



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 02:44 PM UTC

PDB ID : 6I04 / pdb_00006i04
Title : Crystal structure of Sema domain of the Met receptor in complex with FAB
Authors : Casaletto, J.B.; Geddie, M.L.; Abu-Yousif, A.O.; Masson, K.; Fulgham, A.; Boudot, A.; Maiwald, T.; Kearns, J.D.; Kohli, N.; Su, S.; Razlog, M.; Raue, A.; Kalra, A.; Hakansson, M.; Logan, D.T.; Welin, M.; Chattopadhyay, S.; Harms, B.D.; Nielsen, U.B.; Schoeberl, B.; Lugovskoy, A.A.; MacBeath, G.
Deposited on : 2018-10-25
Resolution : 3.10 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

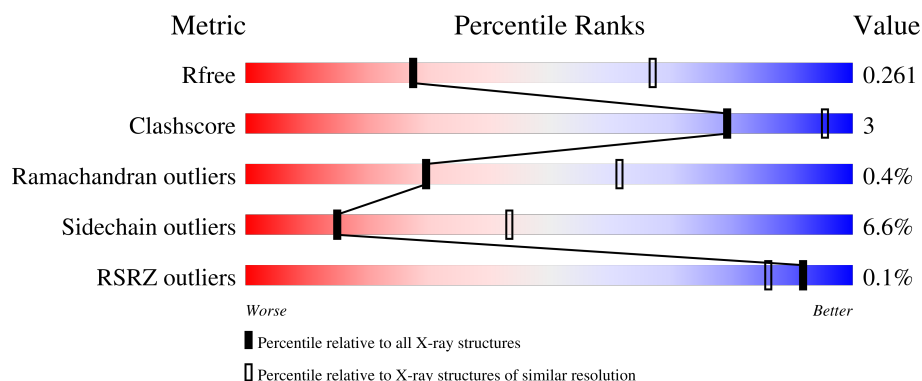
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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	552	
1	B	552	
2	C	230	
2	H	230	
3	D	214	

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Mol	Chain	Length	Quality of chain
3	L	214	90% 9% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13366 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 Hepatocyte growth factor receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	442	Total	C	N	O	S	0	0	0
			3512	2241	588	662	21			
1	B	432	Total	C	N	O	S	0	0	0
			3439	2194	576	648	21			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	565	GLY	-	expression tag	UNP P08581
A	566	GLY	-	expression tag	UNP P08581
A	567	GLY	-	expression tag	UNP P08581
A	568	GLY	-	expression tag	UNP P08581
A	569	GLY	-	expression tag	UNP P08581
A	570	SER	-	expression tag	UNP P08581
A	571	HIS	-	expression tag	UNP P08581
A	572	HIS	-	expression tag	UNP P08581
A	573	HIS	-	expression tag	UNP P08581
A	574	HIS	-	expression tag	UNP P08581
A	575	HIS	-	expression tag	UNP P08581
A	576	HIS	-	expression tag	UNP P08581
B	565	GLY	-	expression tag	UNP P08581
B	566	GLY	-	expression tag	UNP P08581
B	567	GLY	-	expression tag	UNP P08581
B	568	GLY	-	expression tag	UNP P08581
B	569	GLY	-	expression tag	UNP P08581
B	570	SER	-	expression tag	UNP P08581
B	571	HIS	-	expression tag	UNP P08581
B	572	HIS	-	expression tag	UNP P08581
B	573	HIS	-	expression tag	UNP P08581
B	574	HIS	-	expression tag	UNP P08581
B	575	HIS	-	expression tag	UNP P08581
B	576	HIS	-	expression tag	UNP P08581

- Molecule 2 is a protein called Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	211	Total	C	N	O	S	0	0	0
			1588	1016	255	312	5			
2	C	214	Total	C	N	O	S	0	0	0
			1609	1028	259	317	5			

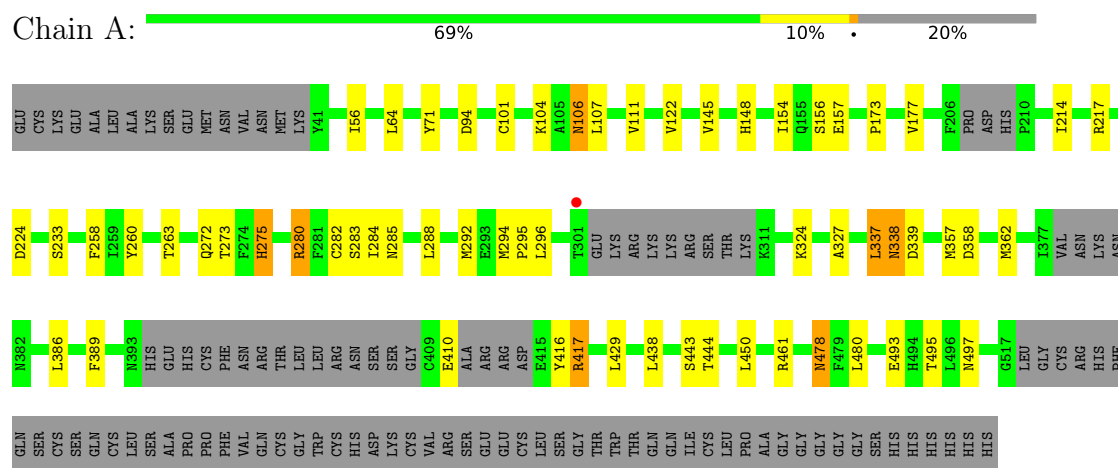
- Molecule 3 is a protein called Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	212	Total	C	N	O	S	0	0	0
			1609	1009	270	325	5			
3	D	212	Total	C	N	O	S	0	0	0
			1609	1009	270	325	5			

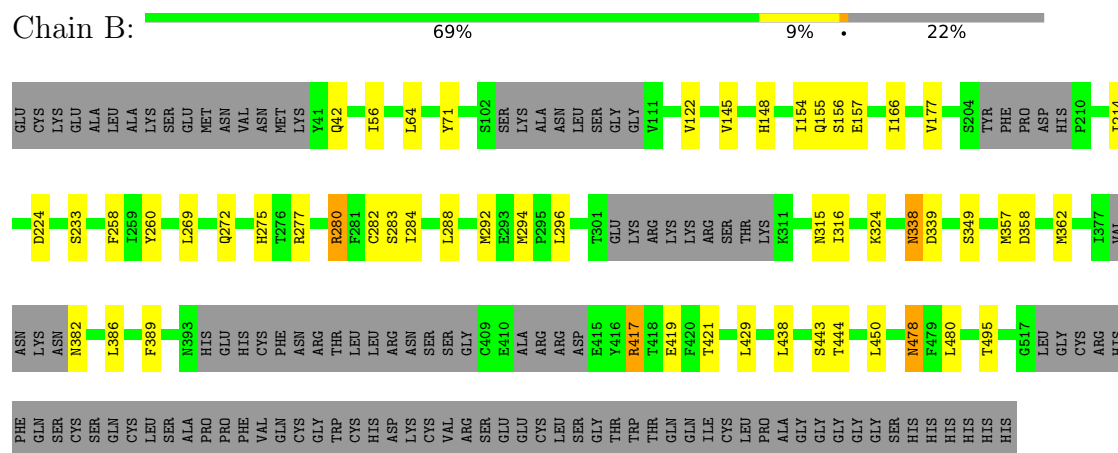
3 Residue-property plots [i](#)

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.

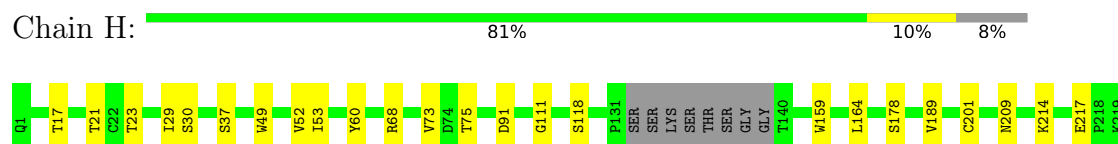
• Molecule 1: Hepatocyte growth factor receptor



• Molecule 1: Hepatocyte growth factor receptor

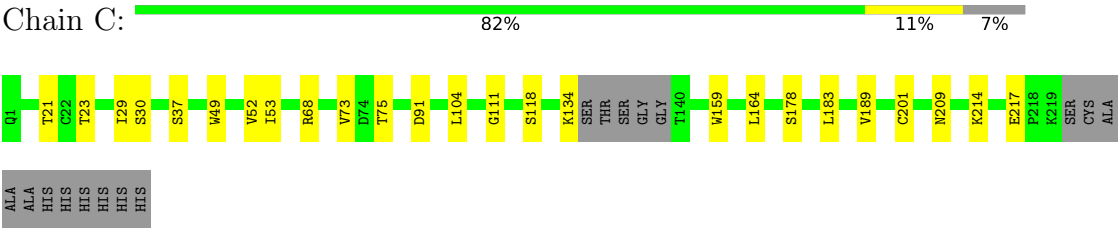


• Molecule 2: Fab heavy chain

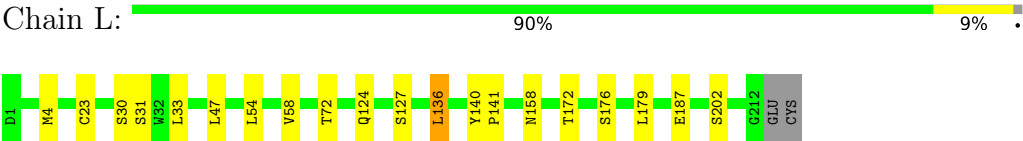


SER
CYS
ALA
ALA
ALA
HIS
HIS
HIS
HIS
HIS
HIS

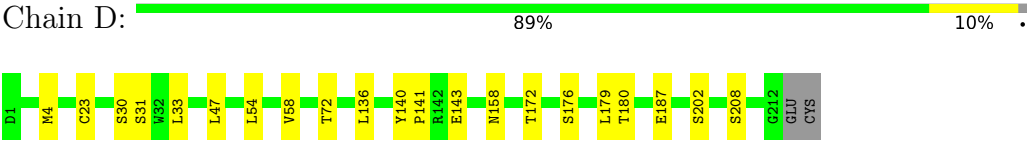
• Molecule 2: Fab heavy chain



• Molecule 3: Fab light chain



• Molecule 3: Fab light chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	73.93Å 85.50Å 101.30Å 77.49° 88.58° 68.76°	Depositor
Resolution (Å)	29.56 – 3.10 29.56 – 3.10	Depositor EDS
% Data completeness (in resolution range)	96.9 (29.56-3.10) 97.0 (29.56-3.10)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.29 (at 3.11Å)	Xtriage
Refinement program	REFMAC 5.8.0232	Depositor
R, R_{free}	0.202 , 0.261 0.206 , 0.261	Depositor DCC
R_{free} test set	1983 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	83.1	Xtriage
Anisotropy	0.067	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 44.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	13366	wwPDB-VP
Average B, all atoms (Å ²)	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.45% 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	0.99	0/3594	1.22	0/4875
1	B	0.98	0/3518	1.21	0/4772
2	C	1.00	0/1650	1.25	1/2256 (0.0%)
2	H	0.98	0/1629	1.23	1/2229 (0.0%)
3	D	1.00	0/1645	1.22	0/2235
3	L	1.00	0/1645	1.22	0/2235
All	All	0.99	0/13681	1.22	2/18602 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	111	GLY	CA-C-O	-6.25	118.16	122.22
2	H	111	GLY	CA-C-O	-5.99	118.33	122.22

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	3512	0	3406	21	0
1	B	3439	0	3336	22	0
2	C	1609	0	1603	11	0
2	H	1588	0	1580	10	0
3	D	1609	0	1570	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	L	1609	0	1570	6	0
All	All	13366	0	13065	72	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 (72) 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:338:ASN:C	1:B:338:ASN:HD22	1.81	0.88
1:A:338:ASN:HD22	1:A:338:ASN:C	1.83	0.87
1:A:338:ASN:HD22	1:A:339:ASP:N	1.84	0.74
3:D:4:MET:HE3	3:D:23:CYS:SG	2.30	0.72
1:B:338:ASN:HD22	1:B:339:ASP:N	1.90	0.68
3:L:4:MET:HE3	3:L:23:CYS:SG	2.35	0.66
2:H:29:ILE:HD11	2:H:75:THR:HA	1.79	0.65
1:A:288:LEU:O	1:A:417:ARG:NH2	2.30	0.64
1:B:282:CYS:SG	1:B:284:ILE:HG12	2.38	0.64
2:C:29:ILE:HD11	2:C:75:THR:HA	1.78	0.64
1:B:288:LEU:O	1:B:417:ARG:NH2	2.31	0.63
1:A:338:ASN:C	1:A:338:ASN:ND2	2.55	0.60
1:A:173:PRO:O	1:A:217:ARG:NH1	2.35	0.60
1:B:386:LEU:HD12	1:B:419:GLU:HG3	1.83	0.60
3:L:158:ASN:HB3	3:L:179:LEU:HD12	1.85	0.59
1:A:282:CYS:SG	1:A:284:ILE:HG12	2.44	0.57
3:D:158:ASN:HB3	3:D:179:LEU:HD12	1.88	0.56
1:B:315:ASN:C	1:B:316:ILE:HD12	2.30	0.55
1:A:56:ILE:HG21	1:A:122:VAL:HG23	1.89	0.55
2:H:37:SER:HB3	2:H:52:VAL:HG22	1.89	0.55
1:A:357:MET:O	1:A:357:MET:HG2	2.07	0.53
1:A:275:HIS:CE1	1:A:295:PRO:HB3	2.43	0.53
1:B:277:ARG:NH1	1:B:419:GLU:OE2	2.42	0.52
1:A:56:ILE:HG21	1:A:122:VAL:CG2	2.40	0.51
1:B:358:ASP:HA	1:B:438:LEU:HB2	1.92	0.50
2:C:37:SER:HB3	2:C:52:VAL:HG22	1.93	0.50
1:B:316:ILE:HD13	1:B:349:SER:HB2	1.93	0.50
1:B:478:ASN:OD1	1:B:478:ASN:C	2.55	0.49
2:H:29:ILE:HD12	2:H:30:SER:N	2.28	0.48
1:B:338:ASN:C	1:B:338:ASN:ND2	2.55	0.47
1:B:258:PHE:CD1	1:B:280:ARG:HD3	2.49	0.47
1:A:258:PHE:CD1	1:A:280:ARG:HD3	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:358:ASP:HA	1:A:438:LEU:HB2	1.95	0.47
1:A:478:ASN:OD1	1:A:478:ASN:C	2.57	0.47
3:L:124:GLN:O	3:L:127:SER:OG	2.32	0.47
3:D:47:LEU:HA	3:D:58:VAL:HG21	1.96	0.47
1:A:260:TYR:CE2	1:A:280:ARG:HG3	2.50	0.47
1:B:56:ILE:HG21	1:B:122:VAL:HG23	1.95	0.47
2:C:134:LYS:HE3	3:D:208:SER:O	2.15	0.47
2:C:52:VAL:HG12	2:C:53:ILE:N	2.30	0.46
1:B:324:LYS:HE3	1:B:338:ASN:O	2.14	0.46
1:B:260:TYR:CE2	1:B:280:ARG:HG3	2.51	0.46
2:H:68:ARG:NH2	2:H:91:ASP:OD2	2.49	0.46
2:C:29:ILE:HD12	2:C:30:SER:N	2.31	0.45
3:L:47:LEU:HA	3:L:58:VAL:HG21	1.99	0.45
2:C:49:TRP:HZ2	2:C:52:VAL:HG23	1.82	0.45
2:C:29:ILE:HD13	2:C:73:VAL:CG1	2.47	0.45
1:B:382:ASN:N	1:B:421:THR:HG1	2.15	0.44
1:A:296:LEU:HD23	1:A:296:LEU:HA	1.88	0.44
2:H:52:VAL:HG12	2:H:53:ILE:N	2.32	0.44
1:B:56:ILE:HG21	1:B:122:VAL:CG2	2.48	0.44
1:B:64:LEU:HB2	1:B:71:TYR:HB2	1.99	0.44
1:A:324:LYS:HE3	1:A:338:ASN:O	2.17	0.44
2:H:29:ILE:HD13	2:H:73:VAL:CG1	2.48	0.43
2:C:49:TRP:CZ2	2:C:52:VAL:HG23	2.54	0.43
2:H:49:TRP:HZ2	2:H:52:VAL:HG23	1.84	0.43
2:C:68:ARG:NH2	2:C:91:ASP:OD2	2.52	0.43
2:C:159:TRP:CH2	2:C:201:CYS:HB3	2.53	0.43
1:A:94:ASP:OD2	2:H:60:TYR:OH	2.32	0.43
1:A:327:ALA:HA	1:A:337:LEU:HD11	2.01	0.43
1:B:166:ILE:HD11	2:C:104:LEU:HD12	2.01	0.42
1:B:296:LEU:HD23	1:B:296:LEU:HA	1.87	0.42
1:A:64:LEU:HB2	1:A:71:TYR:HB2	2.02	0.42
3:D:140:TYR:CG	3:D:141:PRO:HA	2.54	0.42
2:H:49:TRP:CZ2	2:H:52:VAL:HG23	2.55	0.42
2:H:159:TRP:CH2	2:H:201:CYS:HB3	2.55	0.42
1:B:386:LEU:HD23	1:B:389:PHE:HB2	2.02	0.41
3:L:136:LEU:HD23	3:L:136:LEU:N	2.35	0.41
3:L:140:TYR:CG	3:L:141:PRO:HA	2.55	0.41
1:A:145:VAL:HB	1:A:157:GLU:HB3	2.02	0.40
1:B:145:VAL:HB	1:B:157:GLU:HB3	2.03	0.40
1:A:386:LEU:HD23	1:A:389:PHE:HB2	2.03	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	430/552 (78%)	406 (94%)	21 (5%)	3 (1%)	18	49
1	B	418/552 (76%)	399 (96%)	18 (4%)	1 (0%)	43	73
2	C	210/230 (91%)	201 (96%)	9 (4%)	0	100	100
2	H	207/230 (90%)	198 (96%)	9 (4%)	0	100	100
3	D	210/214 (98%)	198 (94%)	11 (5%)	1 (0%)	24	57
3	L	210/214 (98%)	195 (93%)	14 (7%)	1 (0%)	24	57
All	All	1685/1992 (85%)	1597 (95%)	82 (5%)	6 (0%)	30	61

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	106	ASN
1	A	104	LYS
1	A	478	ASN
1	B	478	ASN
3	L	30	SER
3	D	30	SER

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	399/495 (81%)	364 (91%)	35 (9%)	9	33
1	B	392/495 (79%)	366 (93%)	26 (7%)	15	43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	C	188/199 (94%)	178 (95%)	10 (5%)	20	51
2	H	185/199 (93%)	175 (95%)	10 (5%)	20	50
3	D	183/185 (99%)	172 (94%)	11 (6%)	17	47
3	L	183/185 (99%)	174 (95%)	9 (5%)	22	53
All	All	1530/1758 (87%)	1429 (93%)	101 (7%)	15	43

All (101) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	101	CYS
1	A	106	ASN
1	A	107	LEU
1	A	111	VAL
1	A	148	HIS
1	A	154	ILE
1	A	156	SER
1	A	177	VAL
1	A	214	ILE
1	A	224	ASP
1	A	233	SER
1	A	263	THR
1	A	272	GLN
1	A	273	THR
1	A	275	HIS
1	A	280	ARG
1	A	283	SER
1	A	285	ASN
1	A	292	MET
1	A	294	MET
1	A	337	LEU
1	A	338	ASN
1	A	362	MET
1	A	410	GLU
1	A	416	TYR
1	A	417	ARG
1	A	429	LEU
1	A	443	SER
1	A	444	THR
1	A	450	LEU
1	A	461	ARG
1	A	480	LEU

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Mol	Chain	Res	Type
1	A	493	GLU
1	A	495	THR
1	A	497	ASN
2	H	17	THR
2	H	21	THR
2	H	23	THR
2	H	118	SER
2	H	164	LEU
2	H	178	SER
2	H	189	VAL
2	H	209	ASN
2	H	214	LYS
2	H	217	GLU
3	L	31	SER
3	L	33	LEU
3	L	54	LEU
3	L	72	THR
3	L	136	LEU
3	L	172	THR
3	L	176	SER
3	L	187	GLU
3	L	202	SER
1	B	42	GLN
1	B	148	HIS
1	B	154	ILE
1	B	155	GLN
1	B	156	SER
1	B	177	VAL
1	B	214	ILE
1	B	224	ASP
1	B	233	SER
1	B	269	LEU
1	B	272	GLN
1	B	275	HIS
1	B	280	ARG
1	B	283	SER
1	B	292	MET
1	B	294	MET
1	B	338	ASN
1	B	357	MET
1	B	362	MET
1	B	417	ARG

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Mol	Chain	Res	Type
1	B	429	LEU
1	B	443	SER
1	B	444	THR
1	B	450	LEU
1	B	480	LEU
1	B	495	THR
2	C	21	THR
2	C	23	THR
2	C	118	SER
2	C	164	LEU
2	C	178	SER
2	C	183	LEU
2	C	189	VAL
2	C	209	ASN
2	C	214	LYS
2	C	217	GLU
3	D	31	SER
3	D	33	LEU
3	D	54	LEU
3	D	72	THR
3	D	136	LEU
3	D	143	GLU
3	D	172	THR
3	D	176	SER
3	D	180	THR
3	D	187	GLU
3	D	202	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	ASN
1	A	58	HIS
1	A	117	ASN
1	A	142	GLN
1	A	232	GLN
1	A	275	HIS
1	A	289	HIS
1	A	338	ASN
1	A	425	GLN
1	A	433	GLN
1	A	464	GLN

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Mol	Chain	Res	Type
1	A	498	GLN
2	H	169	HIS
3	L	79	GLN
3	L	137	ASN
3	L	160	GLN
1	B	54	ASN
1	B	117	ASN
1	B	142	GLN
1	B	289	HIS
1	B	338	ASN
1	B	388	HIS
1	B	433	GLN
1	B	464	GLN
1	B	498	GLN
2	C	169	HIS
3	D	79	GLN
3	D	137	ASN
3	D	160	GLN
3	D	210	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	442/552 (80%)	-0.38	1 (0%) 91 83	60, 94, 131, 163	0
1	B	432/552 (78%)	-0.30	0 100 100	68, 97, 131, 160	0
2	C	214/230 (93%)	-0.55	0 100 100	52, 77, 116, 137	0
2	H	211/230 (91%)	-0.63	0 100 100	53, 76, 104, 134	0
3	D	212/214 (99%)	-0.51	0 100 100	62, 85, 108, 120	0
3	L	212/214 (99%)	-0.51	0 100 100	55, 82, 105, 116	0
All	All	1723/1992 (86%)	-0.45	1 (0%) 92 86	52, 88, 123, 163	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	301	THR	2.1

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 ⓘ

There are no such residues in this entry.