



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 04:27 PM GMT

PDB ID : 4EVN
Title : Crystal Structure of Fab CR6261 (somatic heavy chain with germline-reverted light chain)
Authors : Whittle, J.R.R.
Deposited on : 2012-04-26
Resolution : 2.85 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

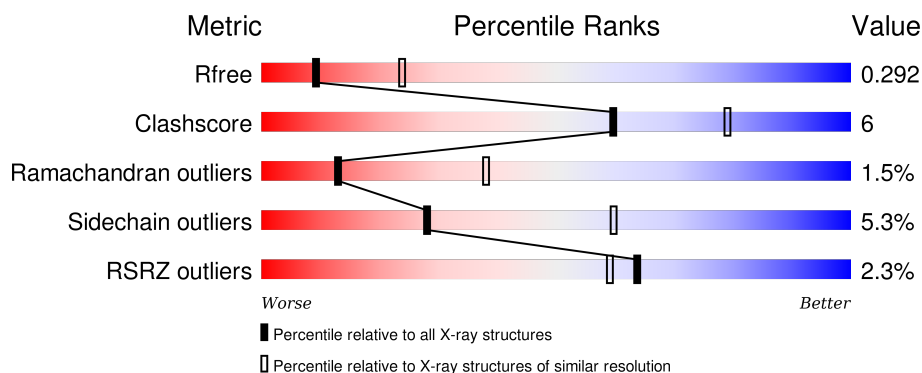
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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}	91344	2228 (2.90-2.82)
Clashscore	102246	2499 (2.90-2.82)
Ramachandran outliers	100387	2439 (2.90-2.82)
Sidechain outliers	100360	2442 (2.90-2.82)
RSRZ outliers	91569	2236 (2.90-2.82)

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. 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	242	<div> <div>3%</div> <div>73% 17% 9%</div> </div>
1	C	242	<div> <div>3%</div> <div>70% 19% 9%</div> </div>
1	E	242	<div> <div>3%</div> <div>71% 18% 9%</div> </div>
1	G	242	<div> <div>3%</div> <div>73% 17% 9%</div> </div>
1	I	242	<div> <div>3%</div> <div>74% 16% 9%</div> </div>

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Mol	Chain	Length	Quality of chain
1	K	242	
1	M	242	
1	O	242	
2	B	217	
2	D	217	
2	F	217	
2	H	217	
2	J	217	
2	L	217	
2	N	217	
2	P	217	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 25293 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 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	221	Total	C	N	O	S	0	0	0
			1623	1028	268	318	9			
1	C	221	Total	C	N	O	S	0	0	0
			1623	1028	268	318	9			
1	E	221	Total	C	N	O	S	0	0	0
			1625	1029	269	318	9			
1	G	221	Total	C	N	O	S	0	0	0
			1623	1028	268	318	9			
1	I	221	Total	C	N	O	S	0	0	0
			1625	1029	269	318	9			
1	K	221	Total	C	N	O	S	0	0	0
			1623	1028	268	318	9			
1	M	221	Total	C	N	O	S	0	0	0
			1623	1028	268	318	9			
1	O	221	Total	C	N	O	S	0	0	0
			1623	1028	268	318	9			

- Molecule 2 is a protein called Fab Lambda Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	213	Total	C	N	O	S	0	0	0
			1541	972	251	314	4			
2	D	213	Total	C	N	O	S	0	0	0
			1537	969	250	314	4			
2	F	213	Total	C	N	O	S	0	0	0
			1537	969	250	314	4			
2	H	213	Total	C	N	O	S	0	0	0
			1537	969	250	314	4			
2	J	213	Total	C	N	O	S	0	0	0
			1537	969	250	314	4			
2	L	213	Total	C	N	O	S	0	0	0
			1540	970	251	315	4			

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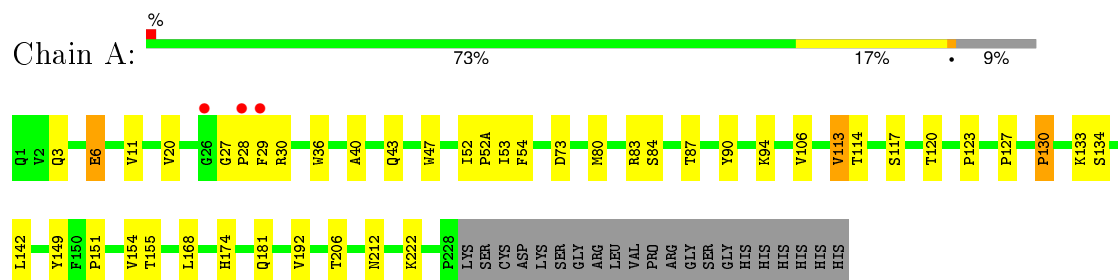
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	N	213	Total	C	N	O	S	0	0	0
			1537	969	250	314	4			
2	P	213	Total	C	N	O	S	0	0	0
			1539	970	251	314	4			

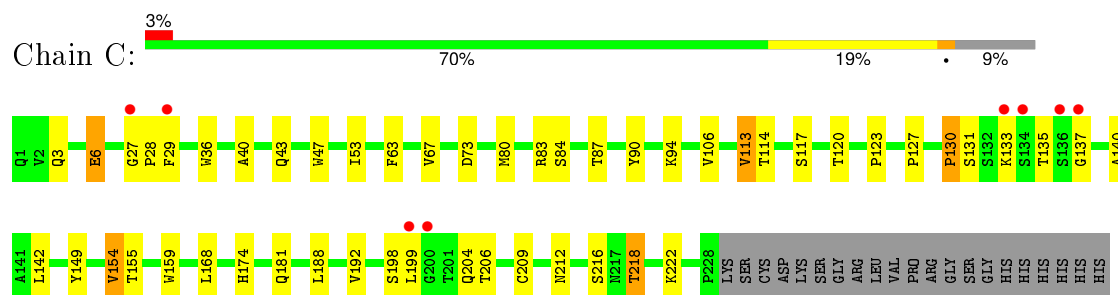
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

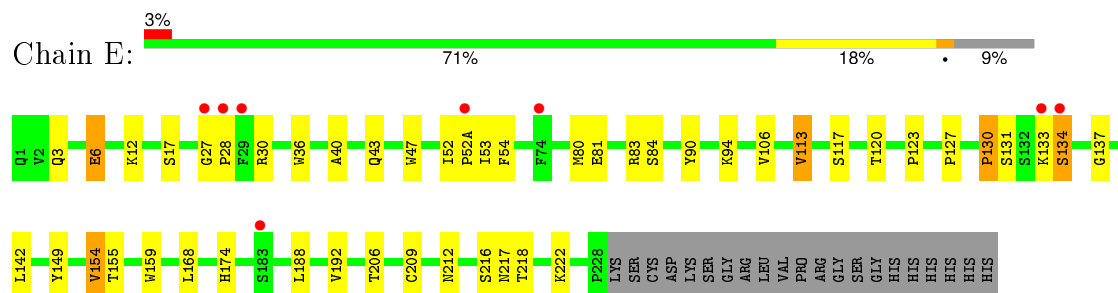
- Molecule 1: Fab Heavy Chain



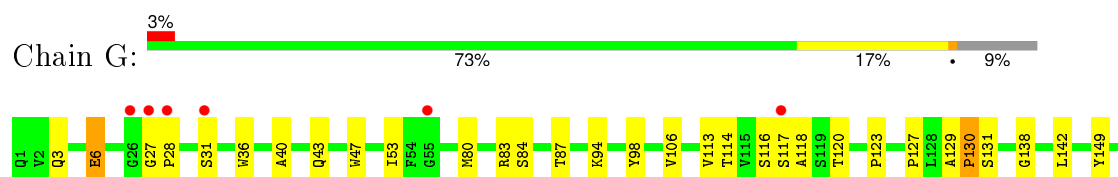
- Molecule 1: Fab Heavy Chain



- Molecule 1: Fab Heavy Chain



- Molecule 1: Fab Heavy Chain

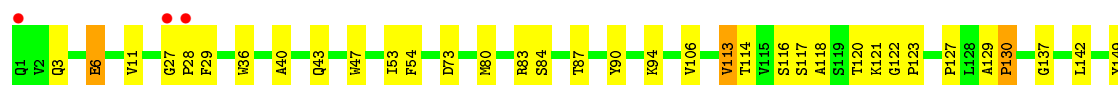




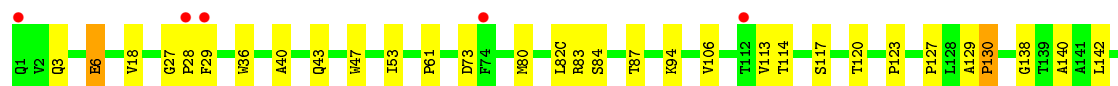
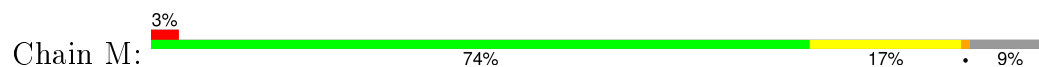
• Molecule 1: Fab Heavy Chain



• Molecule 1: Fab Heavy Chain



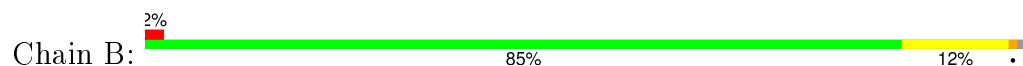
• Molecule 1: Fab Heavy Chain

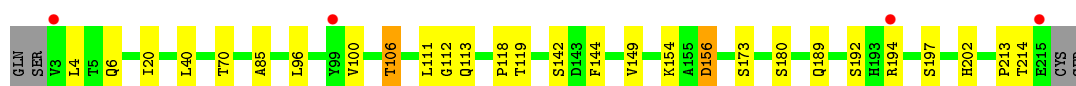


• Molecule 1: Fab Heavy Chain

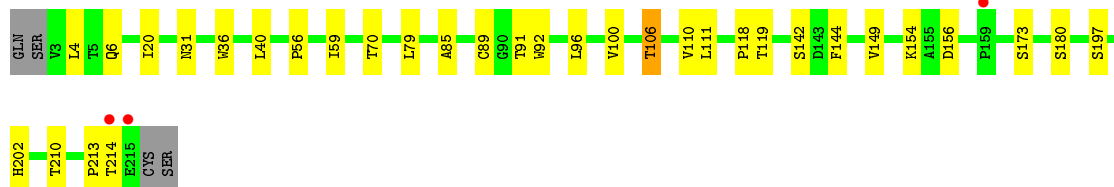
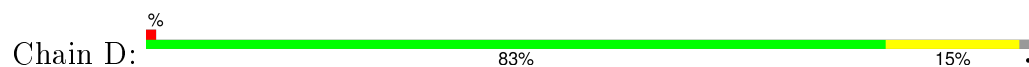


• Molecule 2: Fab Lambda Light Chain

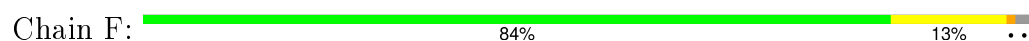




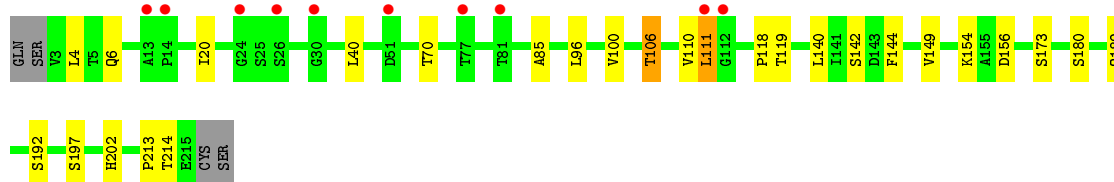
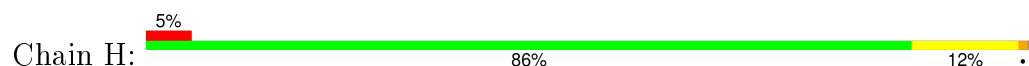
• Molecule 2: Fab Lambda Light Chain



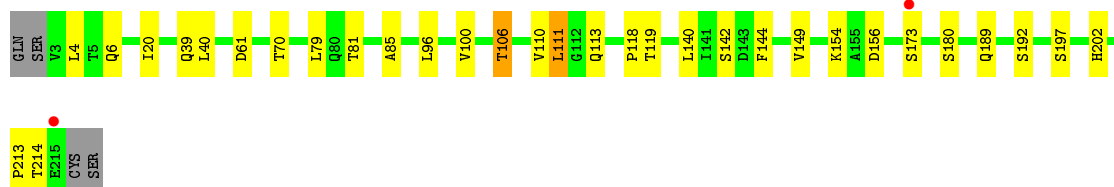
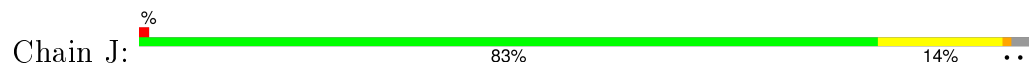
• Molecule 2: Fab Lambda Light Chain



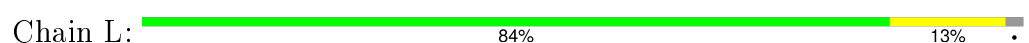
• Molecule 2: Fab Lambda Light Chain



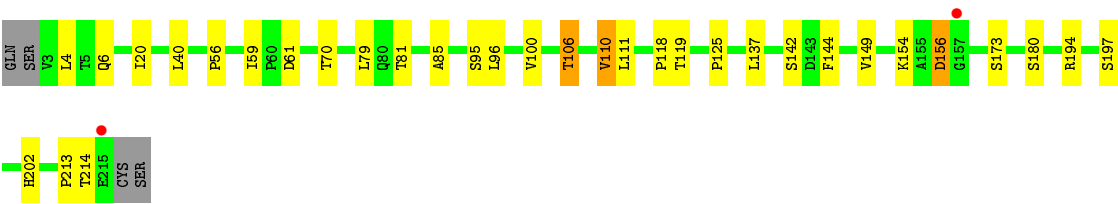
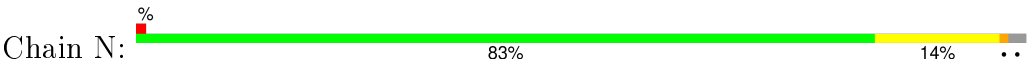
• Molecule 2: Fab Lambda Light Chain



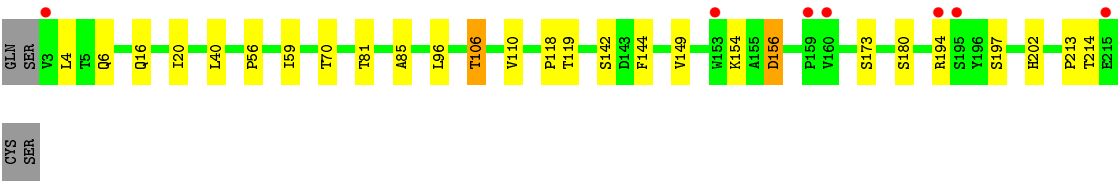
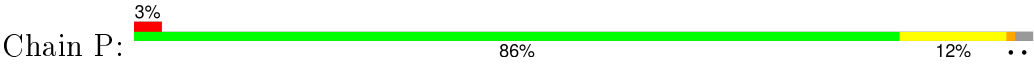
• Molecule 2: Fab Lambda Light Chain



• Molecule 2: Fab Lambda Light Chain



● Molecule 2: Fab Lambda Light Chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	70.11Å 159.27Å 176.44Å 90.00° 89.73° 90.00°	Depositor
Resolution (Å)	55.01 – 2.85 176.44 – 2.85	Depositor EDS
% Data completeness (in resolution range)	96.3 (55.01-2.85) 92.7 (176.44-2.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.17	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.35 (at 2.86Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.230 , 0.293 0.229 , 0.292	Depositor DCC
R_{free} test set	1946 reflections (2.31%)	DCC
Wilson B-factor (Å ²)	54.1	Xtriage
Anisotropy	0.457	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.20 , 2.1	EDS
Estimated twinning fraction	0.073 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	0 of 86892 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	25293	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.09% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.48	0/1664	0.59	0/2270
1	C	0.53	1/1664 (0.1%)	0.62	0/2270
1	E	0.57	0/1666	0.66	0/2272
1	G	0.50	0/1664	0.61	0/2270
1	I	0.52	0/1666	0.63	0/2272
1	K	0.53	0/1664	0.66	0/2270
1	M	0.49	0/1664	0.57	0/2270
1	O	0.51	0/1664	0.62	0/2270
2	B	0.46	0/1580	0.60	1/2168 (0.0%)
2	D	0.48	0/1576	0.61	0/2164
2	F	0.46	0/1576	0.62	0/2164
2	H	0.42	0/1576	0.56	0/2164
2	J	0.44	0/1576	0.59	0/2164
2	L	0.43	0/1579	0.60	0/2168
2	N	0.43	0/1576	0.59	0/2164
2	P	0.45	0/1578	0.60	0/2166
All	All	0.48	1/25933 (0.0%)	0.61	1/35486 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	181	GLN	CD-NE2	6.42	1.49	1.32

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	113	GLN	N-CA-C	-5.67	95.69	111.00

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	1623	0	1580	21	0
1	C	1623	0	1580	23	0
1	E	1625	0	1587	33	0
1	G	1623	0	1580	28	0
1	I	1625	0	1587	23	0
1	K	1623	0	1580	27	0
1	M	1623	0	1580	18	1
1	O	1623	0	1580	25	0
2	B	1541	0	1444	11	0
2	D	1537	0	1433	18	0
2	F	1537	0	1433	15	0
2	H	1537	0	1433	11	0
2	J	1537	0	1433	16	0
2	L	1540	0	1437	15	0
2	N	1537	0	1433	18	0
2	P	1539	0	1440	12	1
All	All	25293	0	24140	282	1

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.

The worst 5 of 282 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:192:SER:HB2	2:P:96:LEU:HD12	1.49	0.94
1:E:81:GLU:OE2	1:O:12:LYS:NZ	2.02	0.93
2:P:81:THR:HA	2:P:110:VAL:HG21	1.52	0.91
1:I:138:GLY:O	1:I:196:SER:N	2.06	0.89
2:D:96:LEU:HD12	2:F:192:SER:HB2	1.51	0.88

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:61:PRO:O	2:P:16:GLN:NE2[2_555]	2.08	0.12

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	219/242 (90%)	211 (96%)	6 (3%)	2 (1%)	21	52
1	C	219/242 (90%)	210 (96%)	6 (3%)	3 (1%)	14	40
1	E	219/242 (90%)	207 (94%)	9 (4%)	3 (1%)	14	40
1	G	219/242 (90%)	207 (94%)	10 (5%)	2 (1%)	21	52
1	I	219/242 (90%)	209 (95%)	7 (3%)	3 (1%)	14	40
1	K	219/242 (90%)	209 (95%)	7 (3%)	3 (1%)	14	40
1	M	219/242 (90%)	209 (95%)	8 (4%)	2 (1%)	21	52
1	O	219/242 (90%)	208 (95%)	7 (3%)	4 (2%)	11	33
2	B	211/217 (97%)	200 (95%)	7 (3%)	4 (2%)	10	32
2	D	211/217 (97%)	202 (96%)	6 (3%)	3 (1%)	14	40
2	F	211/217 (97%)	201 (95%)	7 (3%)	3 (1%)	14	40
2	H	211/217 (97%)	199 (94%)	8 (4%)	4 (2%)	10	32
2	J	211/217 (97%)	200 (95%)	7 (3%)	4 (2%)	10	32
2	L	211/217 (97%)	199 (94%)	7 (3%)	5 (2%)	7	25
2	N	211/217 (97%)	199 (94%)	8 (4%)	4 (2%)	10	32
2	P	211/217 (97%)	202 (96%)	6 (3%)	3 (1%)	14	40
All	All	3440/3672 (94%)	3272 (95%)	116 (3%)	52 (2%)	13	38

5 of 52 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	130	PRO

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Mol	Chain	Res	Type
2	J	111	LEU
2	L	111	LEU
2	N	111	LEU
2	B	214	THR

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	178/202 (88%)	166 (93%)	12 (7%)	20	47
1	C	178/202 (88%)	167 (94%)	11 (6%)	23	51
1	E	179/202 (89%)	168 (94%)	11 (6%)	23	52
1	G	178/202 (88%)	168 (94%)	10 (6%)	26	57
1	I	179/202 (89%)	169 (94%)	10 (6%)	26	57
1	K	178/202 (88%)	168 (94%)	10 (6%)	26	57
1	M	178/202 (88%)	168 (94%)	10 (6%)	26	57
1	O	178/202 (88%)	168 (94%)	10 (6%)	26	57
2	B	164/182 (90%)	156 (95%)	8 (5%)	31	63
2	D	163/182 (90%)	156 (96%)	7 (4%)	35	69
2	F	163/182 (90%)	156 (96%)	7 (4%)	35	69
2	H	163/182 (90%)	154 (94%)	9 (6%)	27	58
2	J	163/182 (90%)	156 (96%)	7 (4%)	35	69
2	L	164/182 (90%)	156 (95%)	8 (5%)	31	63
2	N	163/182 (90%)	155 (95%)	8 (5%)	31	63
2	P	164/182 (90%)	157 (96%)	7 (4%)	35	69
All	All	2733/3072 (89%)	2588 (95%)	145 (5%)	28	60

5 of 145 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	206	THR

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Mol	Chain	Res	Type
1	I	154	VAL
1	O	120	THR
2	H	70	THR
2	H	173	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	217	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 carbohydrates 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	221/242 (91%)	-0.34	3 (1%) 78 75	35, 65, 111, 200	0
1	C	221/242 (91%)	-0.32	8 (3%) 46 39	32, 60, 132, 231	0
1	E	221/242 (91%)	-0.18	8 (3%) 46 39	24, 57, 123, 199	0
1	G	221/242 (91%)	-0.05	7 (3%) 51 44	52, 75, 130, 200	0
1	I	221/242 (91%)	-0.20	8 (3%) 46 39	38, 72, 122, 200	0
1	K	221/242 (91%)	-0.19	5 (2%) 64 59	31, 64, 111, 198	0
1	M	221/242 (91%)	0.09	8 (3%) 46 39	48, 76, 133, 200	0
1	O	221/242 (91%)	-0.24	4 (1%) 71 68	28, 68, 146, 199	0
2	B	213/217 (98%)	-0.24	4 (1%) 70 66	38, 75, 107, 163	0
2	D	213/217 (98%)	-0.33	3 (1%) 78 75	30, 64, 104, 165	0
2	F	213/217 (98%)	-0.38	1 (0%) 91 90	31, 65, 105, 162	0
2	H	213/217 (98%)	0.26	10 (4%) 35 29	55, 92, 141, 207	0
2	J	213/217 (98%)	-0.33	2 (0%) 85 84	42, 76, 114, 161	0
2	L	213/217 (98%)	-0.27	1 (0%) 91 90	34, 71, 118, 163	0
2	N	213/217 (98%)	-0.31	2 (0%) 85 84	40, 77, 113, 183	0
2	P	213/217 (98%)	-0.24	7 (3%) 50 43	32, 73, 114, 164	0
All	All	3472/3672 (94%)	-0.20	81 (2%) 64 59	24, 72, 123, 231	0

The worst 5 of 81 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	M	28	PRO	11.9
1	M	29	PHE	8.3
2	J	173	SER	7.4
1	I	26	GLY	6.8
2	D	215	GLU	6.6

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 carbohydrates 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.