:HB3	1:A:691:GLY:H	1.75	0.42
1:A:473:THR:HA	1:A:476:SER:HB2	2.00	0.41
1:A:764:ASP:HB3	1:A:769:LYS:HD3	2.02	0.41
1:A:815:ARG:CG	1:A:815:ARG:NH1	2.83	0.41
1:A:183:ALA:HB3	1:A:185:ARG:HD3	2.02	0.41
1:A:178:PHE:HB2	1:A:288:GLY:H	1.85	0.41
1:A:606:VAL:HG13	1:A:629:VAL:HG13	2.02	0.41
1:A:634:TRP:HA	1:A:637:ARG:HE	1.85	0.41
1:A:817:GLU:HB2	1:A:824:SER:O	2.21	0.41
1:A:602:GLU:HG2	1:A:605:ASN:HB2	2.03	0.41
1:A:133:SER:H	1:A:292:LYS:HE3	1.85	0.41
1:A:144:ASN:HA	1:A:320:GLY:O	2.21	0.41
1:A:782:LEU:CB	1:A:783:PRO:HD2	2.49	0.41
1:A:863:SER:O	1:A:864:TYR:CD2	2.67	0.41
1:A:867:ARG:CG	1:A:868:LEU:N	2.82	0.41
1:A:991:ILE:O	1:A:993:THR:N	2.49	0.41
1:A:330:THR:N	1:A:331:PRO:HD2	2.36	0.41
1:A:743:ILE:HA	1:A:746:ILE:HD12	2.03	0.41
1:A:864:TYR:CG	1:A:866:GLU:N	2.89	0.41
1:A:439:GLN:HG3	1:A:440:GLY:N	2.36	0.41
1:A:226:LYS:H	1:A:226:LYS:HG3	1.62	0.40
1:A:564:LEU:HA	1:A:565:PRO:HD3	1.92	0.40
1:A:886:LEU:O	1:A:887:CYS:CB	2.68	0.40
1:A:218:GLN:HB3	1:A:233:SER:HA	2.03	0.40
1:A:621:GLY:C	1:A:623:ASN:H	2.24	0.40
1:A:570:GLY:O	1:A:631:LEU:HB2	2.19	0.40
1:A:862:MET:SD	1:A:863:SER:N	2.94	0.40
1:A:1021:PHE:O	1:A:1022:VAL:O	2.40	0.40
1:A:305:ALA:HA	1:A:308:ALA:HB3	2.04	0.40
1:A:453:PHE:C	1:A:471:SER:HB3	2.41	0.40
1:A:28:LEU:C	1:A:30:LEU:H	2.25	0.40
1:A:384:ALA:O	1:A:385:ALA:HB2	2.21	0.40
1:A:930:GLY:HA2	1:A:933:THR:OG1	2.21	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	1012/1053 (96%)	770 (76%)	179 (18%)	63 (6%)	1	21

All (63) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	36	PRO
1	A	150	THR
1	A	166	ILE
1	A	167	SER
1	A	358	PHE
1	A	361	ASN
1	A	386	PHE
1	A	390	ILE
1	A	470	PHE
1	A	489	THR
1	A	703	LEU
1	A	723	ASP
1	A	802	SER
1	A	832	ALA
1	A	837	THR
1	A	971	ARG
1	A	982	PHE
1	A	983	ILE
1	A	1014	ALA
1	A	1022	VAL
1	A	127	VAL
1	A	147	GLY
1	A	256	ASP
1	A	318	PRO
1	A	539	GLY
1	A	557	VAL
1	A	581	GLY
1	A	673	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	674	LEU
1	A	677	ALA
1	A	862	MET
1	A	975	ILE
1	A	991	ILE
1	A	294	ALA
1	A	297	ALA
1	A	344	LEU
1	A	381	ALA
1	A	427	PRO
1	A	538	THR
1	A	638	PRO
1	A	864	TYR
1	A	866	GLU
1	A	867	ARG
1	A	898	PRO
1	A	901	VAL
1	A	954	ASP
1	A	367	ILE
1	A	428	LYS
1	A	579	PRO
1	A	659	LYS
1	A	709	HIS
1	A	713	LEU
1	A	721	LEU
1	A	902	MET
1	A	1013	THR
1	A	226	LYS
1	A	385	ALA
1	A	464	GLY
1	A	809	TRP
1	A	827	ILE
1	A	968	VAL
1	A	1023	PRO
1	A	19	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	826/858 (96%)	702 (85%)	124 (15%)	3 21

All (124) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	ARG
1	A	10	ILE
1	A	13	TRP
1	A	25	LEU
1	A	38	ILE
1	A	49	TYR
1	A	58	GLN
1	A	68	ASN
1	A	108	GLN
1	A	125	GLN
1	A	145	THR
1	A	152	GLU
1	A	162	MET
1	A	176	GLN
1	A	177	LEU
1	A	194	ASN
1	A	208	LYS
1	A	222	THR
1	A	226	LYS
1	A	230	LEU
1	A	239	ARG
1	A	252	LYS
1	A	255	GLN
1	A	261	LEU
1	A	262	LEU
1	A	265	VAL
1	A	277	ILE
1	A	293	LEU
1	A	298	ASN
1	A	313	MET
1	A	330	THR
1	A	344	LEU
1	A	357	LEU
1	A	366	LEU
1	A	375	VAL
1	A	377	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	388	PHE
1	A	391	ASN
1	A	395	MET
1	A	404	LEU
1	A	410	ILE
1	A	415	ASN
1	A	423	GLU
1	A	429	GLU
1	A	432	ARG
1	A	452	VAL
1	A	458	PHE
1	A	469	GLN
1	A	473	THR
1	A	480	LEU
1	A	482	VAL
1	A	483	LEU
1	A	489	THR
1	A	513	PHE
1	A	516	PHE
1	A	518	ARG
1	A	519	MET
1	A	520	PHE
1	A	535	LEU
1	A	540	ARG
1	A	546	LEU
1	A	552	MET
1	A	555	LEU
1	A	556	PHE
1	A	566	ASP
1	A	567	GLU
1	A	568	ASP
1	A	569	GLN
1	A	586	ARG
1	A	588	GLN
1	A	601	LYS
1	A	637	ARG
1	A	643	LYS
1	A	650	ARG
1	A	657	GLN
1	A	659	LYS
1	A	663	VAL
1	A	674	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	693	GLU
1	A	703	LEU
1	A	709	HIS
1	A	714	THR
1	A	743	ILE
1	A	760	ASN
1	A	767	ARG
1	A	795	ASP
1	A	797	GLN
1	A	798	MET
1	A	815	ARG
1	A	820	ASN
1	A	843	LEU
1	A	847	LEU
1	A	853	THR
1	A	858	ASP
1	A	860	THR
1	A	862	MET
1	A	863	SER
1	A	864	TYR
1	A	865	GLN
1	A	868	LEU
1	A	871	ASN
1	A	872	GLN
1	A	884	VAL
1	A	895	TRP
1	A	907	LEU
1	A	913	LEU
1	A	921	LEU
1	A	922	THR
1	A	940	LYS
1	A	944	LEU
1	A	952	LEU
1	A	971	ARG
1	A	972	LEU
1	A	976	LEU
1	A	978	THR
1	A	982	PHE
1	A	984	LEU
1	A	989	LEU
1	A	991	ILE
1	A	1011	MET

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1013	THR
1	A	1022	VAL
1	A	1031	ARG
1	A	1033	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	GLN
1	A	58	GLN
1	A	104	GLN
1	A	108	GLN
1	A	112	GLN
1	A	123	GLN
1	A	151	GLN
1	A	176	GLN
1	A	211	ASN
1	A	228	GLN
1	A	254	ASN
1	A	298	ASN
1	A	360	GLN
1	A	391	ASN
1	A	604	ASN
1	A	605	ASN
1	A	622	GLN
1	A	657	GLN
1	A	687	GLN
1	A	744	ASN
1	A	760	ASN
1	A	820	ASN
1	A	871	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.