



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 01:17 PM UTC

PDB ID : 9F91 / pdb_00009f91
Title : Crystal structure of a designed Respiratory Syncytial Virus immunogen in complex with RSV90 fab
Authors : Castro, K.M.; Correia, B.E.
Deposited on : 2024-05-07
Resolution : 2.43 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:

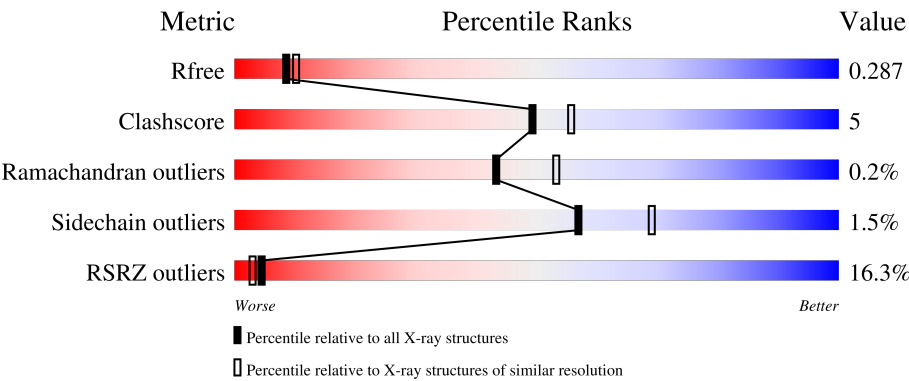
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.43 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	2340 (2.46-2.42)
Clashscore	190562	2400 (2.46-2.42)
Ramachandran outliers	187476	2379 (2.46-2.42)
Sidechain outliers	187428	2379 (2.46-2.42)
RSRZ outliers	180081	2340 (2.46-2.42)

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	228	29% 84% 14% .
1	E	228	12% 84% 14% .
2	B	217	6% 88% 12% .
2	F	217	10% 86% 11% .
3	I	97	15% 54% 16% 28% .

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Mol	Chain	Length	Quality of chain
3	J	97	25% 55% 14% 29%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7713 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 RSV90 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	E	224	Total	C	N	O	S	0	0	0
			1695	1073	285	332	5			
1	A	224	Total	C	N	O	S	0	0	0
			1694	1072	284	333	5			

- Molecule 2 is a protein called RSV90 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	211	Total	C	N	O	S	0	0	0
			1594	998	272	319	5			
2	B	216	Total	C	N	O	S	0	0	0
			1642	1027	279	331	5			

- Molecule 3 is a protein called Designed single epitope Respiratory Syncytial Virus immunogen in complex with RSV90 fab.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	I	70	Total	C	N	O	0	0	0
			527	334	82	111			
3	J	69	Total	C	N	O	0	0	0
			518	329	81	108			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	16	Total	O	0	0
			16	16		
4	F	16	Total	O	0	0
			16	16		
4	A	2	Total	O	0	0
			2	2		
4	B	6	Total	O	0	0
			6	6		

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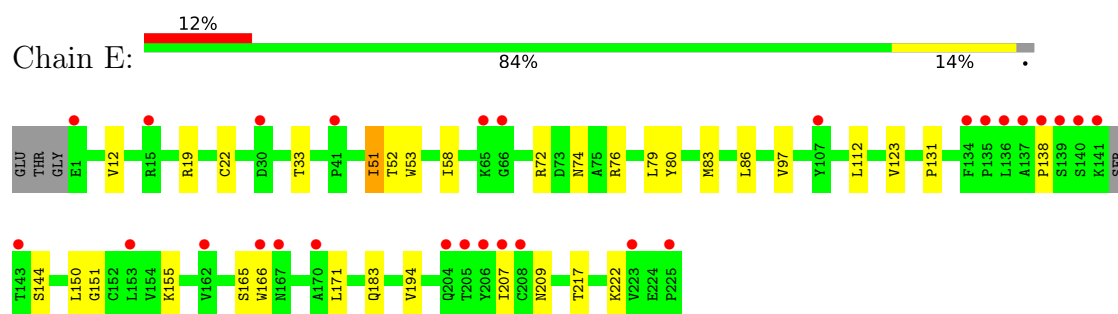
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	I	2	Total	O	0	0
			2	2		
4	J	1	Total	O	0	0
			1	1		

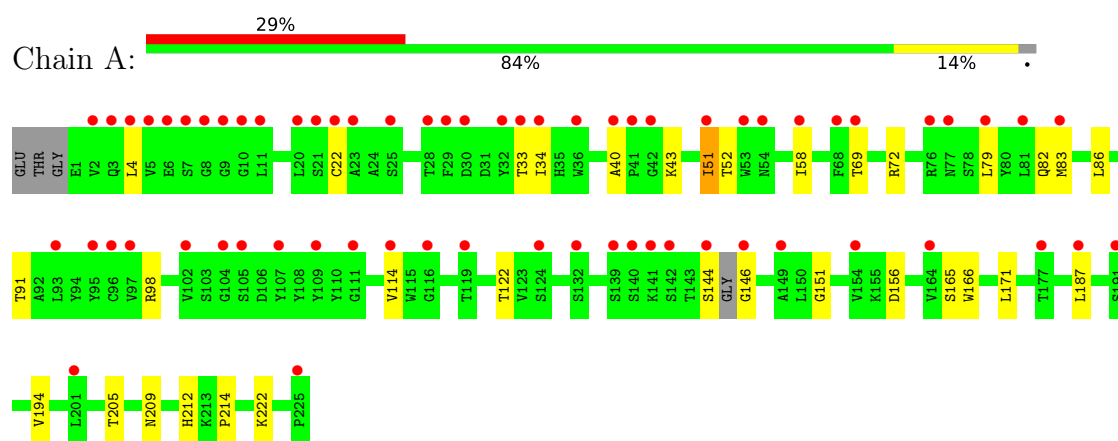
3 Residue-property plots [i](#)

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.

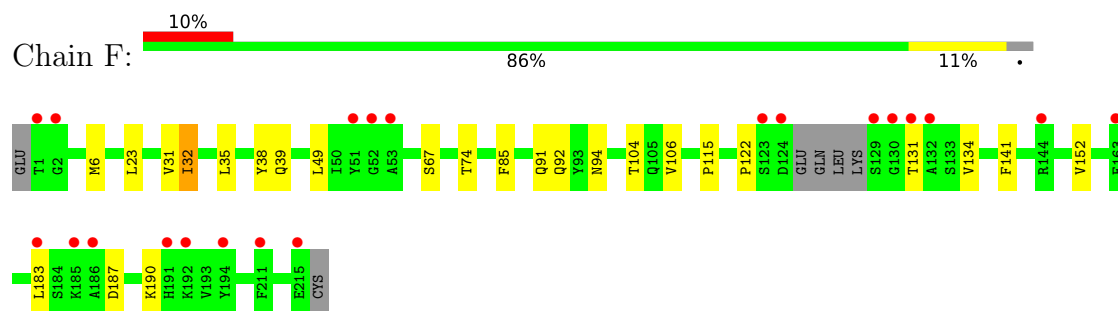
- Molecule 1: RSV90 Fab heavy chain



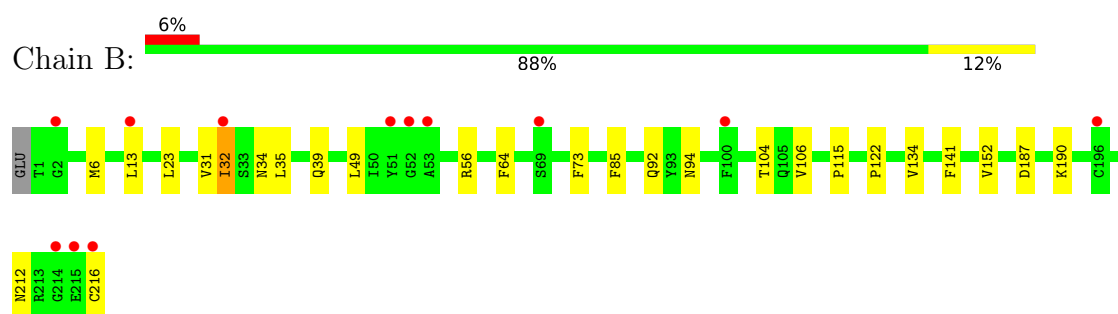
- Molecule 1: RSV90 Fab heavy chain



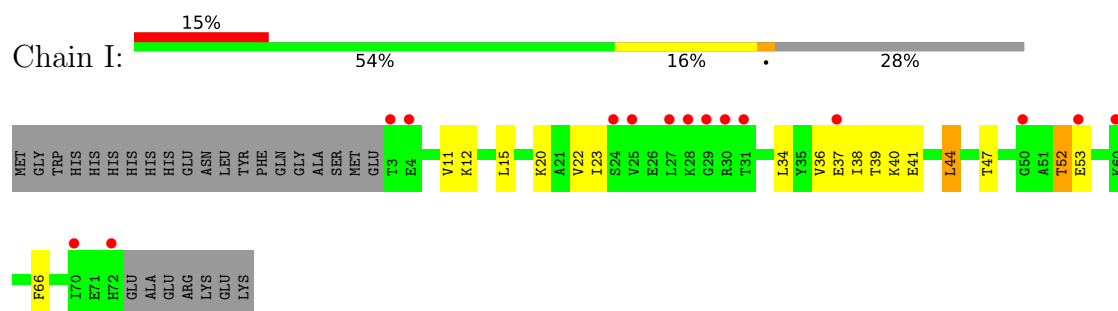
- Molecule 2: RSV90 Fab light chain



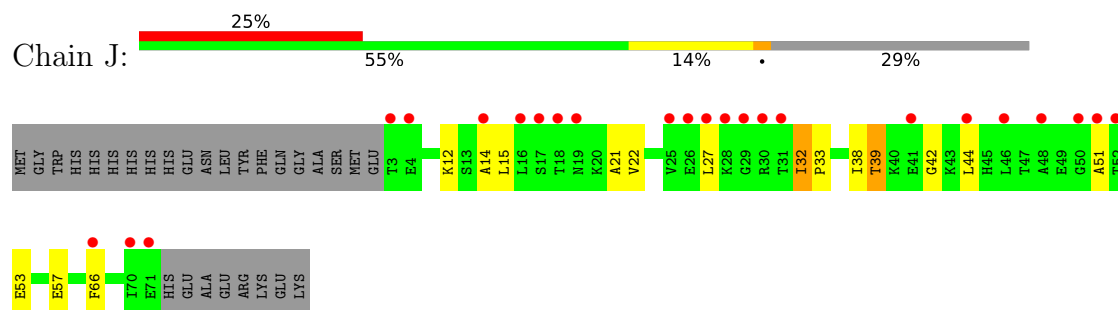
- Molecule 2: RSV90 Fab light chain



- Molecule 3: Designed single epitope Respiratory Syncytial Virus immunogen in complex with RSV90 fab



- Molecule 3: Designed single epitope Respiratory Syncytial Virus immunogen in complex with RSV90 fab



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	113.39Å 137.65Å 87.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	73.83 – 2.43 73.83 – 2.43	Depositor EDS
% Data completeness (in resolution range)	99.8 (73.83-2.43) 99.8 (73.83-2.43)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.61 (at 2.42Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487, PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.251 , 0.287 0.251 , 0.287	Depositor DCC
R_{free} test set	2633 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	52.4	Xtriage
Anisotropy	0.689	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 39.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7713	wwPDB-VP
Average B, all atoms (Å ²)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.46% 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	0.20	0/1736	0.34	0/2369
1	E	0.24	0/1737	0.40	0/2369
2	B	0.10	0/1677	0.27	0/2281
2	F	0.14	0/1628	0.32	0/2215
3	I	0.39	0/530	0.60	0/715
3	J	0.09	0/521	0.25	0/703
All	All	0.20	0/7829	0.35	0/10652

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	1694	0	1634	19	0
1	E	1695	0	1638	21	0
2	B	1642	0	1582	14	0
2	F	1594	0	1533	13	0
3	I	527	0	526	9	0
3	J	518	0	520	9	0
4	A	2	0	0	0	0
4	B	6	0	0	0	0
4	E	16	0	0	0	0
4	F	16	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	I	2	0	0	0	0
4	J	1	0	0	0	0
All	All	7713	0	7433	82	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 5.

All (82) 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:F:31:VAL:HG23	2:F:94:ASN:HB2	1.48	0.91
2:B:31:VAL:HG23	2:B:94:ASN:HB2	1.62	0.82
1:E:53:TRP:HA	1:E:72:ARG:NH1	1.97	0.80
1:E:72:ARG:NE	1:E:74:ASN:OD1	2.20	0.74
2:B:187:ASP:HA	2:B:190:LYS:HE2	1.74	0.69
3:I:20:LYS:HG2	3:I:37:GLU:HG3	1.73	0.68
1:A:22:CYS:HB3	1:A:79:LEU:HB3	1.77	0.65
2:B:122:PRO:HD3	2:B:134:VAL:HG22	1.78	0.65
2:F:23:LEU:HD22	2:F:104:THR:HG21	1.77	0.65
2:F:31:VAL:HG21	2:F:92:GLN:HB2	1.80	0.64
1:E:72:ARG:NH2	1:E:74:ASN:OD1	2.33	0.61
1:E:155:LYS:NZ	1:E:183:GLN:OE1	2.34	0.60
2:B:23:LEU:HD22	2:B:104:THR:HG21	1.83	0.60
2:F:187:ASP:HA	2:F:190:LYS:HE2	1.84	0.60
1:E:76:ARG:HG3	2:B:13:LEU:HD11	1.83	0.60
2:F:67:SER:OG	2:F:74:THR:OG1	2.20	0.59
3:J:15:LEU:HD13	3:J:38:ILE:HB	1.85	0.59
1:A:33:THR:HG22	1:A:52:THR:HA	1.84	0.59
1:A:51:ILE:HG22	1:A:58:ILE:HG12	1.83	0.58
3:J:32:ILE:HD13	3:J:33:PRO:HD2	1.86	0.58
1:A:91:THR:HG23	1:A:122:THR:HA	1.85	0.57
1:E:51:ILE:HG22	1:E:58:ILE:HG12	1.85	0.57
1:E:19:ARG:NH2	1:E:80:TYR:CD1	2.74	0.56
3:J:39:THR:HB	3:J:42:GLY:HA3	1.88	0.56
1:E:165:SER:HB3	1:E:209:ASN:HB2	1.88	0.55
1:A:40:ALA:HB3	1:A:43:LYS:HB2	1.87	0.55
1:A:156:ASP:HB3	1:A:187:LEU:HD13	1.89	0.54
2:B:39:GLN:HB2	2:B:49:LEU:HD11	1.88	0.54
1:E:33:THR:HG22	1:E:52:THR:HA	1.90	0.53
3:J:44:LEU:HD22	3:J:66:PHE:HD2	1.73	0.52
2:F:39:GLN:HB2	2:F:49:LEU:HD11	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:53:TRP:HA	1:E:72:ARG:HH12	1.75	0.52
1:E:72:ARG:CZ	1:E:74:ASN:OD1	2.57	0.52
1:A:51:ILE:HD13	1:A:72:ARG:HD2	1.92	0.50
2:B:115:PRO:HB3	2:B:141:PHE:HB3	1.92	0.50
3:I:44:LEU:HD22	3:I:66:PHE:HD2	1.77	0.50
2:F:6:MET:HE3	2:F:92:GLN:HG2	1.94	0.50
1:A:165:SER:HB3	1:A:209:ASN:HB2	1.94	0.49
2:B:212:ASN:HB2	2:B:216:CYS:HA	1.95	0.49
3:I:12:LYS:HE2	3:I:66:PHE:HE1	1.78	0.48
2:F:115:PRO:HB3	2:F:141:PHE:HB3	1.93	0.48
1:E:51:ILE:HD13	1:E:72:ARG:HD2	1.96	0.48
1:E:171:LEU:HD21	1:E:194:VAL:HG21	1.96	0.47
1:A:171:LEU:HD21	1:A:194:VAL:HG21	1.96	0.47
3:J:14:ALA:HB1	3:J:21:ALA:HB3	1.96	0.47
1:E:138:PRO:HB3	1:E:150:LEU:HB3	1.96	0.47
1:A:205:THR:HG23	1:A:222:LYS:HE3	1.97	0.46
2:B:6:MET:HE3	2:B:92:GLN:HG2	1.96	0.46
1:A:98:ARG:HB3	1:A:114:VAL:HB	1.97	0.46
1:E:22:CYS:HB3	1:E:79:LEU:HB3	1.97	0.45
1:A:83:MET:HB3	1:A:86:LEU:HD21	1.97	0.45
1:E:83:MET:HB3	1:E:86:LEU:HD21	1.99	0.44
1:A:151:GLY:HA2	1:A:166:TRP:CH2	2.52	0.44
1:E:131:PRO:HD2	1:E:217:THR:HG21	1.99	0.44
3:J:53:GLU:O	3:J:57:GLU:HG2	2.17	0.44
1:A:144:SER:C	1:A:146:GLY:N	2.76	0.44
2:B:56:ARG:HD3	2:B:64:PHE:O	2.17	0.43
3:I:52:THR:O	3:I:53:GLU:C	2.60	0.43
3:J:32:ILE:HD11	3:J:51:ALA:HB2	2.01	0.43
2:B:31:VAL:HG22	2:B:34:ASN:HB2	1.98	0.43
3:I:15:LEU:HD13	3:I:38:ILE:HB	1.99	0.43
1:E:151:GLY:HA2	1:E:166:TRP:CH2	2.54	0.43
2:F:85:PHE:HA	2:F:106:VAL:HG23	2.01	0.43
3:I:11:VAL:HG13	3:I:36:VAL:HG11	2.01	0.43
2:F:131:THR:OG1	2:F:183:LEU:O	2.33	0.43
1:A:4:LEU:HD11	1:A:98:ARG:HB2	2.01	0.43
2:B:32:ILE:HD11	3:J:22:VAL:HG21	2.00	0.43
1:A:151:GLY:HA2	1:A:166:TRP:HH2	1.83	0.43
2:B:35:LEU:HD22	2:B:73:PHE:CG	2.54	0.42
1:A:212:HIS:CD2	1:A:214:PRO:HD2	2.55	0.42
2:F:32:ILE:HD11	3:I:22:VAL:HG21	2.00	0.42
1:A:34:ILE:HB	1:A:51:ILE:HD11	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:12:LYS:HE3	3:J:12:LYS:HB2	1.81	0.42
1:E:207:ILE:HD13	1:E:222:LYS:HA	2.01	0.41
2:B:85:PHE:HA	2:B:106:VAL:HG23	2.02	0.41
2:F:122:PRO:HG3	2:F:134:VAL:HG22	2.02	0.41
3:I:23:ILE:HD11	3:I:34:LEU:HD23	2.01	0.41
1:E:97:VAL:CG1	1:E:112:LEU:HB3	2.51	0.41
1:A:69:THR:OG1	1:A:82:GLN:HB3	2.21	0.41
2:F:38:TYR:HE1	2:F:91:GLN:HB3	1.87	0.40
3:I:40:LYS:NZ	3:I:41:GLU:OE2	2.55	0.40
1:E:12:VAL:O	1:E:123:VAL:HA	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	220/228 (96%)	214 (97%)	6 (3%)	0	100	100
1	E	220/228 (96%)	214 (97%)	6 (3%)	0	100	100
2	B	214/217 (99%)	207 (97%)	6 (3%)	1 (0%)	24	29
2	F	207/217 (95%)	202 (98%)	4 (2%)	1 (0%)	24	29
3	I	68/97 (70%)	65 (96%)	3 (4%)	0	100	100
3	J	67/97 (69%)	61 (91%)	6 (9%)	0	100	100
All	All	996/1084 (92%)	963 (97%)	31 (3%)	2 (0%)	43	53

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	32	ILE
2	F	32	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	187/191 (98%)	186 (100%)	1 (0%)	81	87
1	E	186/191 (97%)	184 (99%)	2 (1%)	65	75
2	B	184/188 (98%)	183 (100%)	1 (0%)	81	87
2	F	178/188 (95%)	176 (99%)	2 (1%)	65	75
3	I	55/84 (66%)	51 (93%)	4 (7%)	13	15
3	J	54/84 (64%)	51 (94%)	3 (6%)	19	25
All	All	844/926 (91%)	831 (98%)	13 (2%)	57	69

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	51	ILE
1	E	144	SER
2	F	35	LEU
2	F	152	VAL
1	A	51	ILE
2	B	152	VAL
3	I	39	THR
3	I	44	LEU
3	I	47	THR
3	I	52	THR
3	J	27	LEU
3	J	32	ILE
3	J	39	THR

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

Mol	Chain	Res	Type
1	E	39	GLN
1	E	176	HIS
2	F	40	GLN
2	F	139	ASN

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Mol	Chain	Res	Type
2	F	149	GLN
2	F	201	GLN
2	B	201	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	224/228 (98%)	1.64	65 (29%) 1 1	70, 97, 117, 127	0
1	E	224/228 (98%)	0.98	28 (12%) 8 6	41, 64, 93, 113	0
2	B	216/217 (99%)	0.82	12 (5%) 30 27	49, 68, 92, 98	0
2	F	211/217 (97%)	0.71	21 (9%) 12 10	40, 54, 84, 102	0
3	I	70/97 (72%)	1.27	15 (21%) 2 2	41, 72, 106, 112	0
3	J	69/97 (71%)	1.73	24 (34%) 1 0	79, 106, 121, 124	0
All	All	1014/1084 (93%)	1.10	165 (16%) 4 3	40, 72, 113, 127	0

All (165) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	124	ASP	8.2
2	B	216	CYS	6.0
1	E	134	PHE	4.9
2	F	129	SER	4.9
2	F	132	ALA	4.4
2	F	131	THR	4.3
1	A	144	SER	4.1
3	J	66	PHE	4.1
3	I	27	LEU	4.0
1	A	20	LEU	4.0
2	B	215	GLU	4.0
1	E	143	THR	3.9
1	A	7	SER	3.9
1	A	11	LEU	3.8
1	A	22	CYS	3.8
1	E	223	VAL	3.7
1	E	153	LEU	3.7
1	A	4	LEU	3.7
3	I	28	LYS	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	119	THR	3.7
1	A	2	VAL	3.7
1	A	10	GLY	3.6
1	A	104	GLY	3.5
3	J	48	ALA	3.5
1	A	105	SER	3.5
1	A	146	GLY	3.5
3	J	71	GLU	3.5
1	A	32	TYR	3.3
1	A	97	VAL	3.3
3	J	27	LEU	3.3
3	J	30	ARG	3.3
2	F	52	GLY	3.2
2	F	51	TYR	3.2
1	E	225	PRO	3.2
3	I	29	GLY	3.2
1	A	140	SER	3.2
1	A	5	VAL	3.2
1	A	96	CYS	3.2
2	F	123	SER	3.1
2	B	2	GLY	3.1
1	A	23	ALA	3.1
1	E	30	ASP	3.1
3	I	72	HIS	3.1
2	B	32	ILE	3.1
3	J	3	THR	3.0
1	A	41	PRO	3.0
1	A	79	LEU	3.0
2	B	196	CYS	3.0
1	E	15	ARG	3.0
1	A	51	ILE	3.0
1	A	33	THR	3.0
2	B	51	TYR	3.0
3	I	37	GLU	2.9
3	I	3	THR	2.9
1	A	53	TRP	2.9
1	A	201	LEU	2.9
1	E	206	TYR	2.9
1	A	142	SER	2.9
3	J	28	LYS	2.8
1	E	162	VAL	2.8
3	I	53	GLU	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	9	GLY	2.8
1	E	205	THR	2.8
2	B	53	ALA	2.8
1	A	3	GLN	2.8
3	J	18	THR	2.7
1	A	6	GLU	2.7
3	J	4	GLU	2.7
1	E	135	PRO	2.7
3	I	31	THR	2.7
3	J	14	ALA	2.7
1	A	21	SER	2.7
1	A	116	GLY	2.6
1	E	141	LYS	2.6
1	A	34	ILE	2.6
1	E	1	GLU	2.6
2	F	186	ALA	2.6
2	F	194	TYR	2.6
1	E	208	CYS	2.6
2	F	144	ARG	2.6
3	J	41	GLU	2.6
1	A	177	THR	2.6
2	F	1	THR	2.6
1	A	76	ARG	2.5
1	E	66	GLY	2.5
1	A	149	ALA	2.5
1	E	107	TYR	2.5
2	F	215	GLU	2.5
3	I	4	GLU	2.5
1	A	81	LEU	2.5
2	F	192	LYS	2.5
1	A	107	TYR	2.5
3	I	70	ILE	2.5
2	F	183	LEU	2.5
2	B	52	GLY	2.5
1	A	30	ASP	2.5
1	A	68	PHE	2.5
1	A	8	GLY	2.4
3	I	30	ARG	2.4
1	E	138	PRO	2.4
3	J	25	VAL	2.4
1	E	137	ALA	2.4
3	J	17	SER	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	111	GLY	2.4
1	A	225	PRO	2.4
1	A	139	SER	2.4
1	E	207	ILE	2.4
2	B	13	LEU	2.4
1	A	124	SER	2.3
3	J	29	GLY	2.3
1	A	95	TYR	2.3
1	A	109	TYR	2.3
1	A	154	VAL	2.3
1	A	69	THR	2.3
1	E	140	SER	2.3
3	I	25	VAL	2.3
1	E	139	SER	2.3
1	A	42	GLY	2.3
1	A	93	LEU	2.3
3	J	70	ILE	2.3
3	J	26	GLU	2.3
1	A	54	ASN	2.3
2	B	214	GLY	2.3
1	E	167	ASN	2.2
2	F	2	GLY	2.2
1	E	41	PRO	2.2
3	I	24	SER	2.2
1	A	77	ASN	2.2
2	F	53	ALA	2.2
1	A	36	TRP	2.2
1	A	141	LYS	2.2
1	A	102	VAL	2.1
3	J	19	ASN	2.1
1	A	28	THR	2.1
1	A	83	MET	2.1
2	F	191	HIS	2.1
2	F	130	GLY	2.1
3	I	50	GLY	2.1
3	J	44	LEU	2.1
3	J	46	LEU	2.1
3	J	52	THR	2.1
2	F	163	GLU	2.1
2	B	69	SER	2.1
2	F	211	PHE	2.1
2	B	100	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	164	VAL	2.1
1	E	166	TRP	2.1
1	E	170	ALA	2.1
1	A	40	ALA	2.1
1	E	65	LYS	2.1
1	A	191	SER	2.1
1	A	29	PHE	2.1
3	J	50	GLY	2.1
3	J	31	THR	2.1
1	A	58	ILE	2.1
3	I	60	LYS	2.1
1	A	114	VAL	2.0
3	J	51	ALA	2.0
1	E	136	LEU	2.0
2	F	185	LYS	2.0
1	E	204	GLN	2.0
1	A	187	LEU	2.0
3	J	16	LEU	2.0
1	A	25	SER	2.0
1	A	132	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.