



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 02:46 AM UTC

PDB ID : 8JV0 / pdb_00008jv0
Title : Crystal structure of the SLA-2*1001 allele and ASFV antigenic peptide at 2.2Å resolution
Authors : Wang, S.
Deposited on : 2023-06-27
Resolution : 2.20 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

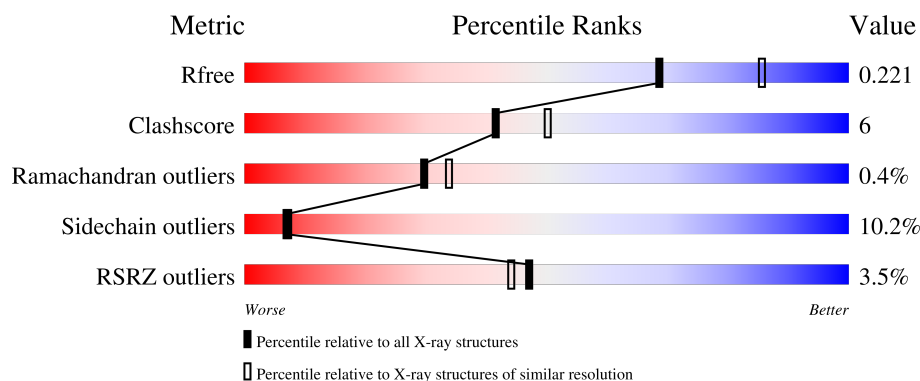
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	275	3% 79% 19% .
1	D	275	5% 81% 17% .
2	B	98	82% 15% ..
2	E	98	2% 66% 27% 7%
3	C	9	44% 56%

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Mol	Chain	Length	Quality of chain
3	F	9	 A horizontal bar chart showing the quality of chain F. The bar is divided into four segments: a small red segment at the beginning labeled '11%', followed by a large green segment labeled '56%', then a yellow segment labeled '33%', and a small orange segment at the end labeled '11%'.

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6333 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 MHC class I antigen.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	275	Total	C	N	O	S	0	0	0
			2235	1391	399	435	10			
1	D	275	Total	C	N	O	S	0	0	0
			2235	1391	399	435	10			

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	97	Total	C	N	O	S	0	0	0
			799	510	140	146	3			
2	E	98	Total	C	N	O	S	0	0	0
			806	515	141	147	3			

- Molecule 3 is a protein called TYR-MET-ASN-CYS-SER-LEU-PRO-THR-TYR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	9	Total	C	N	O	S	0	0	0
			74	48	10	14	2			
3	F	9	Total	C	N	O	S	0	0	0
			75	48	10	15	2			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	39	Total	O	0	0
			39	39		
4	B	23	Total	O	0	0
			23	23		
4	D	33	Total	O	0	0
			33	33		
4	E	13	Total	O	0	0
			13	13		

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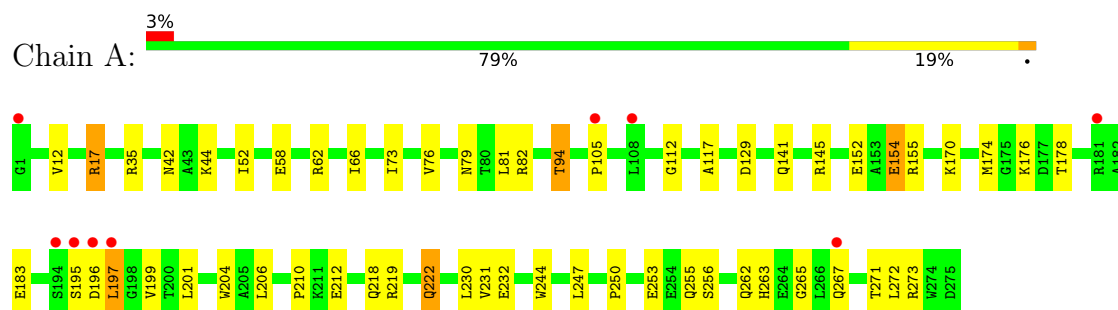
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	F	1	Total	O	0	0
			1	1		

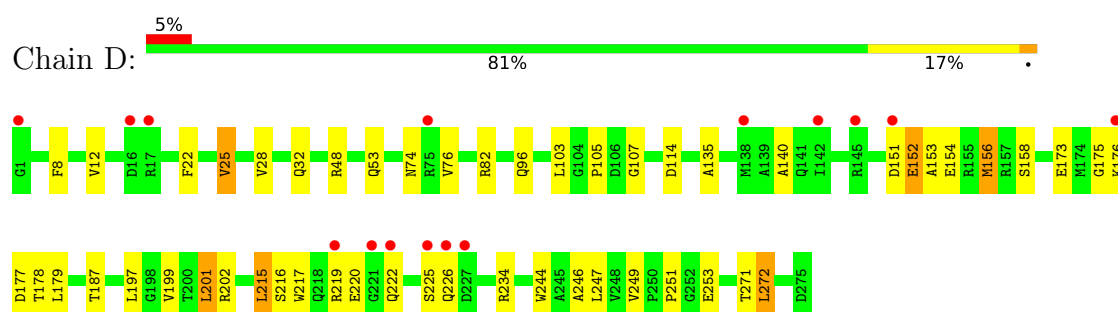
3 Residue-property plots [i](#)

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.

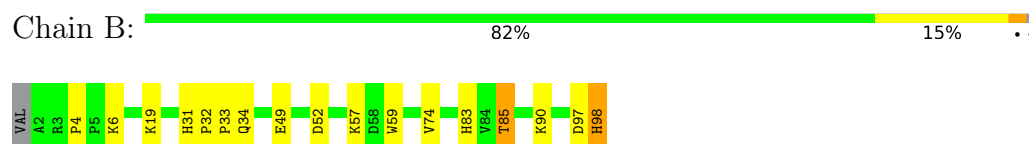
• Molecule 1: MHC class I antigen



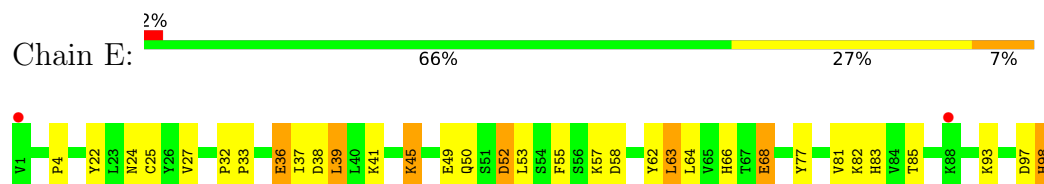
• Molecule 1: MHC class I antigen



• Molecule 2: Beta-2-microglobulin



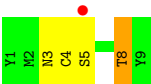
• Molecule 2: Beta-2-microglobulin



• Molecule 3: TYR-MET-ASN-CYS-SER-LEU-PRO-THR-TYR



● Molecule 3: TYR-MET-ASN-CYS-SER-LEU-PRO-THR-TYR



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	41.94Å 105.32Å 221.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.03 – 2.20 49.03 – 2.20	Depositor EDS
% Data completeness (in resolution range)	72.3 (49.03-2.20) 72.3 (49.03-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.91 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.222 , 0.249 (Not available) , 0.221	Depositor DCC
R_{free} test set	1869 reflections (3.66%)	wwPDB-VP
Wilson B-factor (Å ²)	31.1	Xtriage
Anisotropy	0.126	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 17.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6333	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.71% 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	1.03	0/2291	1.44	8/3105 (0.3%)
1	D	1.07	1/2291 (0.0%)	1.40	3/3105 (0.1%)
2	B	1.06	1/824 (0.1%)	1.31	2/1119 (0.2%)
2	E	0.99	0/831	1.28	1/1129 (0.1%)
3	C	0.96	0/76	1.46	1/103 (1.0%)
3	F	0.96	0/77	1.46	0/103
All	All	1.04	2/6390 (0.0%)	1.39	15/8664 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	31	HIS	CE1-NE2	6.98	1.39	1.32
1	D	105	PRO	C-O	-5.29	1.17	1.23

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	129	ASP	CA-CB-CG	6.49	119.09	112.60
1	A	210	PRO	CA-C-N	6.04	128.38	120.28
1	A	210	PRO	C-N-CA	6.04	128.38	120.28
1	A	94	THR	CB-CA-C	5.72	120.68	109.35
2	B	34	GLN	CB-CA-C	5.67	118.33	110.16
1	D	251	PRO	N-CA-C	5.58	121.90	113.81
3	C	9	TYR	CA-C-O	-5.51	111.43	120.80
2	E	58	ASP	CA-CB-CG	5.49	118.09	112.60
1	D	82	ARG	CA-C-N	5.44	126.14	119.99
1	D	82	ARG	C-N-CA	5.44	126.14	119.99
1	A	112	GLY	CA-C-O	-5.26	116.99	121.57
1	A	218	GLN	CA-C-N	5.22	128.64	121.33
1	A	218	GLN	C-N-CA	5.22	128.64	121.33
2	B	49	GLU	CB-CA-C	5.21	119.04	109.46
1	A	230	LEU	CA-C-O	-5.01	115.14	120.40

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	2235	0	2098	29	0
1	D	2235	0	2098	19	0
2	B	799	0	770	12	0
2	E	806	0	782	22	0
3	C	74	0	70	3	0
3	F	75	0	70	4	0
4	A	39	0	0	1	0
4	B	23	0	0	0	0
4	D	33	0	0	1	0
4	E	13	0	0	1	0
4	F	1	0	0	0	0
All	All	6333	0	5888	77	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 6.

All (77) 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)
2:B:4:PRO:HA	2:B:85:THR:HG21	1.49	0.92
2:E:4:PRO:HA	2:E:85:THR:HG21	1.63	0.80
1:A:17:ARG:HH11	1:A:17:ARG:HG3	1.50	0.74
1:D:25:VAL:HG12	1:D:32:GLN:HE21	1.53	0.73
1:A:79:ASN:OD1	1:A:82:ARG:NH1	2.20	0.72
3:F:3:ASN:HD21	3:F:5:SER:HB2	1.56	0.71
2:E:83:HIS:ND1	2:E:85:THR:HG22	2.07	0.69
3:F:4:CYS:SG	3:F:4:CYS:O	2.49	0.69
1:A:62:ARG:CZ	1:A:66:ILE:CD1	2.72	0.67
2:B:97:ASP:C	2:B:98:HIS:HD1	2.03	0.67
2:E:32:PRO:HB2	2:E:33:PRO:HD2	1.81	0.61
2:E:98:HIS:N	2:E:98:HIS:ND1	2.46	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:222:GLN:NE2	4:A:301:HOH:O	2.33	0.61
2:B:98:HIS:HD1	2:B:98:HIS:N	1.99	0.60
4:D:331:HOH:O	2:E:98:HIS:HD2	1.84	0.59
1:A:17:ARG:NH2	1:D:177:ASP:HB3	2.17	0.59
1:A:255:GLN:O	1:A:273:ARG:NH1	2.35	0.58
2:E:97:ASP:C	2:E:98:HIS:ND1	2.61	0.58
2:B:4:PRO:CA	2:B:85:THR:HG21	2.27	0.57
1:A:62:ARG:CZ	1:A:66:ILE:HD11	2.34	0.57
2:B:32:PRO:HB2	2:B:33:PRO:HD2	1.88	0.56
1:A:17:ARG:HG3	1:A:17:ARG:NH1	2.19	0.56
1:A:232:GLU:HB3	2:B:6:LYS:HE2	1.86	0.55
1:D:114:ASP:CG	1:D:156:MET:HE2	2.34	0.53
1:A:62:ARG:CZ	1:A:66:ILE:HD12	2.38	0.52
1:A:62:ARG:NH2	1:A:66:ILE:HD12	2.24	0.52
1:A:73:ILE:HG21	3:C:6:LEU:HD13	1.92	0.52
2:E:25:CYS:HB2	2:E:39:LEU:HD21	1.91	0.51
3:F:3:ASN:ND2	3:F:5:SER:HB2	2.24	0.51
2:B:98:HIS:N	2:B:98:HIS:ND1	2.59	0.51
1:A:152:GLU:OE1	3:C:8:THR:OG1	2.24	0.50
1:D:202:ARG:HD3	1:D:244:TRP:CE3	2.46	0.50
2:E:50:GLN:OE1	2:E:63:LEU:HD22	2.12	0.49
1:D:187:THR:HB	1:D:272:LEU:HD21	1.95	0.48
2:E:22:TYR:CD1	2:E:22:TYR:N	2.82	0.48
2:E:68:GLU:HB3	4:E:108:HOH:O	2.13	0.47
1:A:82:ARG:NH2	2:E:68:GLU:OE1	2.46	0.47
1:A:152:GLU:OE2	3:C:7:PRO:HA	2.14	0.47
1:A:250:PRO:HB2	1:A:253:GLU:HG3	1.95	0.47
1:A:62:ARG:NH1	1:A:66:ILE:HD11	2.31	0.46
1:D:199:VAL:HG13	1:D:249:VAL:HG22	1.98	0.46
1:D:152:GLU:OE2	3:F:8:THR:HG23	2.16	0.46
2:E:36:GLU:O	2:E:81:VAL:HA	2.16	0.46
1:A:42:ASN:ND2	1:A:44:LYS:HE3	2.31	0.45
1:D:22:PHE:CE1	1:D:74:ASN:ND2	2.84	0.45
1:A:52:ILE:HD12	1:A:174:MET:HE1	1.99	0.45
1:A:62:ARG:NH1	1:A:66:ILE:CD1	2.80	0.44
1:A:263:HIS:CD2	1:A:265:GLY:H	2.36	0.44
1:D:135:ALA:HB1	1:D:140:ALA:HB3	2.00	0.44
1:D:234:ARG:HH22	2:E:98:HIS:HE2	1.66	0.44
2:E:83:HIS:ND1	2:E:85:THR:CG2	2.80	0.44
1:A:204:TRP:CE3	1:A:206:LEU:HD21	2.52	0.44
1:D:96:GLN:NE2	2:E:55:PHE:CG	2.85	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:175:GLY:O	1:D:176:LYS:C	2.60	0.43
1:D:8:PHE:HB2	1:D:25:VAL:HG23	1.99	0.43
1:D:201:LEU:O	1:D:246:ALA:HA	2.18	0.43
1:D:103:LEU:HD11	1:D:107:GLY:HA2	2.00	0.43
2:B:83:HIS:ND1	2:B:85:THR:HB	2.32	0.43
1:A:117:ALA:HB2	2:B:59:TRP:CE2	2.54	0.42
1:A:231:VAL:CG1	1:A:244:TRP:CZ2	3.01	0.42
1:D:217:TRP:CG	1:D:247:LEU:HD22	2.54	0.42
1:D:215:LEU:HD23	1:D:215:LEU:HA	1.87	0.42
2:E:37:ILE:HD12	2:E:63:LEU:HD13	2.00	0.42
1:A:35:ARG:HD3	2:B:52:ASP:OD1	2.20	0.42
2:E:37:ILE:CD1	2:E:63:LEU:HD13	2.50	0.42
2:E:38:ASP:OD1	2:E:45:LYS:HE3	2.19	0.42
1:D:28:VAL:HG11	1:D:179:LEU:HD13	2.02	0.41
2:E:41:LYS:HG3	2:E:77:TYR:CE1	2.55	0.41
2:E:24:ASN:HB3	2:E:64:LEU:HD11	2.02	0.41
2:E:27:VAL:O	2:E:62:TYR:HA	2.21	0.41
1:A:244:TRP:HE1	2:B:98:HIS:CD2	2.39	0.41
1:D:152:GLU:O	1:D:153:ALA:C	2.64	0.41
1:A:231:VAL:HG11	1:A:244:TRP:CZ2	2.55	0.41
2:E:49:GLU:HG3	2:E:66:HIS:NE2	2.36	0.40
2:B:97:ASP:C	2:B:98:HIS:ND1	2.76	0.40
1:A:195:SER:HB3	1:A:197:LEU:HD12	2.03	0.40
1:A:154:GLU:HG3	1:A:155:ARG:N	2.34	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	273/275 (99%)	266 (97%)	6 (2%)	1 (0%)	30 34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	273/275 (99%)	263 (96%)	10 (4%)	0	100	100
2	B	95/98 (97%)	94 (99%)	1 (1%)	0	100	100
2	E	96/98 (98%)	90 (94%)	4 (4%)	2 (2%)	5	3
3	C	7/9 (78%)	7 (100%)	0	0	100	100
3	F	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
All	All	751/764 (98%)	726 (97%)	22 (3%)	3 (0%)	30	34

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	53	LEU
2	E	52	ASP
1	A	105	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	235/235 (100%)	209 (89%)	26 (11%)	6	6
1	D	235/235 (100%)	211 (90%)	24 (10%)	7	7
2	B	90/91 (99%)	84 (93%)	6 (7%)	15	17
2	E	91/91 (100%)	81 (89%)	10 (11%)	6	6
3	C	9/9 (100%)	8 (89%)	1 (11%)	6	6
3	F	9/9 (100%)	8 (89%)	1 (11%)	6	6
All	All	669/670 (100%)	601 (90%)	68 (10%)	7	7

All (68) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	VAL
1	A	17	ARG
1	A	58	GLU

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Mol	Chain	Res	Type
1	A	76	VAL
1	A	81	LEU
1	A	94	THR
1	A	141	GLN
1	A	145	ARG
1	A	154	GLU
1	A	170	LYS
1	A	176	LYS
1	A	178	THR
1	A	183	GLU
1	A	196	ASP
1	A	197	LEU
1	A	199	VAL
1	A	201	LEU
1	A	212	GLU
1	A	219	ARG
1	A	222	GLN
1	A	247	LEU
1	A	256	SER
1	A	262	GLN
1	A	267	GLN
1	A	271	THR
1	A	272	LEU
2	B	19	LYS
2	B	57	LYS
2	B	74	VAL
2	B	85	THR
2	B	90	LYS
2	B	98	HIS
3	C	2	MET
1	D	12	VAL
1	D	25	VAL
1	D	48	ARG
1	D	53	GLN
1	D	76	VAL
1	D	151	ASP
1	D	152	GLU
1	D	154	GLU
1	D	156	MET
1	D	158	SER
1	D	173	GLU
1	D	178	THR

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Mol	Chain	Res	Type
1	D	197	LEU
1	D	201	LEU
1	D	215	LEU
1	D	216	SER
1	D	219	ARG
1	D	220	GLU
1	D	222	GLN
1	D	225	SER
1	D	226	GLN
1	D	253	GLU
1	D	271	THR
1	D	272	LEU
2	E	36	GLU
2	E	39	LEU
2	E	45	LYS
2	E	52	ASP
2	E	57	LYS
2	E	63	LEU
2	E	68	GLU
2	E	82	LYS
2	E	93	LYS
2	E	98	HIS
3	F	8	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	42	ASN
1	A	86	ASN
1	A	115	GLN
1	A	141	GLN
1	A	192	HIS
1	A	222	GLN
1	A	263	HIS
2	B	47	ASN
1	D	32	GLN
1	D	141	GLN
1	D	169	GLN
1	D	180	GLN
1	D	192	HIS
1	D	218	GLN
1	D	226	GLN

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Mol	Chain	Res	Type
1	D	260	HIS
1	D	262	GLN
2	E	34	GLN
2	E	98	HIS
3	F	3	ASN

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	275/275 (100%)	0.15	9 (3%) 49 46	14, 29, 61, 110	0
1	D	275/275 (100%)	0.34	15 (5%) 30 27	15, 34, 67, 94	0
2	B	97/98 (98%)	-0.15	0 100 100	15, 25, 48, 57	0
2	E	98/98 (100%)	0.29	2 (2%) 65 62	16, 33, 55, 80	0
3	C	9/9 (100%)	-0.06	0 100 100	18, 23, 32, 32	0
3	F	9/9 (100%)	0.67	1 (11%) 10 8	29, 32, 49, 54	0
All	All	763/764 (99%)	0.20	27 (3%) 47 44	14, 32, 61, 110	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	197	LEU	6.1
2	E	1	VAL	4.5
1	D	138	MET	4.3
1	D	221	GLY	4.3
1	A	194	SER	4.2
1	D	1	GLY	4.1
1	A	196	ASP	3.8
1	A	105	PRO	3.4
1	D	142	ILE	3.1
1	A	267	GLN	3.1
1	D	226	GLN	3.0
1	D	225	SER	2.9
1	A	195	SER	2.8
1	A	181	ARG	2.8
1	D	151	ASP	2.8
1	D	75	ARG	2.8
1	D	227	ASP	2.6
1	D	176	LYS	2.5
1	D	17	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
1	D	219	ARG	2.4
1	A	1	GLY	2.3
2	E	88	LYS	2.2
1	D	222	GLN	2.2
1	D	145	ARG	2.1
1	A	108	LEU	2.1
1	D	16	ASP	2.1
3	F	5	SER	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.