



Full wwPDB X-ray Structure Validation Report ⓘ

May 7, 2026 – 10:43 AM EDT

PDB ID : 4UAQ / pdb_00004uaq
Title : Crystal structure of the accessory translocation ATPase, SecA2, from Mycobacterium tuberculosis
Authors : Swanson-Smith, S.; Ioerger, T.R.; Rigel, N.W.; Miller, B.K.; Braunstein, M.; Sacchettini, J.C.; TB Structural Genomics Consortium (TBSGC)
Deposited on : 2014-08-11
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
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

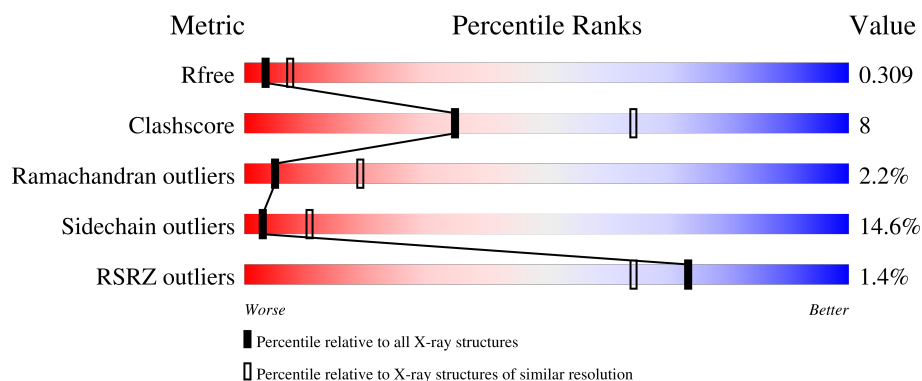
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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	778	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 4961 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 Protein translocase subunit SecA 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	705	Total	C	N	O	S	Se	0	0	0
			4894	3037	898	949	1	9			

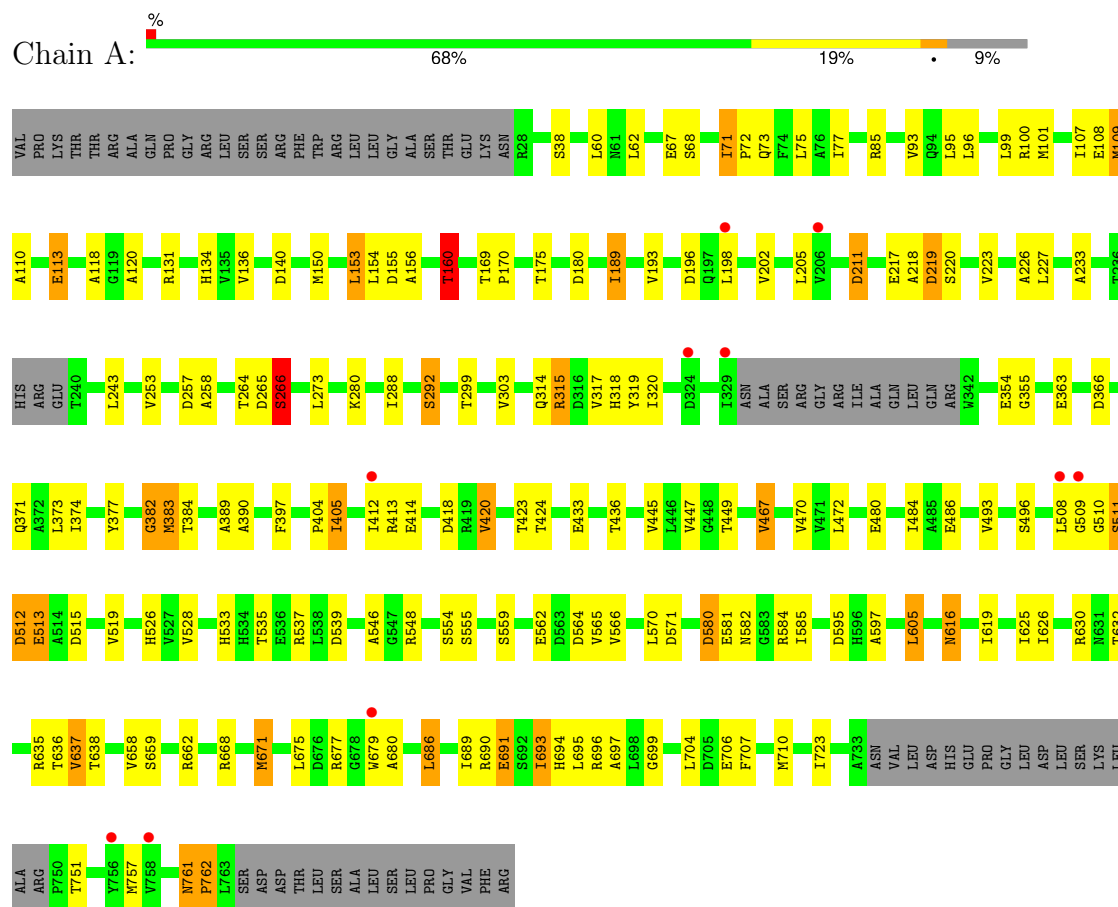
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	67	Total	O	0	0
			67	67		

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: Protein translocase subunit SecA 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	39.60Å 162.09Å 67.31Å 90.00° 95.87° 90.00°	Depositor
Resolution (Å)	35.64 – 2.80 35.64 – 2.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (35.64-2.80) 78.3 (35.64-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.62 (at 2.81Å)	Xtriage
Refinement program	BUSTER 2.8.0	Depositor
R, R_{free}	0.211 , 0.281 0.227 , 0.309	Depositor DCC
R_{free} test set	835 reflections (5.14%)	wwPDB-VP
Wilson B-factor (Å ²)	79.4	Xtriage
Anisotropy	0.251	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 60.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4961	wwPDB-VP
Average B, all atoms (Å ²)	84.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.20% 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 i

5.1 Standard geometry i

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	0.88	0/4958	1.57	49/6778 (0.7%)

There are no bond length outliers.

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	467	VAL	N-CA-C	8.86	115.62	107.56
1	A	218	ALA	CA-C-N	7.67	131.46	120.79
1	A	218	ALA	C-N-CA	7.67	131.46	120.79
1	A	637	VAL	CA-C-N	7.49	130.65	120.54
1	A	637	VAL	C-N-CA	7.49	130.65	120.54
1	A	160	THR	CB-CA-C	6.95	121.89	109.38
1	A	580	ASP	CA-CB-CG	6.74	119.34	112.60
1	A	355	GLY	CA-C-N	-6.57	110.15	121.97
1	A	355	GLY	C-N-CA	-6.57	110.15	121.97
1	A	571	ASP	CA-C-N	6.55	129.36	120.38
1	A	571	ASP	C-N-CA	6.55	129.36	120.38
1	A	220	SER	CA-C-N	6.38	129.12	120.77
1	A	220	SER	C-N-CA	6.38	129.12	120.77
1	A	211	ASP	CA-CB-CG	6.17	118.78	112.60
1	A	257	ASP	CA-C-N	6.13	129.62	120.17
1	A	257	ASP	C-N-CA	6.13	129.62	120.17
1	A	265	ASP	CA-C-N	6.11	133.21	121.54
1	A	265	ASP	C-N-CA	6.11	133.21	121.54
1	A	243	LEU	N-CA-C	-6.06	104.79	111.82
1	A	564	ASP	CA-C-N	5.96	128.14	120.70
1	A	564	ASP	C-N-CA	5.96	128.14	120.70
1	A	196	ASP	CA-CB-CG	5.77	118.37	112.60
1	A	243	LEU	CA-C-N	5.76	128.00	120.28
1	A	243	LEU	C-N-CA	5.76	128.00	120.28
1	A	280	LYS	CA-C-N	5.74	128.62	120.53
1	A	280	LYS	C-N-CA	5.74	128.62	120.53
1	A	658	VAL	N-CA-C	-5.67	106.94	111.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	535	THR	CA-C-N	5.56	128.49	120.38
1	A	535	THR	C-N-CA	5.56	128.49	120.38
1	A	258	ALA	N-CA-C	-5.49	104.44	113.50
1	A	280	LYS	N-CA-C	-5.48	105.00	110.97
1	A	257	ASP	N-CA-C	5.45	119.12	109.96
1	A	693	ILE	CA-C-N	5.35	127.39	120.44
1	A	693	ILE	C-N-CA	5.35	127.39	120.44
1	A	616	ASN	CA-C-N	5.34	127.70	120.44
1	A	616	ASN	C-N-CA	5.34	127.70	120.44
1	A	546	ALA	N-CA-C	5.30	120.39	113.88
1	A	382	GLY	N-CA-C	5.29	118.31	110.42
1	A	597	ALA	CA-C-N	5.27	127.80	120.63
1	A	597	ALA	C-N-CA	5.27	127.80	120.63
1	A	140	ASP	CA-CB-CG	5.21	117.81	112.60
1	A	198	LEU	N-CA-C	-5.18	106.88	114.39
1	A	219	ASP	CA-CB-CG	5.16	117.75	112.60
1	A	580	ASP	CA-C-N	5.14	127.68	120.28
1	A	580	ASP	C-N-CA	5.14	127.68	120.28
1	A	253	VAL	CA-C-N	5.10	125.75	119.99
1	A	253	VAL	C-N-CA	5.10	125.75	119.99
1	A	680	ALA	CA-C-N	5.02	127.93	120.31
1	A	680	ALA	C-N-CA	5.02	127.93	120.31

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	4894	0	4392	70	0
2	A	67	0	0	1	0
All	All	4961	0	4392	70	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 8.

All (70) 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:509:GLY:O	1:A:513:GLU:HB2	1.58	1.00
1:A:219:ASP:OD1	1:A:537:ARG:HD2	1.66	0.95
1:A:109:MSE:HE2	1:A:113:GLU:CG	2.09	0.82
1:A:508:LEU:HD22	1:A:519:VAL:HG12	1.65	0.79
1:A:120:ALA:HB3	1:A:150:MSE:HE2	1.66	0.77
1:A:508:LEU:HD22	1:A:519:VAL:CG1	2.16	0.75
1:A:109:MSE:HE2	1:A:113:GLU:HG3	1.70	0.73
1:A:638:THR:HG21	1:A:668:ARG:HB3	1.72	0.71
1:A:120:ALA:HB2	1:A:150:MSE:HG3	1.74	0.70
1:A:510:GLY:O	1:A:512:ASP:N	2.29	0.66
1:A:472:LEU:HD12	1:A:496:SER:HB3	1.82	0.62
1:A:134:HIS:HD1	1:A:377:TYR:HH	1.49	0.60
1:A:60:LEU:HD11	1:A:77:ILE:HD12	1.85	0.59
1:A:526:HIS:ND1	1:A:554:SER:HB2	2.18	0.58
1:A:160:THR:HG22	1:A:180:ASP:OD1	2.03	0.58
1:A:169:THR:HB	1:A:170:PRO:HD2	1.85	0.58
1:A:131:ARG:NH1	1:A:211:ASP:OD1	2.39	0.55
1:A:616:ASN:HA	1:A:619:ILE:HD12	1.89	0.55
1:A:101:MSE:HE3	1:A:382:GLY:C	2.33	0.54
1:A:314:GLN:O	1:A:318:HIS:HB2	2.10	0.52
1:A:223:VAL:HG21	1:A:390:ALA:HB1	1.92	0.51
1:A:319:TYR:OH	1:A:354:GLU:OE2	2.20	0.51
1:A:136:VAL:HG22	1:A:189:ILE:HD13	1.91	0.51
1:A:363:GLU:CD	1:A:677:ARG:HH22	2.19	0.51
1:A:508:LEU:HD22	1:A:519:VAL:HG11	1.93	0.50
1:A:292:SER:HB2	2:A:809:HOH:O	2.11	0.50
1:A:423:THR:HA	1:A:562:GLU:HG3	1.94	0.50
1:A:619:ILE:HG12	1:A:686:LEU:HD12	1.94	0.50
1:A:108:GLU:HB3	1:A:404:PRO:HA	1.94	0.50
1:A:371:GLN:NE2	1:A:397:PHE:HB3	2.27	0.49
1:A:233:ALA:HA	1:A:363:GLU:O	2.12	0.49
1:A:219:ASP:HB2	1:A:384:THR:HG21	1.95	0.49
1:A:659:SER:HB3	1:A:662:ARG:HB2	1.96	0.48
1:A:72:PRO:HA	1:A:75:LEU:HD12	1.96	0.48
1:A:109:MSE:HE2	1:A:113:GLU:CB	2.44	0.47
1:A:566:VAL:HG13	1:A:570:LEU:HD12	1.96	0.47
1:A:120:ALA:CB	1:A:150:MSE:HE2	2.41	0.47
1:A:635:ARG:O	1:A:637:VAL:HG23	2.15	0.47
1:A:761:ASN:N	1:A:762:PRO:HD3	2.29	0.47
1:A:101:MSE:HE3	1:A:382:GLY:O	2.15	0.47
1:A:110:ALA:O	1:A:113:GLU:HB2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:85:ARG:HD2	1:A:156:ALA:HB2	1.97	0.46
1:A:120:ALA:CB	1:A:150:MSE:HG3	2.45	0.46
1:A:226:ALA:HB1	1:A:371:GLN:HB2	1.96	0.46
1:A:704:LEU:C	1:A:706:GLU:H	2.23	0.46
1:A:315:ARG:HD2	1:A:354:GLU:OE1	2.16	0.46
1:A:100:ARG:HD2	1:A:100:ARG:HA	1.76	0.46
1:A:109:MSE:HE2	1:A:113:GLU:HB3	1.98	0.45
1:A:626:ILE:HG13	1:A:679:TRP:CD1	2.51	0.45
1:A:264:THR:C	1:A:266:SER:H	2.25	0.44
1:A:118:ALA:HB3	1:A:383:MSE:HE1	1.99	0.44
1:A:671:MSE:HE1	1:A:723:ILE:HG22	2.00	0.44
1:A:486:GLU:HA	1:A:510:GLY:HA2	2.00	0.43
1:A:691:GLU:C	1:A:693:ILE:H	2.26	0.43
1:A:467:VAL:HG13	1:A:493:VAL:HG21	2.01	0.43
1:A:695:LEU:C	1:A:697:ALA:H	2.27	0.43
1:A:62:LEU:HD22	1:A:71:ILE:HD12	2.00	0.43
1:A:150:MSE:HE3	1:A:153:LEU:HD22	2.00	0.43
1:A:420:VAL:HA	1:A:559:SER:O	2.19	0.43
1:A:447:VAL:HG22	1:A:528:VAL:HB	2.01	0.42
1:A:299:THR:O	1:A:303:VAL:HG23	2.19	0.42
1:A:189:ILE:HG22	1:A:373:LEU:HD21	2.02	0.42
1:A:433:GLU:HA	1:A:436:THR:HG22	2.01	0.42
1:A:107:ILE:HB	1:A:405:ILE:HD13	2.01	0.41
1:A:533:HIS:ND1	1:A:539:ASP:OD1	2.54	0.41
1:A:189:ILE:O	1:A:193:VAL:HG23	2.20	0.41
1:A:690:ARG:HG3	1:A:707:PHE:CE1	2.56	0.41
1:A:605:LEU:HD12	1:A:605:LEU:HA	1.96	0.41
1:A:108:GLU:HA	1:A:384:THR:O	2.21	0.40
1:A:75:LEU:HD22	1:A:95:LEU:HB3	2.03	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	697/778 (90%)	612 (88%)	70 (10%)	15 (2%)	5	19

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	320	ILE
1	A	511	SER
1	A	636	THR
1	A	751	THR
1	A	762	PRO
1	A	68	SER
1	A	266	SER
1	A	696	ARG
1	A	699	GLY
1	A	315	ARG
1	A	512	ASP
1	A	38	SER
1	A	202	VAL
1	A	389	ALA
1	A	761	ASN

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	419/620 (68%)	358 (85%)	61 (15%)	3	11

All (61) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	67	GLU
1	A	71	ILE
1	A	73	GLN
1	A	93	VAL
1	A	96	LEU
1	A	99	LEU

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Mol	Chain	Res	Type
1	A	109	MSE
1	A	113	GLU
1	A	153	LEU
1	A	154	LEU
1	A	155	ASP
1	A	160	THR
1	A	175	THR
1	A	189	ILE
1	A	205	LEU
1	A	217	GLU
1	A	227	LEU
1	A	266	SER
1	A	273	LEU
1	A	288	ILE
1	A	292	SER
1	A	317	VAL
1	A	366	ASP
1	A	374	ILE
1	A	383	MSE
1	A	405	ILE
1	A	412	ILE
1	A	413	ARG
1	A	414	GLU
1	A	418	ASP
1	A	420	VAL
1	A	424	THR
1	A	445	VAL
1	A	449	THR
1	A	470	VAL
1	A	480	GLU
1	A	484	ILE
1	A	511	SER
1	A	513	GLU
1	A	515	ASP
1	A	548	ARG
1	A	555	SER
1	A	565	VAL
1	A	580	ASP
1	A	581	GLU
1	A	582	ASN
1	A	584	ARG
1	A	585	ILE

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Mol	Chain	Res	Type
1	A	595	ASP
1	A	605	LEU
1	A	625	ILE
1	A	630	ARG
1	A	632	THR
1	A	671	MSE
1	A	675	LEU
1	A	686	LEU
1	A	689	ILE
1	A	691	GLU
1	A	694	HIS
1	A	710	MSE
1	A	757	MSE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	73	GLN
1	A	203	ASN
1	A	408	ASN
1	A	411	ASN
1	A	443	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 [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	695/778 (89%)	0.07	10 (1%) 73 64	30, 82, 120, 182	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	509	GLY	3.8
1	A	758	VAL	3.0
1	A	329	ILE	2.7
1	A	679	TRP	2.7
1	A	198	LEU	2.5
1	A	508	LEU	2.4
1	A	756	TYR	2.4
1	A	412	ILE	2.1
1	A	324	ASP	2.1
1	A	206	VAL	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.