



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 06:00 PM UTC

PDB ID : 5B5V / pdb_00005b5v
Title : Structure of full-length MOB1b
Authors : KIM, S.-Y.; Tachioka, Y.; Mori, T.; Hakoshima, T.
Deposited on : 2016-05-24
Resolution : 2.19 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:

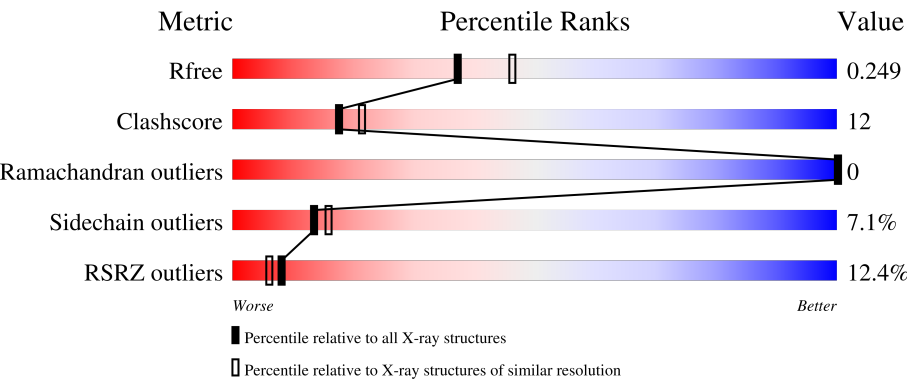
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
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 2.19 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	218	
1	B	218	
1	C	218	
1	D	218	
1	E	218	

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Mol	Chain	Length	Quality of chain
1	F	218	% .. 96%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6325 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 MOB kinase activator 1B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	187	Total	C	N	O	S	0	0	0
			1533	995	248	281	9			
1	B	183	Total	C	N	O	S	0	0	0
			1505	975	243	278	9			
1	C	187	Total	C	N	O	S	0	0	0
			1533	995	248	281	9			
1	D	179	Total	C	N	O	S	0	0	0
			1473	956	239	269	9			
1	E	8	Total	C	N	O		0	0	0
			63	41	11	11				
1	F	8	Total	C	N	O		0	0	0
			63	41	11	11				

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP Q8BPB0
A	0	PRO	-	expression tag	UNP Q8BPB0
B	-1	GLY	-	expression tag	UNP Q8BPB0
B	0	PRO	-	expression tag	UNP Q8BPB0
C	-1	GLY	-	expression tag	UNP Q8BPB0
C	0	PRO	-	expression tag	UNP Q8BPB0
D	-1	GLY	-	expression tag	UNP Q8BPB0
D	0	PRO	-	expression tag	UNP Q8BPB0
E	-1	GLY	-	expression tag	UNP Q8BPB0
E	0	PRO	-	expression tag	UNP Q8BPB0
F	-1	GLY	-	expression tag	UNP Q8BPB0
F	0	PRO	-	expression tag	UNP Q8BPB0

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Zn 1 1	0	0
2	B	1	Total Zn 1 1	0	0
2	C	1	Total Zn 1 1	0	0
2	D	1	Total Zn 1 1	0	0

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Cl 1 1	0	0
3	C	1	Total Cl 1 1	0	0

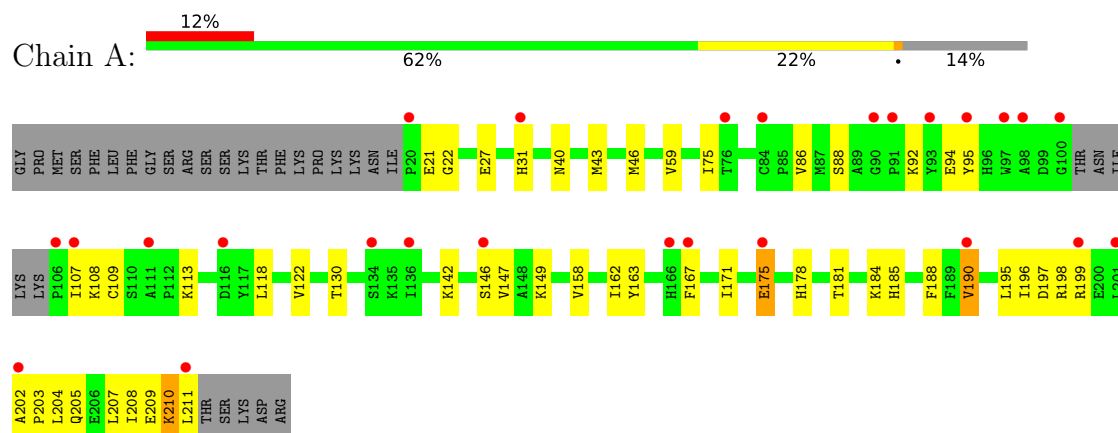
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	30	Total O 30 30	0	0
4	B	47	Total O 47 47	0	0
4	C	34	Total O 34 34	0	0
4	D	38	Total O 38 38	0	0

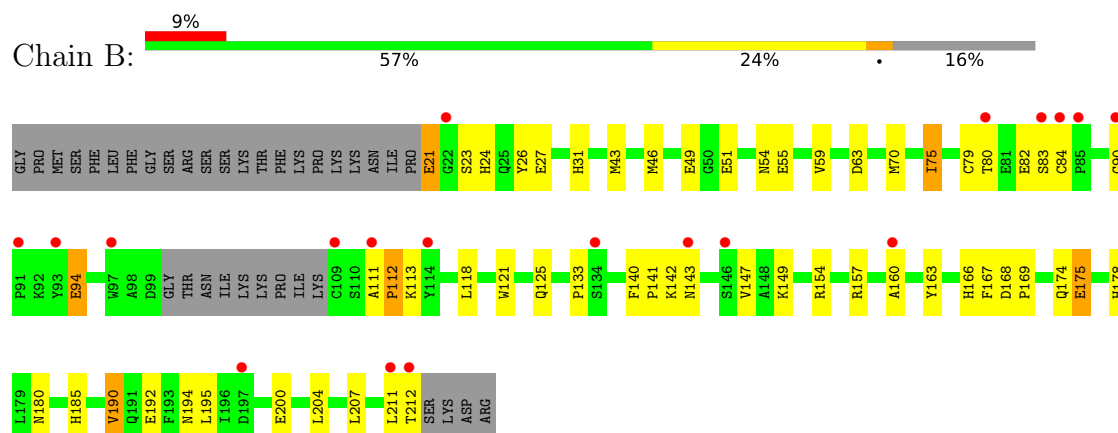
3 Residue-property plots [i](#)

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.

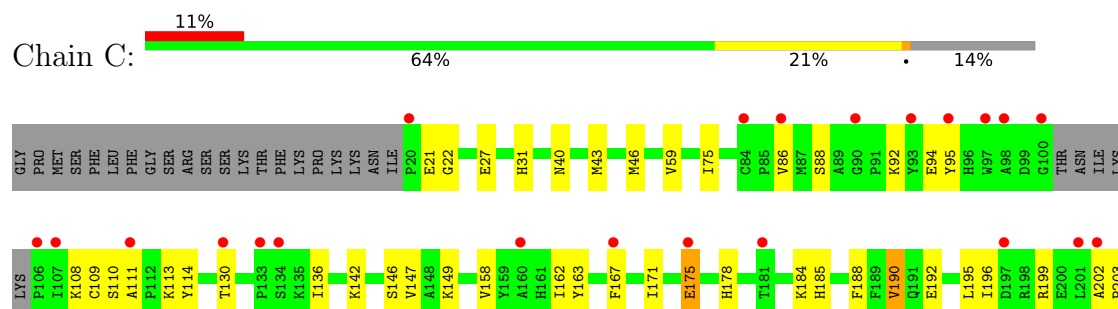
• Molecule 1: MOB kinase activator 1B

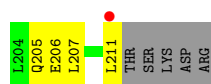


• Molecule 1: MOB kinase activator 1B

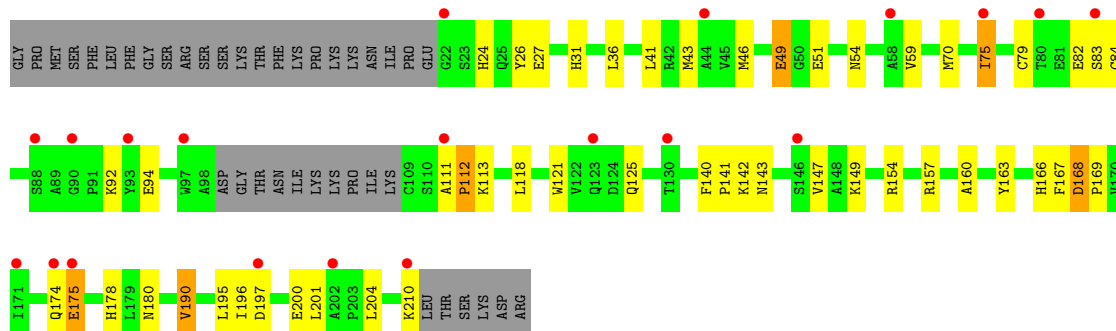


• Molecule 1: MOB kinase activator 1B

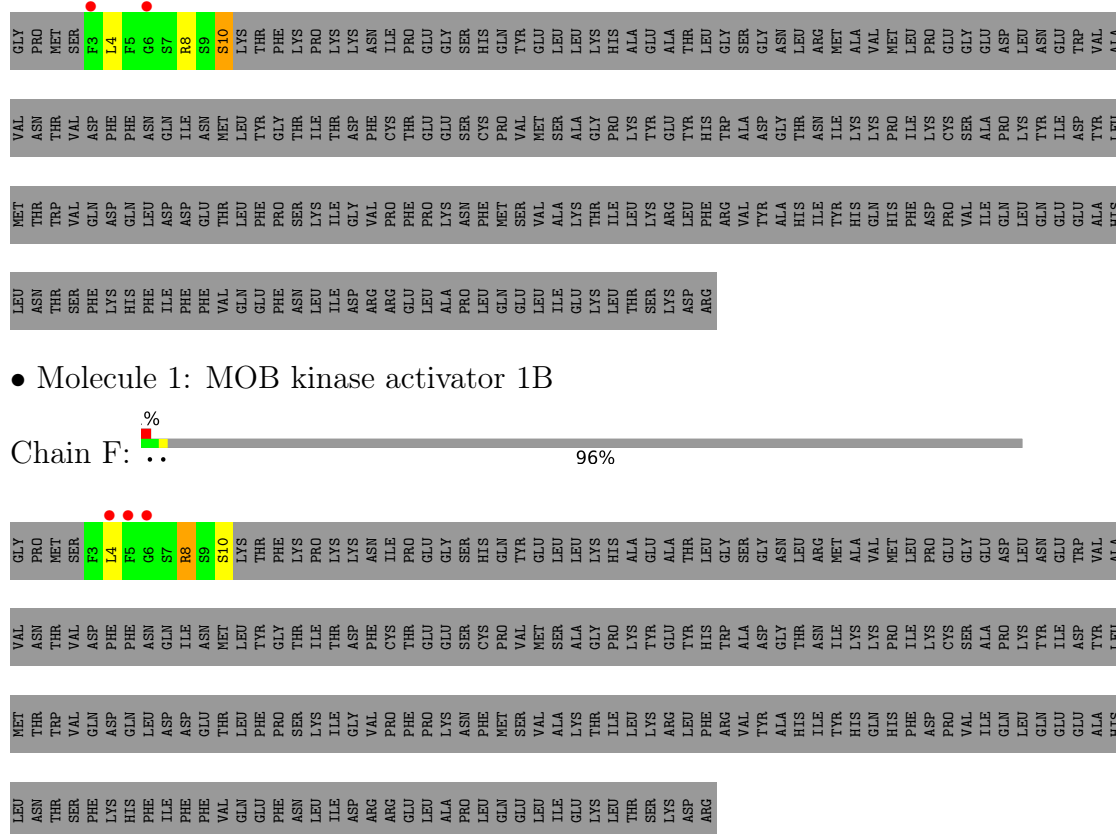




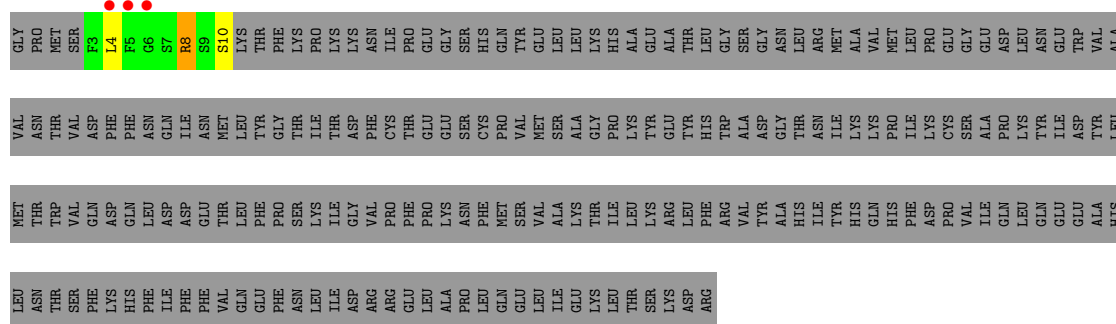
● Molecule 1: MOB kinase activator 1B



● Molecule 1: MOB kinase activator 1B



● Molecule 1: MOB kinase activator 1B



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	59.35Å 127.69Å 59.29Å 90.00° 91.03° 90.00°	Depositor
Resolution (Å)	29.67 – 2.19 29.67 – 2.19	Depositor EDS
% Data completeness (in resolution range)	97.3 (29.67-2.19) 93.1 (29.67-2.19)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.60 (at 2.20Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.233 , 0.246 0.234 , 0.249	Depositor DCC
R_{free} test set	2214 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	46.1	Xtriage
Anisotropy	0.434	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 59.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.219 for -l,k,h 0.258 for -h,-k,l 0.390 for l,-k,h	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6325	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.77% 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

Bond lengths and bond angles in the following residue types are not validated in this section: CL, ZN

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	0.64	0/1577	0.94	4/2138 (0.2%)
1	B	0.71	2/1547 (0.1%)	0.96	3/2099 (0.1%)
1	C	0.63	0/1577	0.91	2/2138 (0.1%)
1	D	0.72	1/1515 (0.1%)	0.93	3/2055 (0.1%)
1	E	1.14	0/64	0.84	0/83
1	F	1.08	0/64	0.90	0/83
All	All	0.69	3/6344 (0.0%)	0.94	12/8596 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	90	GLY	C-N	5.79	1.41	1.34
1	B	112	PRO	N-CD	5.26	1.55	1.47
1	D	112	PRO	N-CD	5.06	1.54	1.47

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	210	LYS	N-CA-C	-6.89	104.60	112.87
1	A	107	ILE	CB-CA-C	-5.99	104.76	111.23
1	A	175	GLU	N-CA-C	-5.61	103.97	111.87
1	C	175	GLU	N-CA-C	-5.59	103.98	111.87
1	A	22	GLY	N-CA-C	-5.37	106.81	115.08
1	C	22	GLY	N-CA-C	-5.34	106.85	115.08
1	B	175	GLU	CG-CD-OE2	5.22	130.41	118.40
1	D	175	GLU	CG-CD-OE2	5.15	130.25	118.40
1	B	84	CYS	CA-C-N	5.08	124.58	119.19
1	B	84	CYS	C-N-CA	5.08	124.58	119.19
1	D	84	CYS	CA-C-N	5.05	124.54	119.19
1	D	84	CYS	C-N-CA	5.05	124.54	119.19

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	1533	0	1481	39	0
1	B	1505	0	1445	45	0
1	C	1533	0	1481	44	1
1	D	1473	0	1417	42	0
1	E	63	0	59	4	0
1	F	63	0	59	9	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
4	A	30	0	0	5	0
4	B	47	0	0	6	0
4	C	34	0	0	6	0
4	D	38	0	0	1	1
All	All	6325	0	5942	150	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 12.

All (150) 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:A:197:ASP:OD2	4:A:401:HOH:O	1.68	1.08
1:A:31:HIS:ND1	1:C:175:GLU:OE2	1.91	1.01
1:C:95:TYR:OH	4:C:401:HOH:O	1.76	1.01
1:A:175:GLU:OE2	1:C:31:HIS:ND1	1.92	1.00
1:B:31:HIS:ND1	1:D:175:GLU:OE2	1.98	0.97
1:B:175:GLU:OE2	1:D:31:HIS:ND1	1.96	0.97
1:D:168:ASP:OD1	4:D:401:HOH:O	1.83	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:114:TYR:OH	4:C:402:HOH:O	1.85	0.93
1:A:185:HIS:HD2	4:A:426:HOH:O	1.57	0.87
1:A:95:TYR:OH	4:A:402:HOH:O	1.94	0.84
1:C:175:GLU:OE2	1:C:178:HIS:ND1	2.15	0.79
1:A:175:GLU:OE2	1:A:178:HIS:ND1	2.15	0.79
1:B:175:GLU:CD	1:B:178:HIS:HD1	1.92	0.78
1:D:175:GLU:CD	1:D:178:HIS:HD1	1.92	0.78
1:C:43:MET:HE3	1:C:46:MET:CE	2.14	0.77
1:B:175:GLU:OE2	1:B:178:HIS:ND1	2.16	0.75
1:D:175:GLU:OE2	1:D:178:HIS:ND1	2.16	0.73
1:B:75:ILE:HD11	1:B:169:PRO:HB2	1.71	0.71
1:C:192:GLU:OE1	4:C:403:HOH:O	2.08	0.71
1:A:203:PRO:HD3	1:E:8:ARG:HH12	1.55	0.71
1:A:92:LYS:O	1:E:10:SER:HA	1.90	0.71
1:D:75:ILE:HD11	1:D:169:PRO:HB2	1.71	0.71
1:A:43:MET:HA	1:A:46:MET:HE2	1.72	0.70
1:B:27:GLU:OE2	1:D:175:GLU:OE2	2.11	0.69
1:A:185:HIS:CD2	4:A:426:HOH:O	2.39	0.69
1:C:43:MET:HE3	1:C:46:MET:HE1	1.75	0.68
1:C:43:MET:HA	1:C:46:MET:HE2	1.74	0.68
1:C:92:LYS:O	1:F:10:SER:CB	2.42	0.67
1:B:24:HIS:HE2	1:B:51:GLU:CD	2.03	0.66
1:A:149:LYS:NZ	4:A:401:HOH:O	2.29	0.65
1:B:94:GLU:OE1	4:B:401:HOH:O	2.15	0.65
1:C:206:GLU:HB2	4:C:411:HOH:O	1.96	0.65
1:B:175:GLU:OE2	1:D:27:GLU:OE2	2.15	0.64
1:B:31:HIS:HD1	1:D:175:GLU:CD	2.04	0.63
1:B:24:HIS:NE2	1:B:51:GLU:OE1	2.28	0.62
1:C:43:MET:CE	1:C:46:MET:HE1	2.29	0.62
1:A:175:GLU:CD	1:C:31:HIS:HD1	2.04	0.62
1:D:163:TYR:OH	1:D:180:ASN:ND2	2.31	0.62
1:A:31:HIS:HD1	1:C:175:GLU:CD	2.02	0.62
1:A:149:LYS:HG2	1:A:195:LEU:HA	1.81	0.62
1:B:157:ARG:NH2	1:B:200:GLU:OE2	2.26	0.61
1:D:111:ALA:HB3	1:D:112:PRO:HD3	1.81	0.61
1:D:157:ARG:NH2	1:D:200:GLU:OE2	2.26	0.61
1:A:203:PRO:HD3	1:E:8:ARG:NH1	2.15	0.61
1:B:111:ALA:HB3	1:B:112:PRO:HD3	1.81	0.61
1:B:175:GLU:OE1	1:B:178:HIS:HB3	2.01	0.61
1:A:27:GLU:OE2	1:C:175:GLU:OE2	2.20	0.60
1:C:149:LYS:HG2	1:C:195:LEU:HA	1.81	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:175:GLU:OE1	1:D:178:HIS:HB3	2.01	0.60
1:B:163:TYR:OH	1:B:180:ASN:ND2	2.31	0.60
1:C:184:LYS:HG3	1:C:211:LEU:HD13	1.83	0.59
1:C:92:LYS:O	1:F:10:SER:HA	2.02	0.59
1:A:204:LEU:O	1:A:208:ILE:HG13	2.04	0.58
1:C:175:GLU:OE1	1:C:178:HIS:ND1	2.37	0.58
1:B:63:ASP:OD2	4:B:402:HOH:O	2.17	0.58
1:C:158:VAL:O	1:C:162:ILE:HG13	2.04	0.58
1:A:175:GLU:OE1	1:A:178:HIS:ND1	2.37	0.57
1:C:175:GLU:CD	1:C:178:HIS:ND1	2.62	0.57
1:A:158:VAL:O	1:A:162:ILE:HG13	2.04	0.57
1:A:175:GLU:OE2	1:C:27:GLU:OE2	2.22	0.57
1:B:175:GLU:CD	1:D:31:HIS:HD1	2.04	0.57
1:A:175:GLU:CD	1:A:178:HIS:ND1	2.62	0.56
1:A:209:GLU:C	1:A:211:LEU:N	2.62	0.56
1:D:43:MET:HA	1:D:46:MET:HE2	1.88	0.55
1:B:43:MET:HA	1:B:46:MET:HE2	1.89	0.55
1:A:209:GLU:C	1:A:211:LEU:H	2.15	0.54
1:D:24:HIS:HE2	1:D:51:GLU:CD	2.15	0.54
1:D:197:ASP:O	1:D:201:LEU:HG	2.07	0.54
1:B:143:ASN:O	1:B:147:VAL:HG23	2.08	0.53
1:D:143:ASN:O	1:D:147:VAL:HG23	2.08	0.53
1:A:92:LYS:HE2	1:E:10:SER:HB3	1.92	0.52
1:B:194:ASN:HA	4:B:404:HOH:O	2.09	0.52
1:D:190:VAL:HG11	1:D:196:ILE:HD12	1.92	0.51
1:A:109:CYS:HB3	1:A:113:LYS:HB3	1.93	0.51
1:A:198:ARG:HH21	1:B:133:PRO:HG2	1.76	0.51
1:C:184:LYS:HE2	1:C:188:PHE:HE2	1.77	0.50
1:C:185:HIS:HE1	4:C:408:HOH:O	1.93	0.50
1:B:118:LEU:HD11	1:B:154:ARG:HB3	1.94	0.50
1:B:192:GLU:OE1	4:B:403:HOH:O	2.19	0.50
1:A:167:PHE:CE2	1:A:171:ILE:HD11	2.47	0.50
1:A:184:LYS:HE2	1:A:188:PHE:HE2	1.77	0.50
1:D:118:LEU:HD11	1:D:154:ARG:HB3	1.94	0.50
1:D:190:VAL:HG22	1:D:195:LEU:HB2	1.94	0.49
1:C:167:PHE:CE2	1:C:171:ILE:HD11	2.47	0.49
1:A:208:ILE:O	1:A:211:LEU:N	2.41	0.49
1:B:190:VAL:HG22	1:B:195:LEU:HB2	1.94	0.49
1:D:121:TRP:O	1:D:125:GLN:HG2	2.13	0.49
1:C:92:LYS:O	1:F:10:SER:CA	2.60	0.49
1:B:160:ALA:HA	1:B:204:LEU:HD11	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:141:PRO:HB2	1:B:143:ASN:OD1	2.13	0.48
1:C:92:LYS:HD2	1:F:10:SER:HB2	1.95	0.48
1:B:121:TRP:O	1:B:125:GLN:HG2	2.13	0.48
1:C:203:PRO:HD3	1:F:8:ARG:NH2	2.29	0.48
1:D:160:ALA:HA	1:D:204:LEU:HD11	1.96	0.48
1:B:175:GLU:CD	1:D:31:HIS:ND1	2.67	0.47
1:C:211:LEU:C	1:C:211:LEU:HD12	2.39	0.47
1:D:141:PRO:HB2	1:D:143:ASN:OD1	2.13	0.47
1:B:49:GLU:HB3	1:D:174:GLN:HG3	1.97	0.47
1:D:196:ILE:HG21	1:D:201:LEU:HD21	1.95	0.47
1:A:198:ARG:NH1	1:B:55:GLU:OE2	2.48	0.47
1:C:109:CYS:HB3	1:C:113:LYS:HB3	1.97	0.47
1:C:110:SER:O	1:C:111:ALA:C	2.57	0.47
1:B:207:LEU:O	1:B:211:LEU:HG	2.15	0.47
1:B:79:CYS:O	1:B:112:PRO:HG3	2.15	0.46
1:C:202:ALA:HA	1:C:205:GLN:HG3	1.98	0.46
1:B:194:ASN:OD1	4:B:404:HOH:O	2.20	0.46
1:D:79:CYS:O	1:D:112:PRO:HG3	2.16	0.46
1:C:92:LYS:O	1:F:10:SER:HB3	2.13	0.46
1:B:31:HIS:ND1	1:D:175:GLU:CD	2.68	0.46
1:A:202:ALA:HA	1:A:205:GLN:HG3	1.97	0.45
1:B:80:THR:N	1:B:83:SER:OG	2.40	0.45
1:B:163:TYR:O	1:B:167:PHE:HB2	2.17	0.45
1:D:196:ILE:HG21	1:D:201:LEU:CD2	2.46	0.45
1:D:163:TYR:O	1:D:167:PHE:HB2	2.17	0.45
1:D:190:VAL:CG2	1:D:196:ILE:HG13	2.46	0.44
1:C:86:VAL:HG21	1:C:94:GLU:OE2	2.18	0.44
1:C:163:TYR:CZ	1:C:207:LEU:HD21	2.52	0.44
1:B:70:MET:HE3	1:D:26:TYR:CE2	2.53	0.44
1:A:181:THR:HG22	4:C:406:HOH:O	2.16	0.44
1:C:190:VAL:HG11	1:C:196:ILE:HD12	2.00	0.44
1:B:185:HIS:HD2	4:B:440:HOH:O	2.01	0.44
1:A:86:VAL:HG21	1:A:94:GLU:OE2	2.18	0.43
1:D:54:ASN:HB3	1:D:140:PHE:CD2	2.52	0.43
1:C:40:ASN:OD1	1:C:43:MET:HG2	2.18	0.43
1:B:54:ASN:HB3	1:B:140:PHE:CD2	2.53	0.43
1:B:166:HIS:O	1:B:169:PRO:HD2	2.18	0.43
1:A:190:VAL:HG11	1:A:196:ILE:HD12	2.00	0.43
1:B:26:TYR:CE2	1:D:70:MET:HE3	2.54	0.43
1:D:175:GLU:OE1	1:D:178:HIS:ND1	2.51	0.43
1:C:43:MET:CE	1:C:46:MET:CE	2.90	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:149:LYS:HG3	1:B:195:LEU:O	2.19	0.42
1:D:166:HIS:O	1:D:169:PRO:HD2	2.19	0.42
1:B:175:GLU:OE1	1:B:178:HIS:ND1	2.52	0.42
1:C:92:LYS:CD	1:F:10:SER:HB2	2.48	0.42
1:B:174:GLN:HG3	1:D:49:GLU:HB3	2.00	0.42
1:A:167:PHE:O	1:A:171:ILE:HG12	2.19	0.42
1:C:92:LYS:CE	1:F:10:SER:HB2	2.50	0.42
1:D:149:LYS:HG3	1:D:195:LEU:O	2.19	0.42
1:C:92:LYS:HE2	1:F:10:SER:HB2	2.02	0.41
1:A:163:TYR:CZ	1:A:207:LEU:HD21	2.55	0.41
1:C:109:CYS:HB3	1:C:113:LYS:HE3	2.02	0.41
1:C:167:PHE:O	1:C:171:ILE:HG12	2.20	0.41
1:A:40:ASN:OD1	1:A:43:MET:HG2	2.20	0.41
1:A:86:VAL:HG11	1:A:94:GLU:OE2	2.21	0.41
1:D:210:LYS:HA	1:D:210:LYS:HD2	1.87	0.41
1:D:36:LEU:HD22	1:D:41:LEU:HD22	2.04	0.40
1:A:118:LEU:O	1:A:122:VAL:HG23	2.21	0.40
1:B:21:GLU:C	1:B:23:SER:H	2.30	0.40
1:C:86:VAL:HG11	1:C:94:GLU:OE2	2.21	0.40
1:D:43:MET:HE3	1:D:43:MET:HB2	1.88	0.40

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:C:136:ILE:CG2	4:D:414:HOH:O[2_658]	2.09	0.11

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	183/218 (84%)	178 (97%)	5 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	179/218 (82%)	172 (96%)	7 (4%)	0	100	100
1	C	183/218 (84%)	176 (96%)	7 (4%)	0	100	100
1	D	175/218 (80%)	168 (96%)	7 (4%)	0	100	100
1	E	6/218 (3%)	6 (100%)	0	0	100	100
1	F	6/218 (3%)	6 (100%)	0	0	100	100
All	All	732/1308 (56%)	706 (96%)	26 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	168/197 (85%)	156 (93%)	12 (7%)	13	16
1	B	165/197 (84%)	155 (94%)	10 (6%)	17	20
1	C	168/197 (85%)	157 (94%)	11 (6%)	15	18
1	D	161/197 (82%)	150 (93%)	11 (7%)	14	17
1	E	7/197 (4%)	5 (71%)	2 (29%)	0	0
1	F	7/197 (4%)	5 (71%)	2 (29%)	0	0
All	All	676/1182 (57%)	628 (93%)	48 (7%)	13	16

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	GLU
1	A	59	VAL
1	A	75	ILE
1	A	88	SER
1	A	108	LYS
1	A	130	THR
1	A	142	LYS
1	A	146	SER

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Mol	Chain	Res	Type
1	A	147	VAL
1	A	190	VAL
1	A	199	ARG
1	A	210	LYS
1	B	21	GLU
1	B	59	VAL
1	B	75	ILE
1	B	82	GLU
1	B	94	GLU
1	B	113	LYS
1	B	142	LYS
1	B	168	ASP
1	B	190	VAL
1	B	212	THR
1	C	21	GLU
1	C	59	VAL
1	C	75	ILE
1	C	88	SER
1	C	108	LYS
1	C	130	THR
1	C	142	LYS
1	C	146	SER
1	C	147	VAL
1	C	190	VAL
1	C	199	ARG
1	D	49	GLU
1	D	59	VAL
1	D	75	ILE
1	D	82	GLU
1	D	83	SER
1	D	92	LYS
1	D	94	GLU
1	D	113	LYS
1	D	142	LYS
1	D	168	ASP
1	D	190	VAL
1	E	4	LEU
1	E	10	SER
1	F	4	LEU
1	F	8	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	96	HIS
1	B	174	GLN
1	B	180	ASN
1	C	96	HIS
1	D	180	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](#)

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	187/218 (85%)	1.00	26 (13%) 6 5	38, 57, 82, 93	0
1	B	183/218 (83%)	0.90	19 (10%) 11 9	38, 56, 78, 95	0
1	C	187/218 (85%)	1.01	23 (12%) 8 6	39, 58, 82, 94	0
1	D	179/218 (82%)	0.95	20 (11%) 10 8	38, 56, 77, 85	0
1	E	8/218 (3%)	1.32	2 (25%) 2 1	66, 75, 83, 87	0
1	F	8/218 (3%)	1.47	3 (37%) 1 0	71, 77, 85, 89	0
All	All	752/1308 (57%)	0.97	93 (12%) 8 6	38, 57, 81, 95	0

All (93) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	97	TRP	5.4
1	A	211	LEU	4.7
1	B	97	TRP	4.3
1	D	197	ASP	4.3
1	D	93	TYR	3.9
1	A	100	GLY	3.8
1	A	134	SER	3.8
1	C	20	PRO	3.6
1	D	22	GLY	3.6
1	C	167	PHE	3.4
1	B	90	GLY	3.3
1	D	80	THR	3.3
1	A	90	GLY	3.3
1	A	97	TRP	3.2
1	D	146	SER	3.2
1	C	106	PRO	3.2
1	F	6	GLY	3.2
1	C	211	LEU	3.2
1	C	134	SER	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	111	ALA	3.1
1	B	91	PRO	3.0
1	C	160	ALA	3.0
1	B	80	THR	3.0
1	C	84	CYS	3.0
1	A	167	PHE	2.9
1	C	100	GLY	2.9
1	A	107	ILE	2.9
1	C	98	ALA	2.9
1	F	5	PHE	2.8
1	C	181	THR	2.8
1	D	88	SER	2.8
1	B	197	ASP	2.8
1	B	84	CYS	2.8
1	C	95	TYR	2.7
1	D	90	GLY	2.7
1	C	93	TYR	2.7
1	B	146	SER	2.7
1	A	98	ALA	2.7
1	B	111	ALA	2.6
1	A	20	PRO	2.6
1	B	211	LEU	2.6
1	C	111	ALA	2.6
1	E	3	PHE	2.5
1	C	90	GLY	2.5
1	E	6	GLY	2.5
1	C	202	ALA	2.5
1	C	86	VAL	2.5
1	D	44	ALA	2.5
1	A	31	HIS	2.5
1	D	75	ILE	2.5
1	D	174	GLN	2.4
1	A	202	ALA	2.4
1	D	210	LYS	2.4
1	C	97	TRP	2.4
1	B	212	THR	2.4
1	C	197	ASP	2.4
1	C	107	ILE	2.4
1	D	83	SER	2.3
1	A	84	CYS	2.3
1	A	116	ASP	2.3
1	F	4	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	93	TYR	2.3
1	B	22	GLY	2.2
1	D	58	ALA	2.2
1	A	136	ILE	2.2
1	D	175	GLU	2.2
1	B	134	SER	2.2
1	D	171	ILE	2.2
1	A	175	GLU	2.2
1	B	83	SER	2.2
1	A	76	THR	2.2
1	B	85	PRO	2.1
1	A	166	HIS	2.1
1	A	91	PRO	2.1
1	A	106	PRO	2.1
1	A	190	VAL	2.1
1	D	202	ALA	2.1
1	D	123	GLN	2.1
1	A	201	LEU	2.1
1	C	201	LEU	2.1
1	C	175	GLU	2.1
1	A	199	ARG	2.1
1	B	114	TYR	2.1
1	C	133	PRO	2.1
1	B	160	ALA	2.1
1	D	111	ALA	2.1
1	B	143	ASN	2.0
1	B	109	CYS	2.0
1	C	130	THR	2.0
1	A	95	TYR	2.0
1	A	146	SER	2.0
1	D	130	THR	2.0
1	B	93	TYR	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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	CL	A	302	1/1	0.91	0.09	70,70,70,70	0
3	CL	C	302	1/1	0.95	0.08	69,69,69,69	0
2	ZN	C	301	1/1	0.96	0.06	60,60,60,60	0
2	ZN	A	301	1/1	0.97	0.04	61,61,61,61	0
2	ZN	B	301	1/1	0.98	0.04	59,59,59,59	0
2	ZN	D	301	1/1	0.99	0.03	58,58,58,58	0

6.5 Other polymers [i](#)

There are no such residues in this entry.