



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 8, 2020 – 02:01 AM BST

PDB ID : 6O25
Title : Crystal structure of 3945 Fab in complex with circumsporozoite protein NANP3 and anti-Kappa VHH domain
Authors : Scally, S.W.; Bosch, A.; Prieto, K.; Murugan, R.; Wardemann, H.; Julien, J.P.
Deposited on : 2019-02-22
Resolution : 2.90 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 : 2.13.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

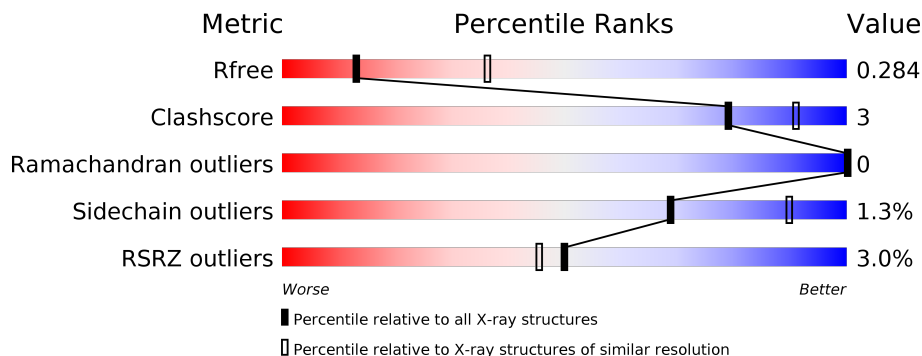
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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}	130704	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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 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	224	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 88%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 10%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: grey;"></div> </div> <p style="margin-left: 20px;">2% 88% 10% •</p>
1	E	224	<div style="display: flex; align-items: center;"> <div style="width: 4%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 89%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 7%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: grey;"></div> </div> <p style="margin-left: 20px;">4% 89% 7% •</p>
1	I	224	<div style="display: flex; align-items: center;"> <div style="width: 0%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 84%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 12%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: grey;"></div> </div> <p style="margin-left: 20px;">% 84% 12% ••</p>
2	B	215	<div style="display: flex; align-items: center;"> <div style="width: 0%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 93%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 6%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: grey;"></div> </div> <p style="margin-left: 20px;">93% 6% •</p>
2	F	215	<div style="display: flex; align-items: center;"> <div style="width: 7%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 91%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 9%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 0%; height: 10px; background-color: grey;"></div> </div> <p style="margin-left: 20px;">7% 91% 9%</p>
2	J	215	<div style="display: flex; align-items: center;"> <div style="width: 0%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 93%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 6%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: grey;"></div> </div> <p style="margin-left: 20px;">93% 6%</p>

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Mol	Chain	Length	Quality of chain
3	C	121	<p>2% 97%</p>
3	G	121	<p>2% 96%</p>
3	K	121	<p>% 97%</p>
4	D	12	<p>8% 67% 25% 8%</p>
4	H	12	<p>33% 67% 33%</p>
4	L	12	<p>8% 67% 8% 8% 17%</p>

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 12136 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 3945 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	220	Total	C	N	O	S	0	0	0
			1665	1054	282	324	5			
1	E	216	Total	C	N	O	S	0	0	0
			1625	1033	271	316	5			
1	I	218	Total	C	N	O	S	0	0	0
			1645	1043	277	320	5			

- Molecule 2 is a protein called 3945 Kappa light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	F	214	Total	C	N	O	S	0	0	0
			1628	1016	275	333	4			
2	B	213	Total	C	N	O	S	0	0	0
			1623	1014	275	330	4			
2	J	214	Total	C	N	O	S	0	0	0
			1622	1013	272	333	4			

- Molecule 3 is a protein called Anti-Kappa VHH domain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	K	119	Total	C	N	O	S	0	0	0
			708	430	134	142	2			
3	C	119	Total	C	N	O	S	0	0	0
			708	430	134	142	2			
3	G	119	Total	C	N	O	S	0	0	0
			708	430	134	142	2			

- Molecule 4 is a protein called Circumsporozoite protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	D	11	Total	C	N	O	0	0	0
			76	44	16	16			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	H	8	Total	C	N	O	0	0	0
			56	32	12	12			
4	L	10	Total	C	N	O	0	0	0
			69	39	15	15			

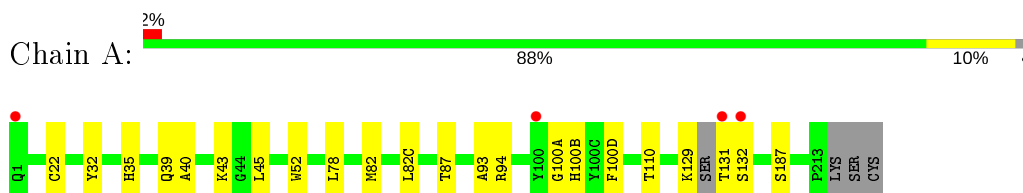
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	O	0	0
			1	1		
5	F	1	Total	O	0	0
			1	1		
5	B	1	Total	O	0	0
			1	1		

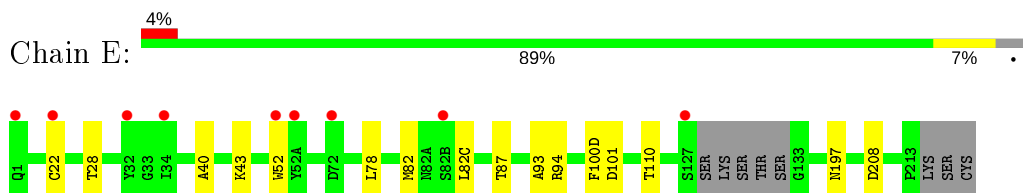
3 Residue-property plots [i](#)

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.

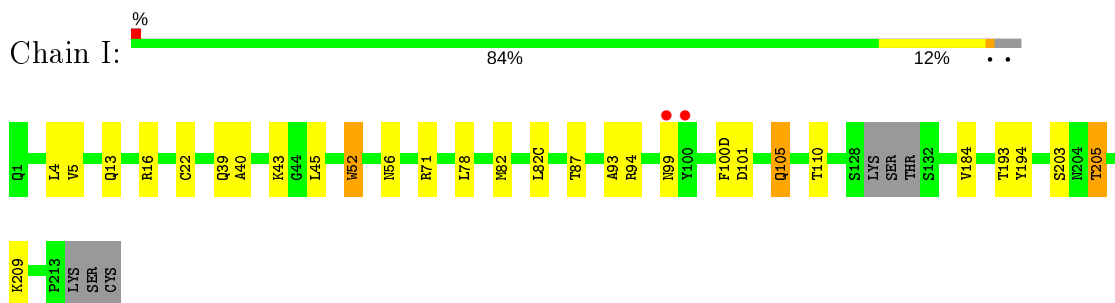
- Molecule 1: 3945 Fab heavy chain



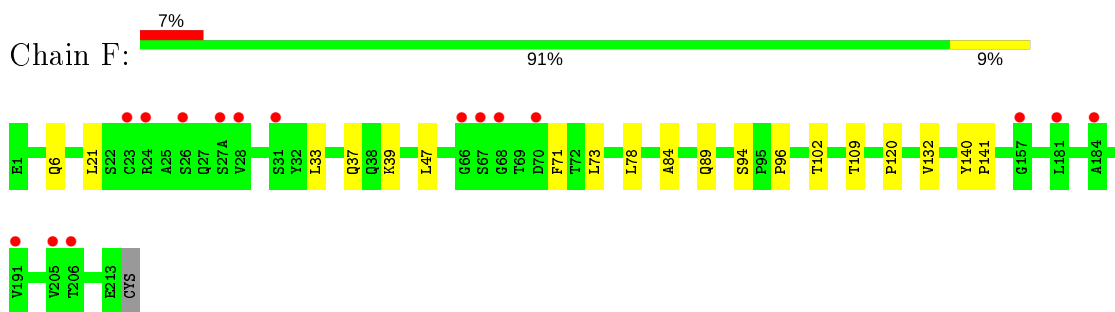
- Molecule 1: 3945 Fab heavy chain



- Molecule 1: 3945 Fab heavy chain



- Molecule 2: 3945 Kappa light chain



- Molecule 2: 3945 Kappa light chain

Chain B:  93% 6%



• Molecule 2: 3945 Kappa light chain

Chain J:  93% 6%



• Molecule 3: Anti-Kappa VHH domain

Chain K:  97%



• Molecule 3: Anti-Kappa VHH domain

Chain C:  97%



• Molecule 3: Anti-Kappa VHH domain

Chain G:  96%



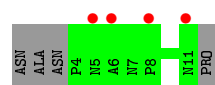
• Molecule 4: Circumsporozoite protein

Chain D:  67% 25% 8%

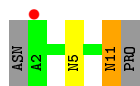


• Molecule 4: Circumsporozoite protein

Chain H:  67% 33%



- Molecule 4: Circumsporozoite protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	156.25Å 230.74Å 48.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.73 – 2.90 39.73 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.9 (39.73-2.90) 94.8 (39.73-2.90)	Depositor EDS
R_{merge}	0.24	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.72 (at 2.90Å)	Xtrriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.215 , 0.268 0.247 , 0.284	Depositor DCC
R_{free} test set	1993 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	50.4	Xtrriage
Anisotropy	0.166	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 36.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	12136	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 40.08 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.8844e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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	0.26	0/1709	0.47	0/2331
1	E	0.25	0/1669	0.46	0/2279
1	I	0.26	0/1689	0.47	0/2304
2	B	0.26	0/1659	0.46	0/2255
2	F	0.25	0/1664	0.46	0/2263
2	J	0.26	0/1658	0.46	0/2256
3	C	0.26	0/342	0.47	0/425
3	G	0.24	0/342	0.47	0/425
3	K	0.26	0/342	0.48	0/425
4	D	0.30	0/78	0.59	0/109
4	H	0.24	0/57	0.42	0/78
4	L	0.26	0/70	0.39	0/97
All	All	0.26	0/11279	0.46	0/15247

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	1665	0	1594	12	0
1	E	1625	0	1547	8	0
1	I	1645	0	1570	17	0
2	B	1623	0	1572	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	1628	0	1567	10	0
2	J	1622	0	1556	8	0
3	C	708	0	405	1	0
3	G	708	0	404	2	0
3	K	708	0	404	1	0
4	D	76	0	65	2	0
4	H	56	0	48	0	0
4	L	69	0	58	2	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	F	1	0	0	0	0
All	All	12136	0	10790	64	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 3.

All (64) 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:I:99:ASN:HD21	3:C:81:GLN:HG2	1.51	0.76
2:J:93:SER:O	4:L:5:ASN:ND2	2.24	0.71
1:I:94:ARG:NH2	1:I:101:ASP:OD2	2.24	0.69
1:A:131:THR:HG21	1:A:187:SER:HA	1.77	0.66
2:F:37:GLN:HB2	2:F:47:LEU:HD11	1.77	0.66
1:I:4:LEU:O	1:I:105:GLN:NE2	2.32	0.62
1:A:93:ALA:HB1	1:A:100(D):PHE:HB3	1.82	0.61
1:I:93:ALA:HB1	1:I:100(D):PHE:HB3	1.83	0.60
1:I:5:VAL:HA	1:I:105:GLN:HE21	1.68	0.58
2:B:93:SER:O	4:D:5:ASN:ND2	2.37	0.58
1:I:13:GLN:OE1	1:I:16:ARG:NH1	2.38	0.57
2:J:37:GLN:HB2	2:J:47:LEU:HD11	1.87	0.57
1:A:32:TYR:CD1	1:A:94:ARG:HD3	2.40	0.56
1:I:203:SER:HG	1:I:205:THR:HG1	1.50	0.56
1:E:87:THR:HG23	1:E:110:THR:HA	1.89	0.55
1:E:197:ASN:ND2	1:E:208:ASP:OD2	2.30	0.55
1:I:82:MET:HB3	1:I:82(C):LEU:HD21	1.90	0.54
2:F:120:PRO:HD3	2:F:132:VAL:HG22	1.89	0.54
1:I:82:MET:HE2	1:I:82(C):LEU:HD21	1.89	0.54
2:F:21:LEU:HD22	2:F:102:THR:HG21	1.89	0.53
2:B:83:PHE:HA	2:B:104:VAL:HG23	1.90	0.53
1:A:40:ALA:HB3	1:A:43:LYS:HB2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:22:CYS:HB3	1:E:78:LEU:HB3	1.91	0.53
1:E:40:ALA:HB3	1:E:43:LYS:HB2	1.92	0.52
1:A:35:HIS:CE1	1:A:100(B):HIS:HB3	2.45	0.52
1:E:93:ALA:HB1	1:E:100(D):PHE:HB3	1.92	0.51
1:A:129:LYS:H	1:A:132:SER:HB2	1.76	0.51
1:A:82:MET:HE2	1:A:82(C):LEU:HD21	1.93	0.51
1:I:40:ALA:HB3	1:I:43:LYS:HB2	1.91	0.51
1:E:94:ARG:NH2	1:E:101:ASP:OD2	2.37	0.50
1:A:22:CYS:HB3	1:A:78:LEU:HB3	1.94	0.49
1:I:52:TRP:O	1:I:71:ARG:NH1	2.47	0.48
2:J:21:LEU:HD23	2:J:102:THR:HB	1.96	0.47
2:J:66:GLY:HA3	2:J:71:PHE:HA	1.94	0.47
1:A:87:THR:HG23	1:A:110:THR:HA	1.95	0.47
4:L:11:ASN:OD1	4:L:11:ASN:N	2.48	0.47
1:E:82:MET:HB3	1:E:82(C):LEU:HD21	1.95	0.47
1:I:87:THR:HG23	1:I:110:THR:HA	1.96	0.47
2:F:33:LEU:HD22	2:F:71:PHE:CG	2.50	0.46
2:F:89:GLN:HE21	2:F:96:PRO:HB3	1.80	0.46
2:F:39:LYS:HG2	2:F:84:ALA:HB2	1.97	0.45
1:E:82:MET:HE2	1:E:82(C):LEU:HD21	1.97	0.45
1:A:100(A):GLY:HA3	2:B:91:TYR:HD2	1.81	0.45
1:A:39:GLN:HB2	1:A:45:LEU:HD23	1.98	0.45
2:B:61:ARG:NE	2:B:82:ASP:OD2	2.45	0.45
1:A:82:MET:HB3	1:A:82(C):LEU:HD21	1.97	0.45
2:B:37:GLN:HB2	2:B:47:LEU:HD11	1.98	0.45
2:F:21:LEU:HD12	2:F:73:LEU:HD23	1.99	0.44
2:B:21:LEU:HD22	2:B:102:THR:HG21	2.00	0.44
1:I:22:CYS:HB3	1:I:78:LEU:HB3	1.99	0.44
3:G:66:ARG:NH2	3:G:86:ASP:OD1	2.51	0.44
1:I:39:GLN:HB2	1:I:45:LEU:HD23	2.00	0.44
2:J:61:ARG:NE	2:J:82:ASP:OD2	2.48	0.43
2:F:109:THR:HG21	3:G:61:ASP:HA	2.01	0.43
2:J:140:TYR:CG	2:J:141:PRO:HA	2.54	0.41
1:I:184:VAL:HG11	1:I:194:TYR:CE1	2.56	0.41
1:I:43:LYS:HD3	1:I:43:LYS:HA	1.84	0.41
2:J:197:THR:OG1	3:K:100(A):UNK:O	2.38	0.41
2:B:35:TRP:CZ3	2:B:88:CYS:HB3	2.56	0.41
1:I:52:TRP:CD2	1:I:56:ASN:HB2	2.56	0.40
2:F:78:LEU:HD12	2:F:78:LEU:HA	1.91	0.40
4:D:9:ASN:HB2	4:D:12:PRO:HG3	2.04	0.40
2:F:140:TYR:CG	2:F:141:PRO:HA	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:33:LEU:HD22	2:J:71:PHE:CG	2.56	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	216/224 (96%)	210 (97%)	6 (3%)	0	100	100
1	E	212/224 (95%)	207 (98%)	5 (2%)	0	100	100
1	I	214/224 (96%)	209 (98%)	5 (2%)	0	100	100
2	B	211/215 (98%)	204 (97%)	7 (3%)	0	100	100
2	F	212/215 (99%)	203 (96%)	9 (4%)	0	100	100
2	J	212/215 (99%)	205 (97%)	7 (3%)	0	100	100
3	C	46/121 (38%)	43 (94%)	3 (6%)	0	100	100
3	G	46/121 (38%)	43 (94%)	3 (6%)	0	100	100
3	K	46/121 (38%)	43 (94%)	3 (6%)	0	100	100
4	D	9/12 (75%)	7 (78%)	2 (22%)	0	100	100
4	H	6/12 (50%)	6 (100%)	0	0	100	100
4	L	8/12 (67%)	7 (88%)	1 (12%)	0	100	100
All	All	1438/1716 (84%)	1387 (96%)	51 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	182/188 (97%)	181 (100%)	1 (0%)	88	96
1	E	176/188 (94%)	174 (99%)	2 (1%)	73	92
1	I	179/188 (95%)	174 (97%)	5 (3%)	43	76
2	B	183/186 (98%)	182 (100%)	1 (0%)	88	96
2	F	183/186 (98%)	181 (99%)	2 (1%)	73	92
2	J	182/186 (98%)	180 (99%)	2 (1%)	73	92
3	C	38/39 (97%)	37 (97%)	1 (3%)	46	77
3	G	38/39 (97%)	38 (100%)	0	100	100
3	K	38/39 (97%)	37 (97%)	1 (3%)	46	77
4	D	8/9 (89%)	8 (100%)	0	100	100
4	H	6/9 (67%)	6 (100%)	0	100	100
4	L	7/9 (78%)	6 (86%)	1 (14%)	3	10
All	All	1220/1266 (96%)	1204 (99%)	16 (1%)	69	90

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	TRP
1	E	28	THR
1	E	52	TRP
2	F	6	GLN
2	F	94	SER
2	B	100	GLN
1	I	52	TRP
1	I	105	GLN
1	I	193	THR
1	I	205	THR
1	I	209	LYS
2	J	20	THR
2	J	197	THR
3	K	68	THR
3	C	3	GLN
4	L	11	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such

sidechains are listed below:

Mol	Chain	Res	Type
1	E	56	ASN
1	I	99	ASN
1	I	105	GLN
3	C	3	GLN
4	D	5	ASN
4	L	5	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 monosaccharides 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	220/224 (98%)	-0.11	4 (1%) 68 67	23, 37, 67, 89	0
1	E	216/224 (96%)	0.37	9 (4%) 36 32	28, 52, 85, 101	0
1	I	218/224 (97%)	-0.09	2 (0%) 84 84	26, 43, 70, 98	0
2	B	213/215 (99%)	-0.15	0 100 100	21, 39, 73, 136	0
2	F	214/215 (99%)	0.36	16 (7%) 14 11	30, 53, 91, 136	0
2	J	214/215 (99%)	-0.04	1 (0%) 91 91	24, 43, 87, 123	0
3	C	48/121 (39%)	0.39	2 (4%) 36 32	33, 55, 104, 128	0
3	G	48/121 (39%)	0.74	3 (6%) 20 16	39, 72, 111, 135	0
3	K	48/121 (39%)	0.02	1 (2%) 63 61	23, 42, 67, 100	0
4	D	11/12 (91%)	0.43	1 (9%) 9 6	41, 60, 100, 102	0
4	H	8/12 (66%)	1.63	4 (50%) 0 0	81, 90, 109, 114	0
4	L	10/12 (83%)	0.28	1 (10%) 7 5	49, 69, 79, 93	0
All	All	1468/1716 (85%)	0.10	44 (2%) 50 45	21, 45, 87, 136	0

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	41	PRO	4.1
3	G	39	GLN	4.0
1	E	127	SER	3.9
3	G	41	PRO	3.6
2	F	27(A)	SER	3.4
4	H	6	ALA	3.3
2	F	67	SER	3.2
4	L	2	ALA	3.1
1	E	72	ASP	3.0
2	F	24	ARG	3.0
1	E	34	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
1	E	22	CYS	2.8
2	F	66	GLY	2.7
2	F	206	THR	2.7
2	F	70	ASP	2.7
1	E	1	GLN	2.7
2	F	191	VAL	2.7
4	H	11	ASN	2.6
1	E	52(A)	TYR	2.6
3	G	82(C)	LEU	2.6
2	F	28	VAL	2.5
1	I	100	TYR	2.5
2	J	94	SER	2.5
3	C	111	VAL	2.5
2	F	31	SER	2.5
1	E	52	TRP	2.4
1	A	132	SER	2.4
2	F	184	ALA	2.4
4	D	12	PRO	2.4
1	E	82(B)	SER	2.3
2	F	157	GLY	2.2
1	E	32	TYR	2.2
1	A	131	THR	2.2
4	H	8	PRO	2.2
4	H	5	ASN	2.2
1	I	99	ASN	2.2
2	F	68	GLY	2.1
2	F	23	CYS	2.1
2	F	26	SER	2.1
3	K	2	VAL	2.1
2	F	181	LEU	2.1
2	F	205	VAL	2.0
1	A	100	TYR	2.0
1	A	1	GLN	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 monosaccharides in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.