



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 12:08 AM UTC

PDB ID : 9MVG / pdb_00009mvg
Title : Structure of SciW variant L66A bound to the Rhs1 transmembrane domain
Authors : Van Schepdael, M.A.; Prehna, G.
Deposited on : 2025-01-15
Resolution : 3.05 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

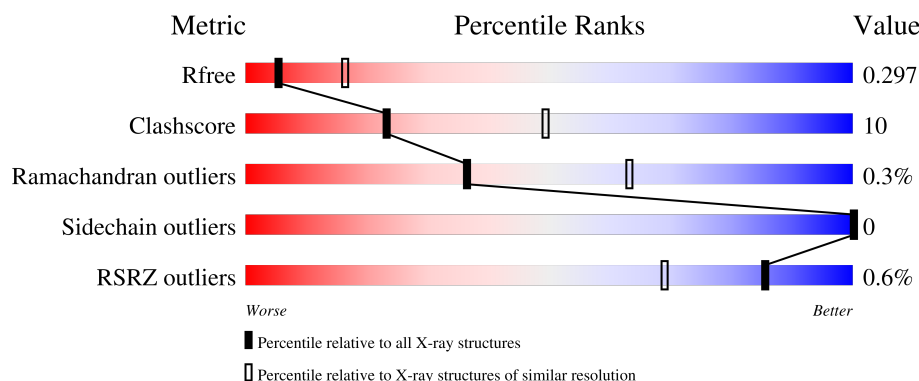
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.05 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	2469 (3.10-3.02)
Clashscore	190562	2569 (3.10-3.02)
Ramachandran outliers	187476	2424 (3.10-3.02)
Sidechain outliers	187428	2423 (3.10-3.02)
RSRZ outliers	180081	2469 (3.10-3.02)

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	148	% 83% 12% 5%
1	B	148	% 75% 22% .
1	D	148	73% 19% 8%
1	E	148	% 70% 21% . 9%
2	C	66	36% 18% . 44%

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Mol	Chain	Length	Quality of chain
2	F	66	42% 14% 44%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9794 atoms, of which 4879 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 SciW protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	141	Total	C	H	N	O	S	0	0	0
			2206	700	1099	194	209	4			
1	B	143	Total	C	H	N	O	S	0	0	0
			2242	710	1116	199	213	4			
1	D	136	Total	C	H	N	O	S	0	0	0
			2124	674	1058	189	200	3			
1	E	135	Total	C	H	N	O	S	0	0	0
			2112	673	1054	184	198	3			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	66	ALA	LEU	variant	UNP H9L4F1
B	66	ALA	LEU	variant	UNP H9L4F1
D	66	ALA	LEU	variant	UNP H9L4F1
E	66	ALA	LEU	variant	UNP H9L4F1

- Molecule 2 is a protein called Rhs1 protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	C	37	Total	C	H	N	O	S	0	0	0
			536	179	276	38	41	2			
2	F	37	Total	C	H	N	O	S	0	0	0
			536	179	276	38	41	2			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	0	MET	-	initiating methionine	UNP A0A767UFH6
C	1	GLY	-	expression tag	UNP A0A767UFH6
C	60	HIS	-	expression tag	UNP A0A767UFH6
C	61	HIS	-	expression tag	UNP A0A767UFH6

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Chain	Residue	Modelled	Actual	Comment	Reference
C	62	HIS	-	expression tag	UNP A0A767UFH6
C	63	HIS	-	expression tag	UNP A0A767UFH6
C	64	HIS	-	expression tag	UNP A0A767UFH6
C	65	HIS	-	expression tag	UNP A0A767UFH6
F	0	MET	-	initiating methionine	UNP A0A767UFH6
F	1	GLY	-	expression tag	UNP A0A767UFH6
F	60	HIS	-	expression tag	UNP A0A767UFH6
F	61	HIS	-	expression tag	UNP A0A767UFH6
F	62	HIS	-	expression tag	UNP A0A767UFH6
F	63	HIS	-	expression tag	UNP A0A767UFH6
F	64	HIS	-	expression tag	UNP A0A767UFH6
F	65	HIS	-	expression tag	UNP A0A767UFH6

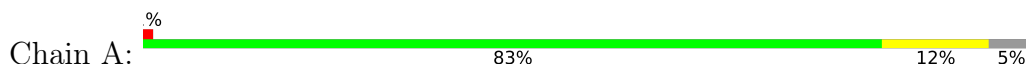
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	22	Total O 22 22	0	0
3	B	12	Total O 12 12	0	0
3	C	2	Total O 2 2	0	0
3	D	2	Total O 2 2	0	0

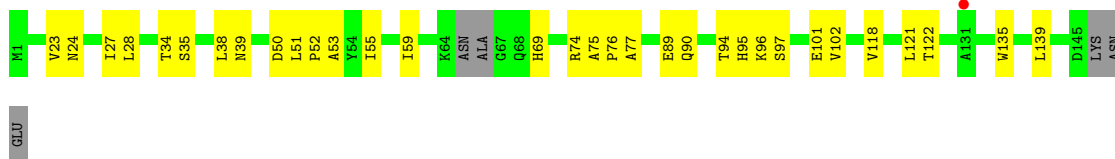
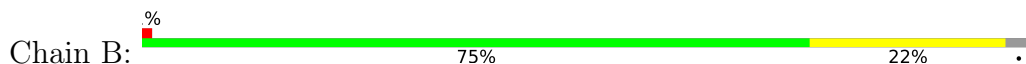
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

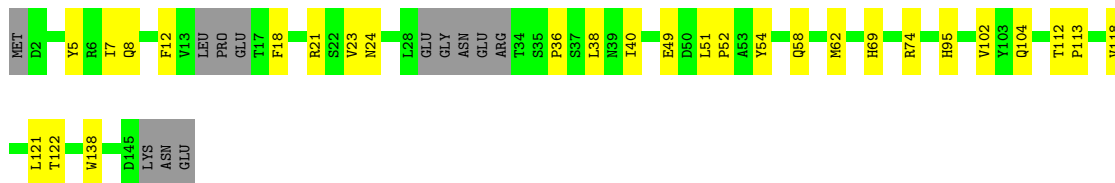
- Molecule 1: SciW protein



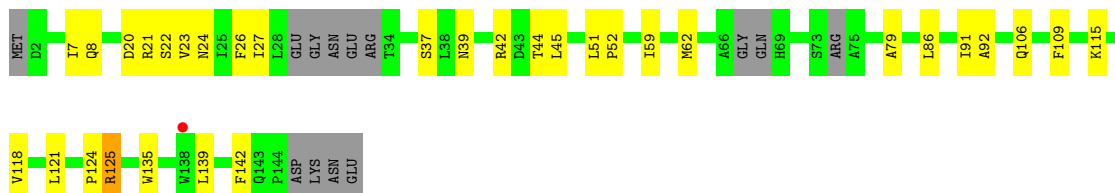
- Molecule 1: SciW protein



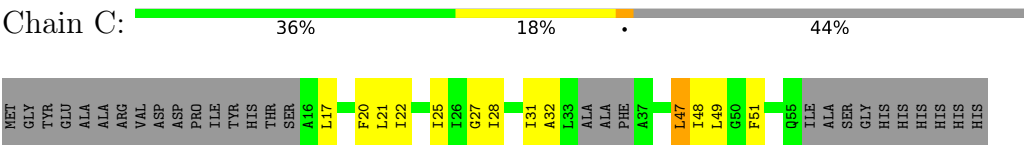
- Molecule 1: SciW protein



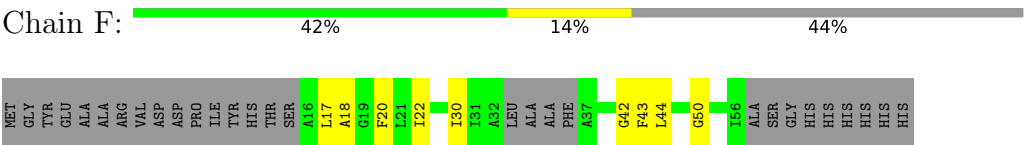
- Molecule 1: SciW protein



● Molecule 2: Rhs1 protein



● Molecule 2: Rhs1 protein



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	90.67Å 52.02Å 177.45Å 90.00° 99.77° 90.00°	Depositor
Resolution (Å)	45.16 – 3.05 45.16 – 3.05	Depositor EDS
% Data completeness (in resolution range)	99.1 (45.16-3.05) 99.7 (45.16-3.05)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.35 (at 3.06Å)	Xtriage
Refinement program	PHENIX 1.21.2_5419	Depositor
R, R_{free}	0.262 , 0.299 0.260 , 0.297	Depositor DCC
R_{free} test set	752 reflections (4.51%)	wwPDB-VP
Wilson B-factor (Å ²)	92.9	Xtriage
Anisotropy	0.321	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 173.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.005 for $1/2^*h-3/2^*k,-1/2^*h-1/2^*k,-1/2^*h+1/2^*k-l$ 0.023 for $1/2^*h+3/2^*k,1/2^*h-1/2^*k,-1/2^*h-1/2^*k-l$	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	9794	wwPDB-VP
Average B, all atoms (Å ²)	194.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.13% 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	0.17	0/1131	0.36	0/1534
1	B	0.15	0/1150	0.37	0/1558
1	D	0.13	0/1088	0.39	0/1474
1	E	0.13	0/1080	0.34	0/1464
2	C	0.12	0/263	0.33	0/352
2	F	0.10	0/263	0.32	0/352
All	All	0.14	0/4975	0.36	0/6734

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	1107	1099	1098	16	0
1	B	1126	1116	1115	30	0
1	D	1066	1058	1055	26	0
1	E	1058	1054	1050	28	0
2	C	260	276	275	18	0
2	F	260	276	275	11	0
3	A	22	0	0	0	0
3	B	12	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	4915	4879	4868	100	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 10.

All (100) 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:B:28:LEU:HD12	1:B:35:SER:HB3	1.64	0.80
2:C:17:LEU:HB3	2:C:22:ILE:HD13	1.72	0.71
2:F:17:LEU:HB3	2:F:22:ILE:HD13	1.74	0.70
1:B:97:SER:HB2	2:C:28:ILE:HD11	1.75	0.69
1:E:44:THR:HG22	1:E:115:LYS:HG2	1.75	0.68
1:D:122:THR:HG21	2:F:50:GLY:O	1.97	0.63
1:B:55:ILE:HD13	1:B:89:GLU:OE1	1.98	0.63
1:D:24:ASN:HA	1:E:22:SER:HB2	1.81	0.60
1:E:21:ARG:NH2	2:F:18:ALA:HB2	2.17	0.60
1:B:122:THR:HG21	2:C:27:GLY:CA	2.32	0.59
2:C:47:LEU:HD22	2:C:48:ILE:HD12	1.83	0.59
1:B:122:THR:HG21	2:C:27:GLY:HA3	1.84	0.59
1:A:104:GLN:HG2	1:A:122:THR:HG23	1.84	0.59
1:E:37:SER:OG	2:F:30:ILE:HG21	2.03	0.58
1:A:23:VAL:HG11	2:C:49:LEU:CD1	2.34	0.58
1:E:21:ARG:CZ	2:F:18:ALA:HB2	2.35	0.57
1:D:7:ILE:HG22	1:D:8:GLN:N	2.20	0.57
1:E:59:ILE:HA	1:E:62:MET:HE3	1.85	0.57
1:B:95:HIS:CD2	2:C:28:ILE:HD12	2.41	0.56
2:C:47:LEU:O	2:C:51:PHE:HD1	1.89	0.55
1:B:74:ARG:HG3	1:B:89:GLU:OE2	2.07	0.55
1:A:27:ILE:HG22	1:A:28:LEU:N	2.21	0.55
1:E:135:TRP:CZ2	1:E:139:LEU:HD11	2.42	0.55
1:E:86:LEU:HD13	1:E:109:PHE:HB3	1.89	0.54
1:B:38:LEU:HD23	1:B:121:LEU:HD13	1.89	0.54
1:D:7:ILE:HG22	1:D:8:GLN:H	1.72	0.54
1:D:112:THR:HB	1:D:113:PRO:HD2	1.89	0.54
1:A:69:HIS:HA	1:A:95:HIS:HB3	1.90	0.54
1:A:23:VAL:HG11	2:C:49:LEU:HD13	1.90	0.54
1:B:51:LEU:HB3	1:B:52:PRO:HD3	1.90	0.54
1:E:91:ILE:HD12	1:E:92:ALA:N	2.24	0.53
1:D:23:VAL:HA	1:D:40:ILE:O	2.09	0.53
1:B:55:ILE:O	1:B:59:ILE:HG12	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:102:VAL:CG1	2:C:31:ILE:HD11	2.40	0.51
1:E:86:LEU:HD12	1:E:86:LEU:C	2.35	0.51
1:A:27:ILE:HG22	1:A:28:LEU:H	1.75	0.51
1:D:5:TYR:HA	1:E:8:GLN:OE1	2.10	0.51
1:E:22:SER:OG	1:E:42:ARG:NH2	2.44	0.51
1:B:34:THR:HG22	1:B:34:THR:O	2.11	0.50
1:B:23:VAL:O	1:B:23:VAL:HG23	2.11	0.50
1:E:106:GLN:OE1	1:E:118:VAL:HG12	2.12	0.50
1:B:102:VAL:HG12	2:C:31:ILE:HD11	1.93	0.49
1:E:23:VAL:O	1:E:23:VAL:HG23	2.12	0.49
1:A:121:LEU:C	1:A:121:LEU:HD23	2.38	0.49
1:B:69:HIS:HA	1:B:95:HIS:HB3	1.95	0.49
1:D:51:LEU:HG	1:D:52:PRO:HD3	1.94	0.49
1:D:102:VAL:HG12	1:D:104:GLN:HG3	1.95	0.49
1:A:51:LEU:HB3	1:A:52:PRO:HD3	1.94	0.48
1:D:69:HIS:HA	1:D:95:HIS:HB3	1.96	0.48
1:D:118:VAL:HG13	2:F:43:PHE:CD1	2.49	0.48
1:A:104:GLN:CG	1:A:122:THR:HG23	2.43	0.48
1:D:38:LEU:HD13	1:D:138:TRP:CD1	2.48	0.47
1:A:62:MET:CE	2:C:47:LEU:HD12	2.45	0.46
1:D:62:MET:HE1	2:F:44:LEU:N	2.30	0.46
2:C:31:ILE:HG13	2:C:32:ALA:N	2.31	0.46
1:E:51:LEU:HB3	1:E:52:PRO:HD3	1.97	0.46
1:B:77:ALA:HB2	1:B:90:GLN:HB3	1.97	0.45
1:E:91:ILE:HD12	1:E:91:ILE:C	2.42	0.45
1:B:95:HIS:O	1:B:102:VAL:HG22	2.17	0.45
1:B:94:THR:OG1	1:B:101:GLU:OE2	2.22	0.45
1:D:12:PHE:HB3	1:E:142:PHE:HA	1.97	0.45
1:D:49:GLU:OE2	1:D:54:TYR:HA	2.17	0.44
1:B:135:TRP:CZ2	1:B:139:LEU:HD11	2.53	0.44
1:A:102:VAL:HG12	1:A:104:GLN:HG3	2.00	0.44
2:C:47:LEU:HD23	2:C:51:PHE:CE1	2.52	0.44
1:B:89:GLU:OE2	1:B:90:GLN:O	2.35	0.43
1:B:118:VAL:HG11	2:C:20:PHE:HA	2.01	0.43
1:B:97:SER:HB2	2:C:28:ILE:CD1	2.47	0.43
1:D:40:ILE:HA	1:D:118:VAL:O	2.19	0.43
1:B:74:ARG:HB3	1:D:74:ARG:HB3	1.99	0.43
1:D:36:PRO:HA	1:D:122:THR:O	2.18	0.43
1:D:118:VAL:HG21	2:F:42:GLY:HA2	2.00	0.43
1:E:24:ASN:O	1:E:39:ASN:HA	2.20	0.42
1:D:121:LEU:C	1:D:121:LEU:HD23	2.44	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:18:PHE:HB3	1:E:26:PHE:HB3	2.02	0.42
1:A:7:ILE:HG12	1:A:10:GLY:O	2.19	0.42
1:A:102:VAL:HB	2:C:51:PHE:CE2	2.54	0.42
1:E:124:PRO:O	1:E:125:ARG:HG2	2.19	0.42
1:B:75:ALA:HB1	1:B:76:PRO:HD2	2.02	0.42
1:E:79:ALA:HB2	1:E:109:PHE:CZ	2.54	0.42
1:E:27:ILE:HG12	2:F:30:ILE:HD12	2.02	0.42
1:A:21:ARG:HG3	1:B:27:ILE:HD11	2.02	0.42
1:E:7:ILE:HG13	1:E:8:GLN:H	1.85	0.42
1:E:45:LEU:HD12	1:E:45:LEU:O	2.19	0.41
1:B:50:ASP:OD1	1:B:53:ALA:CB	2.69	0.41
1:D:24:ASN:HD21	1:E:7:ILE:HD13	1.85	0.41
1:D:51:LEU:N	1:D:52:PRO:HD2	2.35	0.41
1:A:24:ASN:HB2	1:A:40:ILE:HB	2.02	0.41
1:B:95:HIS:N	1:B:101:GLU:OE2	2.54	0.41
1:E:20:ASP:OD2	1:E:42:ARG:NH2	2.53	0.41
1:D:58:GLN:O	1:D:62:MET:HG2	2.20	0.41
1:D:21:ARG:O	1:D:21:ARG:HG3	2.21	0.41
1:D:118:VAL:HG13	2:F:43:PHE:HD1	1.85	0.41
1:B:38:LEU:CD2	1:B:121:LEU:HD13	2.49	0.40
1:B:96:LYS:CG	1:B:101:GLU:OE1	2.68	0.40
1:E:106:GLN:HG2	2:F:20:PHE:CD2	2.56	0.40
1:B:24:ASN:O	1:B:39:ASN:HA	2.21	0.40
2:C:21:LEU:O	2:C:25:ILE:HG12	2.21	0.40
1:A:58:GLN:O	1:A:62:MET:HG2	2.21	0.40
1:E:121:LEU:HD23	1:E:121:LEU:C	2.46	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	137/148 (93%)	131 (96%)	6 (4%)	0	100	100
1	B	139/148 (94%)	134 (96%)	5 (4%)	0	100	100
1	D	130/148 (88%)	121 (93%)	9 (7%)	0	100	100
1	E	127/148 (86%)	120 (94%)	6 (5%)	1 (1%)	16	42
2	C	33/66 (50%)	32 (97%)	0	1 (3%)	3	15
2	F	33/66 (50%)	33 (100%)	0	0	100	100
All	All	599/724 (83%)	571 (95%)	26 (4%)	2 (0%)	36	63

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	47	LEU
1	E	125	ARG

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	119/125 (95%)	119 (100%)	0	100	100
1	B	121/125 (97%)	121 (100%)	0	100	100
1	D	114/125 (91%)	114 (100%)	0	100	100
1	E	114/125 (91%)	114 (100%)	0	100	100
2	C	23/45 (51%)	23 (100%)	0	100	100
2	F	23/45 (51%)	23 (100%)	0	100	100
All	All	514/590 (87%)	514 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	104	GLN

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Mol	Chain	Res	Type
1	B	69	HIS
1	B	95	HIS
1	B	136	ASN
1	D	58	GLN
1	D	106	GLN
1	E	69	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	141/148 (95%)	0.24	2 (1%) 73 51	58, 109, 225, 252	0
1	B	143/148 (96%)	0.05	1 (0%) 84 66	85, 163, 233, 289	0
1	D	136/148 (91%)	-0.18	0 100 100	162, 229, 272, 316	0
1	E	135/148 (91%)	-0.06	1 (0%) 84 66	204, 252, 300, 357	0
2	C	37/66 (56%)	0.41	0 100 100	108, 166, 207, 210	0
2	F	37/66 (56%)	0.04	0 100 100	188, 249, 301, 342	0
All	All	629/724 (86%)	0.04	4 (0%) 85 69	58, 203, 275, 357	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	69	HIS	3.7
1	E	138	TRP	3.1
1	B	131	ALA	2.9
1	A	110	ILE	2.9

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.