



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 05:53 PM GMT

PDB ID : 2J0T
Title : CRYSTAL STRUCTURE OF THE CATALYTIC DOMAIN OF MMP-1 IN
COMPLEX WITH THE INHIBITORY DOMAIN OF TIMP-1
Authors : Iyer, S.; Wei, S.; Brew, K.; Acharya, K.R.
Deposited on : 2006-08-04
Resolution : 2.54 Å(reported)

This is a full wwPDB validation 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/ValidationPDFNotes.html>

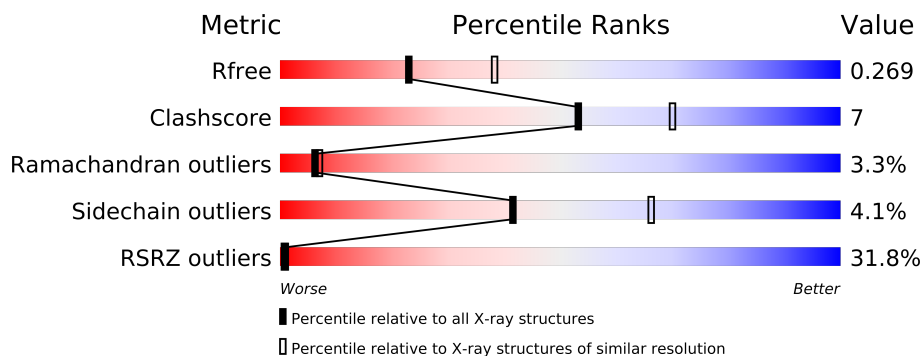
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.54 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}	66092	3413 (2.58-2.50)
Clashscore	79885	4284 (2.58-2.50)
Ramachandran outliers	78287	4193 (2.58-2.50)
Sidechain outliers	78261	4195 (2.58-2.50)
RSRZ outliers	66119	3414 (2.58-2.50)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	170	
1	B	170	
1	C	170	
2	D	126	
2	E	126	
2	F	126	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6547 atoms, of which 0 are hydrogen and 0 are deuterium.

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 INTERSTITIAL COLLAGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	161	Total	C	N	O	S	0	0	0
			1268	791	227	248	2			
1	B	162	Total	C	N	O	S	0	0	0
			1261	787	224	248	2			
1	C	159	Total	C	N	O	S	0	0	0
			1228	769	218	239	2			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	100	MET	-	EXPRESSION TAG	UNP P03956
B	100	MET	-	EXPRESSION TAG	UNP P03956
C	100	MET	-	EXPRESSION TAG	UNP P03956

- Molecule 2 is a protein called METALLOPROTEINASE INHIBITOR 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	124	Total	C	N	O	S	0	0	0
			906	574	156	167	9			
2	E	124	Total	C	N	O	S	0	0	0
			907	575	156	167	9			
2	F	124	Total	C	N	O	S	0	0	0
			921	582	161	169	9			

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Zn	0	0
			2	2		
3	A	2	Total	Zn	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	2	Total	Zn	0	0
			2	2		

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	3	Total	Ca	0	0
			3	3		
4	A	3	Total	Ca	0	0
			3	3		
4	C	3	Total	Ca	0	0
			3	3		

- Molecule 5 is water.

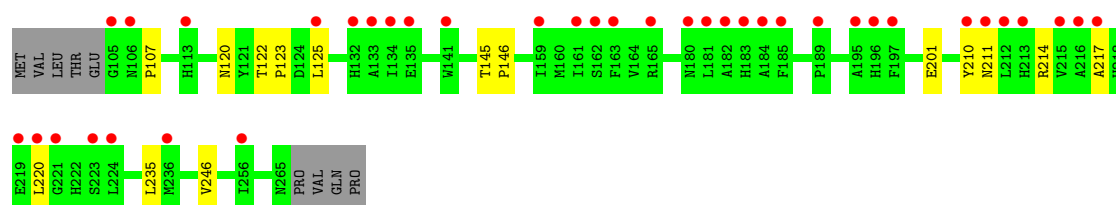
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	18	Total	O	0	0
			18	18		
5	B	9	Total	O	0	0
			9	9		
5	C	8	Total	O	0	0
			8	8		
5	D	3	Total	O	0	0
			3	3		
5	E	1	Total	O	0	0
			1	1		
5	F	2	Total	O	0	0
			2	2		

3 Residue-property plots

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 ($\text{RSRZ} > 2$). 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.

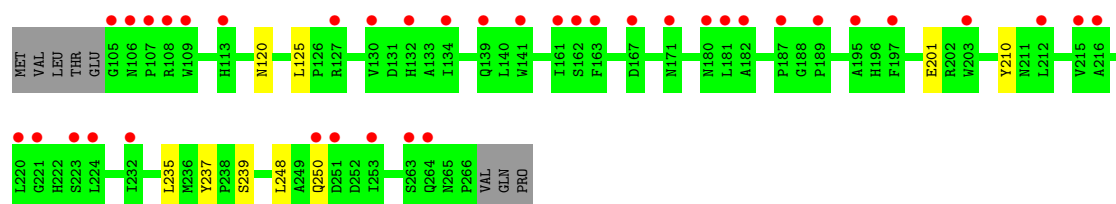
• Molecule 1: INTERSTITIAL COLLAGENASE

Chain A: 



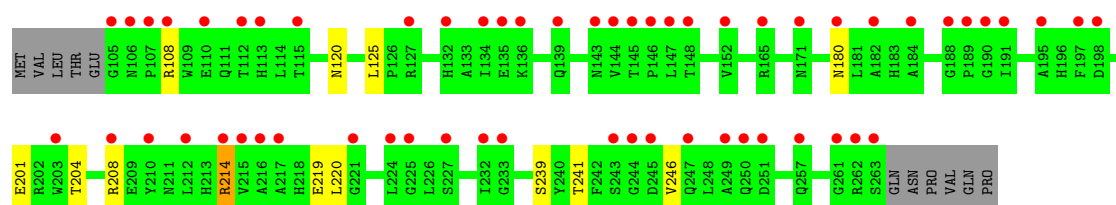
• Molecule 1: INTERSTITIAL COLLAGENASE

Chain B: 



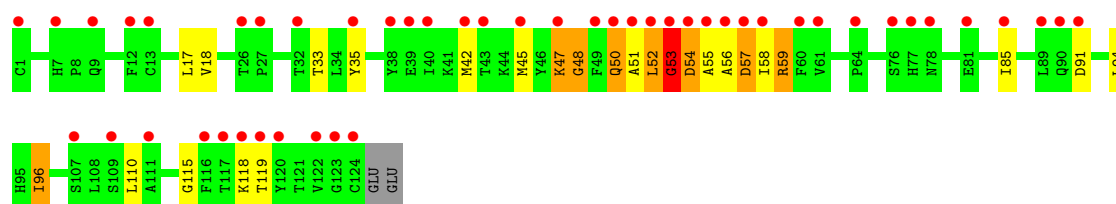
• Molecule 1: INTERSTITIAL COLLAGENASE

Chain C: 



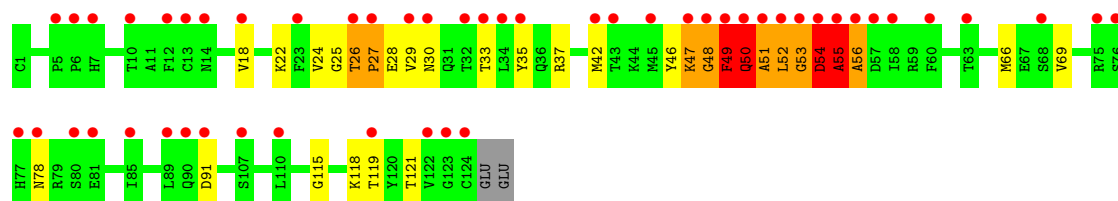
• Molecule 2: METALLOPROTEINASE INHIBITOR 1

Chain D: 



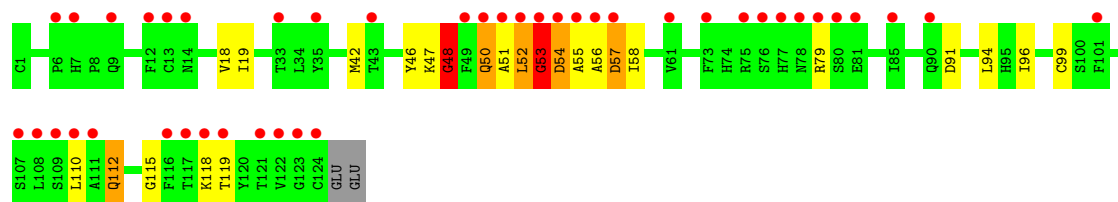
- Molecule 2: METALLOPROTEINASE INHIBITOR 1

Chain E: 



- Molecule 2: METALLOPROTEINASE INHIBITOR 1

Chain F: 



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	158.10Å 67.85Å 86.24Å 90.00° 100.29° 90.00°	Depositor
Resolution (Å)	23.00 – 2.54 17.99 – 2.54	Depositor EDS
% Data completeness (in resolution range)	98.3 (23.00-2.54) 98.5 (17.99-2.54)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.75 (at 2.56Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.248 , 0.275 0.248 , 0.269	Depositor DCC
R_{free} test set	997 reflections (3.52%)	DCC
Wilson B-factor (Å ²)	48.1	Xtriage
Anisotropy	0.030	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 30.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	2 of 29346 reflections (0.007%)	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	6547	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 50.09 % 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 6.7994e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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

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	0.33	0/1305	0.47	0/1776
1	B	0.32	0/1298	0.47	0/1766
1	C	0.32	0/1264	0.46	0/1719
2	D	0.35	0/929	0.48	0/1260
2	E	0.44	0/931	0.52	0/1260
2	F	0.43	0/945	0.51	0/1280
All	All	0.36	0/6672	0.48	0/9061

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	D	0	8
2	E	0	11
2	F	0	7
All	All	0	26

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (26) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	47	LYS	Peptide
2	D	48	GLY	Peptide
2	D	50	GLN	Peptide
2	D	52	LEU	Peptide

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Mol	Chain	Res	Type	Group
2	D	53	GLY	Peptide
2	D	54	ASP	Peptide
2	D	55	ALA	Peptide
2	D	57	ASP	Peptide
2	E	24	VAL	Peptide
2	E	25	GLY	Peptide
2	E	26	THR	Peptide
2	E	47	LYS	Peptide
2	E	48	GLY	Peptide
2	E	49	PHE	Peptide
2	E	50	GLN	Peptide
2	E	52	LEU	Peptide
2	E	53	GLY	Peptide
2	E	54	ASP	Peptide
2	E	55	ALA	Peptide
2	F	48	GLY	Peptide
2	F	50	GLN	Peptide
2	F	52	LEU	Peptide
2	F	53	GLY	Peptide
2	F	54	ASP	Peptide
2	F	55	ALA	Peptide
2	F	57	ASP	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1268	0	1156	4	0
1	B	1261	0	1139	2	0
1	C	1228	0	1114	4	0
2	D	906	0	831	25	0
2	E	907	0	830	27	0
2	F	921	0	851	27	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	3	0	0	0	0
4	B	3	0	0	0	0
4	C	3	0	0	0	0
5	A	18	0	0	0	0
5	B	9	0	0	0	0
5	C	8	0	0	0	0
5	D	3	0	0	0	0
5	E	1	0	0	0	0
5	F	2	0	0	0	0
All	All	6547	0	5921	87	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 7.

All (87) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:F:42:MET:CE	2:F:58:ILE:HG21	1.42	1.47
2:F:42:MET:CE	2:F:58:ILE:CG2	2.00	1.39
2:F:42:MET:HE3	2:F:58:ILE:CG2	1.59	1.28
2:D:59:ARG:HG2	2:D:59:ARG:HH11	1.01	1.15
2:D:51:ALA:O	2:D:53:GLY:O	1.69	1.11
2:F:51:ALA:O	2:F:53:GLY:O	1.69	1.11
2:F:42:MET:HE3	2:F:58:ILE:HG23	1.10	1.06
2:F:42:MET:HE1	2:F:58:ILE:CG2	1.71	1.05
2:D:45:MET:SD	2:D:48:GLY:HA3	2.02	0.99
2:E:26:THR:OG1	2:E:27:PRO:HD2	1.64	0.98
2:E:47:LYS:HG2	2:E:48:GLY:H	1.22	0.97
2:E:49:PHE:CA	2:E:51:ALA:N	2.30	0.95
2:D:59:ARG:HG2	2:D:59:ARG:NH1	1.72	0.90
2:E:49:PHE:CA	2:E:51:ALA:CA	2.51	0.88
2:D:59:ARG:HG3	2:D:59:ARG:O	1.76	0.86
2:F:42:MET:HE1	2:F:58:ILE:HG21	0.82	0.81
2:E:50:GLN:CA	2:E:53:GLY:O	2.30	0.79
2:E:26:THR:OG1	2:E:27:PRO:CD	2.30	0.79
2:E:47:LYS:HG2	2:E:48:GLY:N	1.90	0.79
2:D:59:ARG:HH11	2:D:59:ARG:CG	1.89	0.76
2:E:18:VAL:HG22	2:E:47:LYS:HB3	1.68	0.74
2:F:51:ALA:C	2:F:53:GLY:O	2.26	0.73
2:D:51:ALA:C	2:D:53:GLY:O	2.26	0.73
1:C:180:ASN:HB3	2:F:99:CYS:SG	2.29	0.72
2:F:58:ILE:HG23	2:F:58:ILE:O	1.91	0.70
2:E:115:GLY:HA2	2:E:119:THR:HB	1.71	0.70

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:D:58:ILE:O	2:D:58:ILE:HG23	1.90	0.70
2:F:52:LEU:C	2:F:53:GLY:O	2.30	0.70
2:E:50:GLN:O	2:E:53:GLY:C	2.30	0.69
2:D:52:LEU:C	2:D:53:GLY:O	2.30	0.69
2:D:85:ILE:HG23	2:D:96:ILE:HD11	1.74	0.69
2:E:53:GLY:O	2:E:55:ALA:CA	2.42	0.68
2:D:18:VAL:HG22	2:D:47:LYS:HB3	1.78	0.65
1:C:214:ARG:HH21	1:C:241:THR:H	1.44	0.65
2:E:50:GLN:O	2:E:54:ASP:N	2.30	0.64
2:E:49:PHE:CA	2:E:51:ALA:H	2.12	0.63
1:A:217:ALA:HB1	1:A:235:LEU:HD21	1.79	0.63
2:D:52:LEU:CA	2:D:53:GLY:O	2.47	0.62
2:F:52:LEU:CA	2:F:53:GLY:O	2.47	0.62
2:F:56:ALA:O	2:F:58:ILE:N	2.34	0.61
2:D:56:ALA:O	2:D:58:ILE:N	2.34	0.61
2:F:18:VAL:HG22	2:F:47:LYS:HB3	1.81	0.61
2:D:58:ILE:HD11	2:D:94:LEU:HB3	1.82	0.61
2:F:58:ILE:CD1	2:F:94:LEU:HB2	2.31	0.60
2:F:58:ILE:HD11	2:F:94:LEU:CB	2.32	0.60
2:D:59:ARG:NH1	2:D:59:ARG:CG	2.55	0.60
1:A:211:ASN:HD22	1:A:214:ARG:H	1.47	0.60
2:F:19:ILE:HD13	2:F:42:MET:HE2	1.86	0.56
2:F:18:VAL:HG23	2:F:46:TYR:HB2	1.87	0.56
1:C:204:THR:HG21	1:C:208:ARG:HB3	1.87	0.56
2:E:30:ASN:HD22	2:E:33:THR:HG22	1.70	0.56
2:F:58:ILE:HD11	2:F:94:LEU:HB3	1.88	0.56
2:E:53:GLY:C	2:E:55:ALA:CA	2.75	0.55
2:E:33:THR:HG23	2:E:35:TYR:H	1.72	0.55
2:E:49:PHE:C	2:E:51:ALA:N	2.58	0.54
2:D:115:GLY:HA2	2:D:119:THR:HB	1.89	0.53
2:F:115:GLY:HA2	2:F:119:THR:HB	1.91	0.53
2:E:53:GLY:C	2:E:55:ALA:N	2.63	0.52
2:D:47:LYS:HG2	2:D:48:GLY:N	2.24	0.51
2:F:18:VAL:HG22	2:F:47:LYS:CB	2.41	0.50
2:E:50:GLN:O	2:E:53:GLY:O	2.30	0.50
2:E:55:ALA:O	2:E:56:ALA:O	2.30	0.50
2:D:47:LYS:HG2	2:D:48:GLY:H	1.75	0.50
2:D:85:ILE:HG23	2:D:96:ILE:CD1	2.40	0.49
2:D:56:ALA:O	2:D:58:ILE:HB	2.13	0.49
2:F:56:ALA:O	2:F:58:ILE:HB	2.13	0.48
2:F:58:ILE:HD13	2:F:94:LEU:HB2	1.95	0.48
2:E:66:MET:HB2	2:E:69:VAL:HG12	1.95	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:E:18:VAL:HG23	2:E:46:TYR:HB2	1.95	0.48
2:E:26:THR:HA	2:E:27:PRO:HD3	1.40	0.47
2:D:58:ILE:O	2:D:58:ILE:CG2	2.61	0.46
1:A:145:THR:HB	1:A:146:PRO:HD2	1.98	0.45
2:E:26:THR:HG1	2:E:27:PRO:HD2	1.76	0.44
2:E:28:GLU:OE1	2:E:37:ARG:NE	2.43	0.43
2:D:17:LEU:HA	2:D:47:LYS:O	2.17	0.43
2:D:58:ILE:CD1	2:D:94:LEU:HB3	2.48	0.43
2:E:26:THR:CB	2:E:27:PRO:CD	2.87	0.43
1:C:180:ASN:CB	2:F:99:CYS:SG	3.04	0.43
1:A:122:THR:HA	1:A:123:PRO:HD3	1.92	0.42
2:D:58:ILE:HD11	2:D:94:LEU:CB	2.50	0.42
2:D:33:THR:HG23	2:D:35:TYR:HB2	2.01	0.41
2:F:79:ARG:HG2	2:F:79:ARG:H	1.74	0.41
1:B:237:TYR:CE2	1:B:239:SER:HB2	2.56	0.41
1:B:235:LEU:HD23	1:B:248:LEU:HD23	2.01	0.41
2:F:110:LEU:C	2:F:112:GLN:H	2.24	0.41
2:F:48:GLY:O	2:F:51:ALA:CA	2.69	0.41
2:E:50:GLN:C	2:E:53:GLY:O	2.59	0.41

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	159/170 (94%)	155 (98%)	2 (1%)	2 (1%)	18	29
1	B	160/170 (94%)	157 (98%)	2 (1%)	1 (1%)	33	54
1	C	157/170 (92%)	150 (96%)	7 (4%)	0	100	100
2	D	122/126 (97%)	105 (86%)	11 (9%)	6 (5%)	3	3
2	E	122/126 (97%)	98 (80%)	12 (10%)	12 (10%)	1	0
2	F	122/126 (97%)	101 (83%)	14 (12%)	7 (6%)	3	2
All	All	842/888 (95%)	766 (91%)	48 (6%)	28 (3%)	6	7

All (28) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	50	GLN
2	D	53	GLY
2	D	57	ASP
2	D	118	LYS
2	E	49	PHE
2	E	52	LEU
2	E	55	ALA
2	E	56	ALA
2	E	118	LYS
2	F	50	GLN
2	F	53	GLY
2	F	57	ASP
1	A	210	TYR
2	D	54	ASP
2	E	51	ALA
2	E	54	ASP
2	F	54	ASP
1	A	107	PRO
2	E	27	PRO
2	E	78	ASN
2	E	50	GLN
2	F	91	ASP
2	F	118	LYS
1	B	210	TYR
2	D	91	ASP
2	E	91	ASP
2	E	29	VAL
2	F	48	GLY

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	132/142 (93%)	127 (96%)	5 (4%)	44	70
1	B	130/142 (92%)	126 (97%)	4 (3%)	52	78
1	C	125/142 (88%)	116 (93%)	9 (7%)	21	35

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	D	92/109 (84%)	88 (96%)	4 (4%)	40	64
2	E	92/109 (84%)	89 (97%)	3 (3%)	50	75
2	F	95/109 (87%)	93 (98%)	2 (2%)	66	88
All	All	666/753 (88%)	639 (96%)	27 (4%)	41	66

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	120	ASN
1	A	125	LEU
1	A	201	GLU
1	A	220	LEU
1	A	246	VAL
1	B	120	ASN
1	B	125	LEU
1	B	201	GLU
1	B	250	GLN
1	C	108	ARG
1	C	120	ASN
1	C	125	LEU
1	C	201	GLU
1	C	214	ARG
1	C	219	GLU
1	C	220	LEU
1	C	239	SER
1	C	246	VAL
2	D	42	MET
2	D	59	ARG
2	D	96	ILE
2	D	110	LEU
2	E	22	LYS
2	E	42	MET
2	E	121	THR
2	F	96	ILE
2	F	112	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	113	HIS

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Mol	Chain	Res	Type
1	A	120	ASN
1	A	211	ASN
1	B	120	ASN
1	C	111	GLN
1	C	120	ASN
1	C	257	GLN
2	D	30	ASN
2	E	30	ASN
2	E	106	ASN
2	F	9	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 15 ligands modelled in this entry, 15 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.

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 ⓘ

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	161/170 (94%)	1.48	38 (23%) 1 1	41, 46, 51, 57	0
1	B	162/170 (95%)	1.44	38 (23%) 1 1	40, 45, 51, 55	0
1	C	159/170 (93%)	1.96	58 (36%) 1 0	41, 45, 47, 48	0
2	D	124/126 (98%)	2.10	48 (38%) 1 0	26, 44, 47, 48	0
2	E	124/126 (98%)	2.05	51 (41%) 1 0	39, 44, 47, 50	0
2	F	124/126 (98%)	2.15	43 (34%) 1 1	26, 44, 47, 49	0
All	All	854/888 (96%)	1.83	276 (32%) 1 1	26, 45, 49, 57	0

All (276) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	56	ALA	14.1
1	C	105	GLY	12.9
2	E	124	CYS	11.0
2	E	52	LEU	9.5
2	D	56	ALA	8.9
2	D	124	CYS	8.7
2	F	55	ALA	8.6
2	D	53	GLY	8.5
2	E	77	HIS	8.5
2	F	54	ASP	8.4
1	B	105	GLY	7.9
2	F	52	LEU	7.9
2	D	122	VAL	7.9
2	F	124	CYS	7.6
2	F	53	GLY	7.5
2	E	55	ALA	7.2
2	D	54	ASP	7.2
2	D	57	ASP	6.9
2	F	110	LEU	6.9

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Mol	Chain	Res	Type	RSRZ
2	D	13	CYS	6.7
2	D	55	ALA	6.7
2	F	57	ASP	6.6
2	E	54	ASP	6.4
2	E	123	GLY	6.3
2	D	77	HIS	6.3
1	B	106	ASN	5.9
1	C	106	ASN	5.7
1	A	105	GLY	5.6
1	A	106	ASN	5.6
2	F	107	SER	5.5
1	C	232	ILE	5.5
2	E	51	ALA	5.5
2	F	78	ASN	5.4
1	A	197	PHE	5.3
1	C	107	PRO	5.3
2	F	123	GLY	5.2
1	B	212	LEU	5.2
2	D	52	LEU	5.0
2	F	122	VAL	5.0
2	E	56	ALA	5.0
2	E	45	MET	5.0
1	C	233	GLY	5.0
2	E	57	ASP	4.9
1	B	264	GLN	4.9
1	C	262	ARG	4.9
1	C	261	GLY	4.9
1	C	112	THR	4.9
2	E	91	ASP	4.8
2	F	77	HIS	4.8
2	F	121	THR	4.8
1	C	212	LEU	4.7
1	B	197	PHE	4.7
1	C	263	SER	4.6
2	E	53	GLY	4.6
2	D	76	SER	4.5
1	A	212	LEU	4.5
1	C	135	GLU	4.5
2	D	123	GLY	4.5
1	C	108	ARG	4.4
2	F	51	ALA	4.4
2	E	35	TYR	4.4

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Mol	Chain	Res	Type	RSRZ
1	B	253	ILE	4.3
2	F	109	SER	4.3
2	D	12	PHE	4.2
2	F	13	CYS	4.2
2	F	7	HIS	4.2
1	C	171	ASN	4.1
2	D	50	GLN	4.1
2	F	50	GLN	4.1
1	C	127	ARG	4.1
2	E	89	LEU	4.1
2	F	117	THR	4.1
2	E	26	THR	4.1
1	A	256	ILE	4.0
1	C	249	ALA	4.0
1	A	221	GLY	4.0
1	C	257	GLN	3.9
1	A	161	ILE	3.9
1	C	188	GLY	3.9
2	D	120	TYR	3.9
2	D	43	THR	3.8
1	C	146	PRO	3.8
1	C	197	PHE	3.8
1	C	250	GLN	3.7
2	E	76	SER	3.7
1	A	195	ALA	3.7
1	A	132	HIS	3.6
2	E	12	PHE	3.6
1	A	215	VAL	3.6
2	F	49	PHE	3.6
1	B	134	ILE	3.6
1	B	161	ILE	3.6
1	C	189	PRO	3.6
1	C	139	GLN	3.6
2	E	58	ILE	3.5
2	F	35	TYR	3.5
1	A	220	LEU	3.5
2	D	89	LEU	3.5
2	D	119	THR	3.5
2	E	85	ILE	3.5
2	F	12	PHE	3.5
2	E	43	THR	3.5
2	F	111	ALA	3.5

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Mol	Chain	Res	Type	RSRZ
1	C	132	HIS	3.4
1	B	182	ALA	3.4
2	D	107	SER	3.4
2	D	58	ILE	3.4
1	A	182	ALA	3.4
2	D	85	ILE	3.4
1	C	136	LYS	3.4
2	F	118	LYS	3.4
1	B	220	LEU	3.3
1	B	224	LEU	3.3
1	B	221	GLY	3.3
1	C	113	HIS	3.2
2	D	26	THR	3.2
2	F	101	PHE	3.2
1	B	141	TRP	3.2
2	F	108	LEU	3.2
1	A	224	LEU	3.2
1	A	141	TRP	3.2
2	D	117	THR	3.2
1	B	167	ASP	3.1
1	A	134	ILE	3.1
2	E	90	GLN	3.1
2	E	13	CYS	3.1
2	D	9	GLN	3.1
1	A	184	ALA	3.1
1	C	144	VAL	3.1
2	D	78	ASN	3.0
1	A	216	ALA	3.0
2	E	30	ASN	3.0
2	E	60	PHE	3.0
2	D	27	PRO	3.0
2	F	43	THR	3.0
1	A	133	ALA	3.0
2	D	7	HIS	3.0
2	E	48	GLY	3.0
2	E	75	ARG	3.0
2	E	80	SER	3.0
1	B	171	ASN	2.9
1	C	165	ARG	2.9
1	C	147	LEU	2.9
1	B	232	ILE	2.9
2	D	116	PHE	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	113	HIS	2.9
2	E	122	VAL	2.9
1	C	203	TRP	2.9
1	B	127	ARG	2.9
1	B	195	ALA	2.9
1	C	134	ILE	2.9
1	C	243	SER	2.9
2	F	119	THR	2.9
2	D	111	ALA	2.8
1	C	195	ALA	2.8
1	C	210	TYR	2.8
2	F	14	ASN	2.8
1	A	196	HIS	2.8
2	F	61	VAL	2.8
1	A	125	LEU	2.8
2	F	85	ILE	2.8
1	C	180	ASN	2.7
1	C	115	THR	2.7
1	C	143	ASN	2.7
1	B	223	SER	2.7
2	D	49	PHE	2.7
1	C	244	GLY	2.7
2	D	42	MET	2.7
1	A	162	SER	2.7
2	E	34	LEU	2.7
1	B	215	VAL	2.7
2	E	27	PRO	2.7
1	C	190	GLY	2.7
1	B	263	SER	2.7
2	E	14	ASN	2.7
1	A	181	LEU	2.7
2	F	75	ARG	2.7
2	E	78	ASN	2.7
1	C	225	GLY	2.6
1	B	180	ASN	2.6
1	A	211	ASN	2.6
1	A	223	SER	2.6
2	F	73	PHE	2.6
2	F	80	SER	2.6
1	A	217	ALA	2.6
2	D	51	ALA	2.6
2	D	45	MET	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	162	SER	2.6
1	C	110	GLU	2.6
1	C	152	VAL	2.6
2	E	10	THR	2.6
1	B	203	TRP	2.5
2	F	90	GLN	2.5
2	E	32	THR	2.5
1	B	132	HIS	2.5
1	B	181	LEU	2.5
2	E	47	LYS	2.5
1	A	159	ILE	2.5
2	D	40	ILE	2.5
2	E	33	THR	2.5
1	A	210	TYR	2.5
1	B	250	GLN	2.5
1	B	163	PHE	2.5
1	C	184	ALA	2.5
2	F	33	THR	2.5
1	A	185	PHE	2.5
1	B	216	ALA	2.5
2	D	1	CYS	2.5
1	C	247	GLN	2.5
1	A	189	PRO	2.4
1	C	216	ALA	2.4
1	A	113	HIS	2.4
2	D	61	VAL	2.4
2	E	7	HIS	2.4
1	B	251	ASP	2.4
1	C	245	ASP	2.4
2	D	81	GLU	2.4
1	C	251	ASP	2.3
1	C	227	SER	2.3
2	D	90	GLN	2.3
2	D	60	PHE	2.3
2	F	79	ARG	2.3
2	E	119	THR	2.3
2	E	23	PHE	2.3
1	C	182	ALA	2.3
1	C	145	THR	2.3
2	E	50	GLN	2.3
1	A	183	HIS	2.3
2	E	5	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
2	E	49	PHE	2.3
2	F	116	PHE	2.3
1	A	165	ARG	2.2
2	D	38	TYR	2.2
1	A	180	ASN	2.2
1	C	224	LEU	2.2
2	E	110	LEU	2.2
2	E	81	GLU	2.2
1	C	208	ARG	2.2
1	C	221	GLY	2.2
2	F	76	SER	2.2
2	E	18	VAL	2.2
2	E	107	SER	2.2
1	B	108	ARG	2.2
1	B	130	VAL	2.2
2	D	91	ASP	2.2
1	C	191	ILE	2.2
2	F	9	GLN	2.2
2	E	29	VAL	2.2
1	C	217	ALA	2.2
1	C	198	ASP	2.1
2	D	32	THR	2.1
2	E	63	THR	2.1
1	C	214	ARG	2.1
1	A	213	HIS	2.1
2	E	68	SER	2.1
1	A	219	GLU	2.1
1	A	236	MET	2.1
1	C	215	VAL	2.1
1	A	163	PHE	2.1
1	B	189	PRO	2.1
2	D	35	TYR	2.1
2	F	81	GLU	2.1
1	C	148	THR	2.1
2	F	6	PRO	2.1
2	D	109	SER	2.1
2	E	42	MET	2.1
1	B	107	PRO	2.1
1	B	139	GLN	2.1
2	D	118	LYS	2.1
1	A	135	GLU	2.0
2	E	6	PRO	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	109	TRP	2.0
1	B	187	PRO	2.0
2	D	39	GLU	2.0
2	D	47	LYS	2.0
2	D	64	PRO	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	CA	A	1269	1/1	0.14	-1.37	42,42,42,42	0
4	CA	C	1266	1/1	0.13	-1.59	66,66,66,66	0
4	CA	C	1267	1/1	0.15	-1.63	40,40,40,40	0
4	CA	B	1270	1/1	0.13	-1.64	40,40,40,40	0
3	ZN	A	1266	1/1	0.16	-1.74	33,33,33,33	0
3	ZN	A	1267	1/1	0.17	-1.85	29,29,29,29	0
3	ZN	C	1264	1/1	0.16	-1.87	45,45,45,45	0
4	CA	A	1270	1/1	0.14	-2.06	51,51,51,51	0
3	ZN	B	1267	1/1	0.14	-2.07	30,30,30,30	0
4	CA	B	1271	1/1	0.12	-2.73	48,48,48,48	0
4	CA	C	1268	1/1	0.10	-2.94	43,43,43,43	0
3	ZN	B	1268	1/1	0.13	-2.94	34,34,34,34	0
4	CA	B	1269	1/1	0.07	-2.99	40,40,40,40	0
4	CA	A	1268	1/1	0.06	-3.85	32,32,32,32	0
3	ZN	C	1265	1/1	0.09	-4.36	46,46,46,46	0

6.5 Other polymers ⓘ

There are no such residues in this entry.