



Full wwPDB X-ray Structure Validation Report

Feb 26, 2014 – 09:47 PM GMT

PDB ID : 1E4X
Title : CROSSREACTIVE BINDING OF A CIRCULARIZED PEPTIDE TO AN ANTI-TGFALPHA ANTIBODY FAB-FRAGMENT
Authors : Hahn, M.; Winkler, D.; Misselwitz, R.; Wessner, H.; Welfle, K.; Zahn, G.; Schneider-Mergener, J.; Hoehne, W.
Deposited on : 2000-07-12
Resolution : 1.90 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>

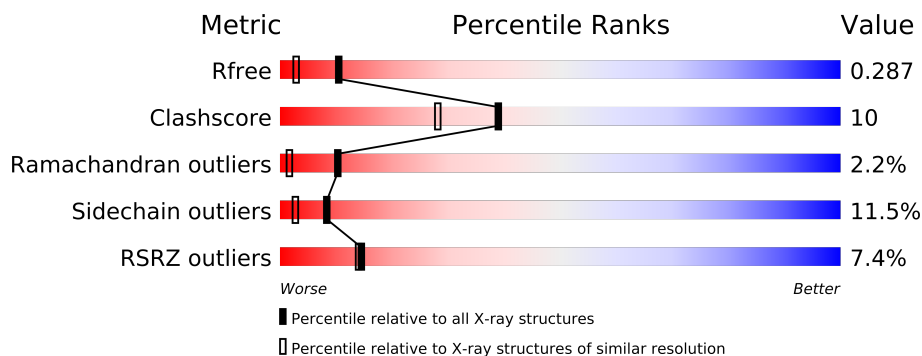
The following versions of software and data (see [references](#)) were used in the production of this report:

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 1.90 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}	66092	3684 (1.90-1.90)
Clashscore	79885	4465 (1.90-1.90)
Ramachandran outliers	78287	4413 (1.90-1.90)
Sidechain outliers	78261	4414 (1.90-1.90)
RSRZ outliers	66119	3686 (1.90-1.90)

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. 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	H	217	
2	I	217	
3	L	214	
3	M	214	
4	P	7	
4	Q	7	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7115 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 TAB2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	216	Total	C	N	O	S	0	0	0
			1634	1032	270	325	7			

- Molecule 2 is a protein called TAB2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	I	217	Total	C	N	O	S	0	0	0
			1644	1040	271	326	7			

- Molecule 3 is a protein called TAB2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	214	Total	C	N	O	S	0	0	0
			1657	1032	276	342	7			
3	M	214	Total	C	N	O	S	0	0	0
			1657	1032	276	342	7			

- Molecule 4 is a protein called CYCLIC PEPTIDE.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	P	7	Total	C	N	O	0	0	0
			58	36	10	12			
4	Q	7	Total	C	N	O	0	0	0
			58	36	10	12			

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	67	Total	O	0	0
			67	67		
5	I	91	Total	O	0	0
			91	91		

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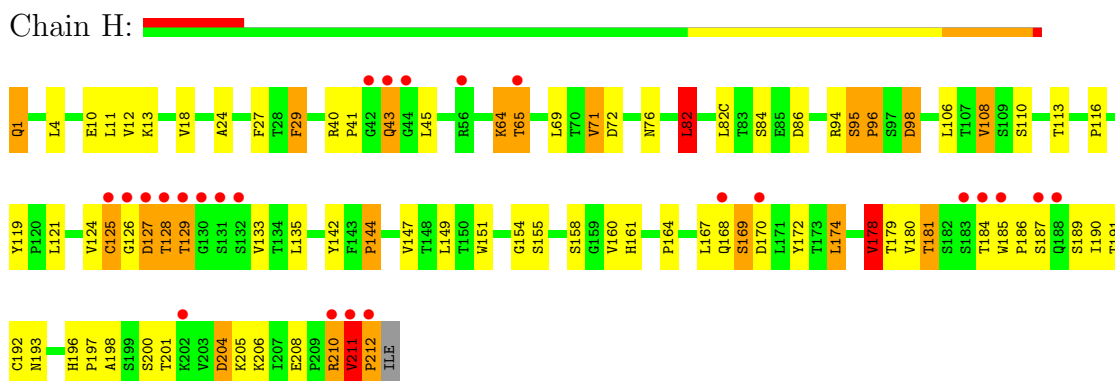
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	L	130	Total 130	O 130	0	0
5	M	116	Total 116	O 116	0	0
5	P	2	Total 2	O 2	0	0
5	Q	1	Total 1	O 1	0	0

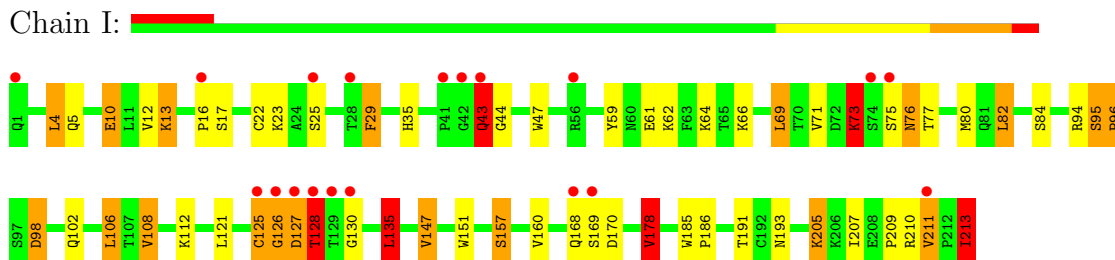
3 Residue-property plots

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 ($RSRZ > 2$). 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.

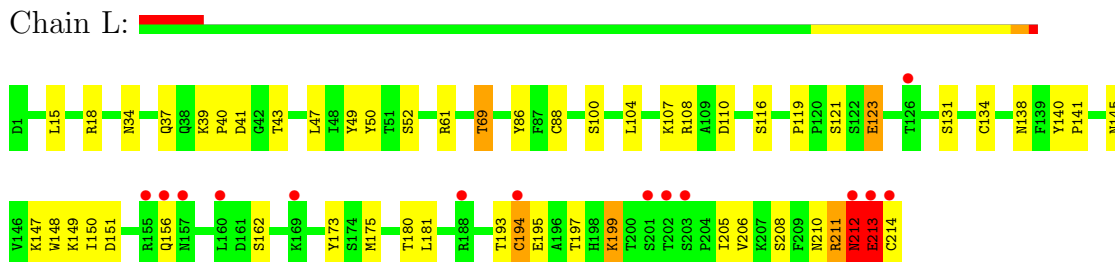
• Molecule 1: TAB2



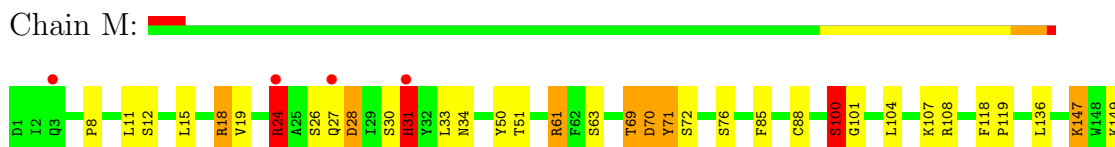
• Molecule 2: TAB2

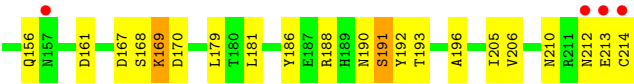


• Molecule 3: TAB2



• Molecule 3: TAB2





● Molecule 4: CYCLIC PEPTIDE

Chain P:



● Molecule 4: CYCLIC PEPTIDE

Chain Q:



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	173.82Å 45.09Å 120.41Å 90.00° 99.13° 90.00°	Depositor
Resolution (Å)	20.00 – 1.90 19.90 – 1.90	Depositor EDS
% Data completeness (in resolution range)	94.6 (20.00-1.90) 92.8 (19.90-1.90)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.65 (at 1.90Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.245 , 0.311 0.232 , 0.287	Depositor DCC
R_{free} test set	3426 reflections (5.30%)	DCC
Wilson B-factor (Å ²)	23.9	Xtriage
Anisotropy	0.151	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 44.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 68027 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7115	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.04% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	H	0.65	0/1677	1.54	24/2293 (1.0%)
2	I	0.68	0/1688	1.58	30/2309 (1.3%)
3	L	0.69	0/1694	1.48	21/2298 (0.9%)
3	M	0.72	0/1694	1.56	19/2298 (0.8%)
4	P	0.99	0/59	1.55	2/78 (2.6%)
4	Q	0.94	1/59 (1.7%)	1.18	0/78
All	All	0.69	1/6871 (0.0%)	1.54	96/9354 (1.0%)

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
1	H	0	2
2	I	0	2
All	All	0	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	Q	7	ASP	C-OXT	5.64	1.34	1.23

All (96) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	M	18	ARG	CD-NE-CZ	14.59	144.02	123.60
3	M	31	HIS	CA-CB-CG	13.00	135.70	113.60
3	M	24	ARG	NE-CZ-NH1	12.48	126.54	120.30
2	I	127	ASP	C-N-CA	11.41	150.24	121.70
2	I	98	ASP	CB-CG-OD2	-10.89	108.50	118.30
2	I	128	THR	N-CA-CB	10.54	130.33	110.30
2	I	98	ASP	CB-CG-OD1	9.67	127.00	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	76	ASN	CA-CB-CG	9.65	134.62	113.40
1	H	65	THR	N-CA-CB	9.51	128.37	110.30
3	L	18	ARG	NE-CZ-NH1	8.80	124.70	120.30
3	L	69	THR	N-CA-CB	-8.65	93.87	110.30
1	H	211	VAL	CB-CA-C	8.63	127.80	111.40
3	M	188	ARG	NE-CZ-NH1	8.57	124.58	120.30
3	L	61	ARG	CD-NE-CZ	8.51	135.51	123.60
2	I	178	VAL	CG1-CB-CG2	8.40	124.34	110.90
2	I	178	VAL	CB-CA-C	-8.37	95.50	111.40
3	M	108	ARG	NE-CZ-NH2	-8.31	116.15	120.30
1	H	204	ASP	CB-CG-OD2	8.20	125.68	118.30
1	H	127	ASP	CA-CB-CG	8.05	131.12	113.40
1	H	98	ASP	CB-CG-OD1	7.98	125.48	118.30
2	I	10	GLU	CA-CB-CG	7.97	130.93	113.40
1	H	95	SER	CA-C-O	-7.91	103.49	120.10
3	L	50	TYR	CB-CG-CD2	7.86	125.72	121.00
2	I	96	PRO	N-CA-CB	7.82	112.69	103.30
1	H	72	ASP	CB-CG-OD1	7.80	125.32	118.30
2	I	95	SER	CA-C-O	-7.72	103.89	120.10
2	I	211	VAL	N-CA-CB	-7.27	95.51	111.50
2	I	96	PRO	CA-N-CD	-7.25	101.36	111.50
3	L	50	TYR	CB-CG-CD1	-7.24	116.65	121.00
3	L	49	TYR	CB-CG-CD1	-7.18	116.69	121.00
3	M	214	CYS	CA-CB-SG	7.00	126.61	114.00
2	I	157	SER	N-CA-CB	-7.00	100.01	110.50
3	M	61	ARG	NE-CZ-NH2	-6.91	116.84	120.30
3	L	213	GLU	C-N-CA	6.88	138.91	121.70
3	M	161	ASP	CB-CG-OD2	6.80	124.42	118.30
1	H	86	ASP	CB-CG-OD1	6.75	124.38	118.30
1	H	94	ARG	NE-CZ-NH2	-6.65	116.97	120.30
1	H	178	VAL	CB-CA-C	-6.59	98.88	111.40
2	I	94	ARG	NE-CZ-NH2	6.58	123.59	120.30
2	I	29	PHE	CB-CG-CD1	6.52	125.36	120.80
3	M	100	SER	N-CA-CB	-6.51	100.73	110.50
1	H	86	ASP	CB-CG-OD2	-6.50	112.45	118.30
3	M	167	ASP	CB-CG-OD2	-6.49	112.46	118.30
3	M	186	TYR	CB-CG-CD1	-6.39	117.17	121.00
3	L	212	ASN	CA-CB-CG	6.35	127.36	113.40
3	M	192	TYR	CB-CG-CD1	-6.33	117.20	121.00
1	H	211	VAL	C-N-CD	6.27	141.56	128.40
3	L	69	THR	CA-CB-CG2	6.25	121.15	112.40
3	L	108	ARG	NE-CZ-NH1	6.21	123.40	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	M	170	ASP	CB-CG-OD1	6.20	123.88	118.30
1	H	212	PRO	CA-N-CD	-6.16	102.87	111.50
4	P	7	ASP	CB-CG-OD1	6.07	123.76	118.30
1	H	96	PRO	N-CA-CB	6.03	110.53	103.30
2	I	29	PHE	CB-CG-CD2	-6.01	116.59	120.80
3	L	181	LEU	CA-CB-CG	6.00	129.10	115.30
3	L	43	THR	CA-CB-CG2	-5.94	104.08	112.40
1	H	64	LYS	CA-C-N	5.90	130.18	117.20
1	H	1	GLN	CA-CB-CG	-5.88	100.47	113.40
3	M	108	ARG	NE-CZ-NH1	5.83	123.22	120.30
2	I	106	LEU	CA-CB-CG	5.81	128.66	115.30
1	H	40	ARG	NE-CZ-NH1	-5.79	117.41	120.30
3	L	52	SER	N-CA-CB	-5.79	101.82	110.50
3	L	100	SER	CA-CB-OG	-5.74	95.72	111.20
2	I	135	LEU	CA-CB-CG	5.73	128.48	115.30
2	I	147	VAL	N-CA-CB	-5.71	98.93	111.50
1	H	71	VAL	N-CA-CB	-5.68	99.01	111.50
3	M	12	SER	N-CA-CB	5.65	118.98	110.50
3	L	194	CYS	CB-CA-C	-5.53	99.35	110.40
1	H	174	LEU	CA-CB-CG	5.48	127.91	115.30
2	I	96	PRO	N-CD-CG	5.47	111.41	103.20
3	L	61	ARG	NE-CZ-NH2	-5.47	117.57	120.30
3	M	71	TYR	CB-CG-CD1	-5.45	117.73	121.00
1	H	64	LYS	O-C-N	-5.43	114.01	122.70
2	I	213	ILE	CB-CA-C	-5.42	100.77	111.60
2	I	76	ASN	CB-CA-C	5.40	121.19	110.40
3	L	123	GLU	OE1-CD-OE2	-5.39	116.83	123.30
3	L	86	TYR	CB-CG-CD2	-5.38	117.77	121.00
2	I	178	VAL	N-CA-CB	5.38	123.33	111.50
1	H	40	ARG	NE-CZ-NH2	-5.37	117.61	120.30
2	I	10	GLU	N-CA-CB	5.30	120.14	110.60
3	M	24	ARG	CG-CD-NE	5.25	122.82	111.80
3	M	188	ARG	NH1-CZ-NH2	-5.19	113.69	119.40
1	H	211	VAL	CA-CB-CG2	5.19	118.69	110.90
2	I	210	ARG	CD-NE-CZ	5.14	130.79	123.60
4	P	5	PHE	CB-CG-CD2	-5.12	117.22	120.80
2	I	213	ILE	N-CA-CB	5.11	122.56	110.80
3	M	61	ARG	NE-CZ-NH1	5.11	122.85	120.30
3	L	175	MET	CA-CB-CG	5.10	121.97	113.30
2	I	127	ASP	O-C-N	-5.09	114.55	122.70
3	L	41	ASP	CB-CG-OD1	5.07	122.86	118.30
1	H	82	LEU	CA-CB-CG	5.05	126.92	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	40	ARG	NH1-CZ-NH2	5.04	124.95	119.40
2	I	73	LYS	C-N-CA	5.02	134.26	121.70
2	I	205	LYS	O-C-N	5.01	130.72	122.70
3	L	173	TYR	CB-CG-CD2	-5.00	118.00	121.00
2	I	76	ASN	N-CA-C	-5.00	97.49	111.00

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	H	95	SER	Mainchain,Peptide
2	I	95	SER	Mainchain,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	H	1634	0	1603	40	0
2	I	1644	0	1615	41	0
3	L	1657	0	1576	27	0
3	M	1657	0	1576	28	0
4	P	58	0	51	0	0
4	Q	58	0	51	0	0
5	H	67	0	0	1	0
5	I	91	0	0	3	0
5	L	130	0	0	3	0
5	M	116	0	0	6	0
5	P	2	0	0	0	0
5	Q	1	0	0	0	0
All	All	7115	0	6472	128	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 10.

All (128) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:H:211:VAL:HG22	1:H:212:PRO:HD3	1.45	0.97
1:H:191:THR:HG22	1:H:206:LYS:HG3	1.51	0.91
2:I:126:GLY:H	2:I:211:VAL:HG21	1.35	0.89
2:I:125:CYS:HA	2:I:211:VAL:HG11	1.64	0.79
3:M:8:PRO:HG3	3:M:11:LEU:HD13	1.65	0.77
1:H:211:VAL:HG22	1:H:212:PRO:CD	2.17	0.74
1:H:160:VAL:HG22	1:H:178:VAL:HG13	1.68	0.74
3:L:193:THR:HG23	3:L:208:SER:HB3	1.71	0.73
3:M:27:GLN:O	3:M:28:ASP:C	2.26	0.72
1:H:196:HIS:HB3	1:H:201:THR:HG22	1.71	0.72
1:H:180:VAL:HG11	1:H:190:ILE:HD11	1.70	0.71
3:M:24:ARG:HD2	3:M:70:ASP:OD1	1.89	0.71
2:I:126:GLY:N	2:I:211:VAL:HG21	2.05	0.70
2:I:191:THR:HG23	5:I:2048:HOH:O	1.91	0.70
1:H:196:HIS:HB3	1:H:201:THR:CG2	2.22	0.69
3:L:211:ARG:O	3:L:212:ASN:HB2	1.91	0.69
2:I:135:LEU:HG	2:I:207:ILE:HG21	1.74	0.68
2:I:75:SER:HB2	2:I:77:THR:OG1	1.94	0.68
2:I:59:TYR:HB2	2:I:64:LYS:HE3	1.76	0.67
1:H:29:PHE:H	1:H:76:ASN:HD21	1.42	0.67
3:M:69:THR:HG22	3:M:70:ASP:OD1	1.98	0.63
3:M:30:SER:O	3:M:31:HIS:HB2	1.98	0.63
3:L:210:ASN:O	3:L:212:ASN:N	2.32	0.63
3:L:147:LYS:HE3	3:L:149:LYS:HE3	1.82	0.62
2:I:13:LYS:O	2:I:16:PRO:HD2	1.99	0.61
1:H:169:SER:OG	1:H:170:ASP:N	2.34	0.60
3:L:131:SER:HG	3:L:180:THR:HG1	1.50	0.59
2:I:69:LEU:HD12	2:I:80:MET:HG3	1.84	0.59
2:I:160:VAL:HG22	2:I:178:VAL:HG13	1.83	0.59
2:I:126:GLY:H	2:I:211:VAL:CG2	2.11	0.59
3:M:11:LEU:HD23	3:M:19:VAL:HG13	1.86	0.58
3:M:147:LYS:HD2	3:M:149:LYS:HE3	1.85	0.57
3:M:50:TYR:O	3:M:51:THR:HB	2.05	0.57
3:M:18:ARG:NE	5:M:2013:HOH:O	2.38	0.57
3:L:211:ARG:O	3:L:212:ASN:CB	2.53	0.56
3:L:148:TRP:CH2	3:L:194:CYS:SG	2.99	0.56
3:M:100:SER:HB2	5:M:2053:HOH:O	2.06	0.56
1:H:210:ARG:NH2	3:L:121:SER:HA	2.20	0.56
2:I:191:THR:HG21	5:I:2018:HOH:O	2.06	0.55
3:M:136:LEU:HD21	3:M:196:ALA:HB2	1.87	0.55
1:H:125:CYS:HA	1:H:210:ARG:O	2.07	0.55
2:I:23:LYS:HE2	2:I:75:SER:HB3	1.88	0.55
1:H:154:GLY:HA3	2:I:16:PRO:HB3	1.89	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:I:61:GLU:HA	2:I:64:LYS:HG3	1.89	0.55
3:M:169:LYS:HB3	3:M:169:LYS:NZ	2.22	0.54
3:M:149:LYS:HB2	3:M:193:THR:HB	1.90	0.54
1:H:161:HIS:HE1	3:L:138:ASN:OD1	1.91	0.54
1:H:125:CYS:SG	3:L:214:CYS:O	2.65	0.53
1:H:18:VAL:HG12	1:H:82:LEU:HB2	1.90	0.53
2:I:35:HIS:HD1	2:I:47:TRP:HE1	0.69	0.52
3:M:179:LEU:HG	3:M:181:LEU:HD13	1.91	0.51
1:H:193:ASN:HA	1:H:204:ASP:OD1	2.10	0.51
3:L:37:GLN:HB2	3:L:47:LEU:HD11	1.93	0.51
2:I:12:VAL:O	2:I:108:VAL:HA	2.11	0.51
2:I:61:GLU:HA	2:I:64:LYS:HZ3	1.76	0.50
2:I:4:LEU:HG	2:I:22:CYS:SG	2.51	0.50
2:I:151:TRP:CE2	2:I:178:VAL:HG22	2.47	0.50
3:L:213:GLU:HG3	3:L:214:CYS:N	2.26	0.50
3:M:18:ARG:NH1	3:M:76:SER:OG	2.45	0.50
1:H:144:PRO:HD2	1:H:198:ALA:CB	2.42	0.50
3:L:123:GLU:HB2	5:L:2104:HOH:O	2.11	0.50
2:I:126:GLY:H	2:I:211:VAL:HG11	1.77	0.49
3:L:110:ASP:OD2	3:L:199:LYS:HD2	2.12	0.49
3:L:195:GLU:HG2	3:L:206:VAL:HB	1.93	0.49
2:I:169:SER:OG	2:I:170:ASP:N	2.45	0.49
1:H:144:PRO:O	1:H:196:HIS:HE1	1.96	0.49
1:H:181:THR:OG1	1:H:184:THR:HG23	2.13	0.49
1:H:116:PRO:HB3	1:H:142:TYR:HB3	1.96	0.48
2:I:209:PRO:HB3	2:I:213:ILE:HD11	1.96	0.48
1:H:151:TRP:CZ3	1:H:192:CYS:HB3	2.49	0.48
3:L:197:THR:HG23	5:L:2128:HOH:O	2.15	0.47
3:M:205:ILE:HD11	5:M:2113:HOH:O	2.14	0.47
2:I:5:GLN:NE2	2:I:23:LYS:HD3	2.30	0.47
1:H:133:VAL:O	1:H:179:THR:HA	2.14	0.47
1:H:24:ALA:HB1	1:H:27:PHE:CE1	2.50	0.47
3:M:18:ARG:NH2	5:M:2013:HOH:O	2.47	0.47
2:I:59:TYR:HB3	2:I:64:LYS:HG2	1.97	0.47
1:H:189:SER:OG	1:H:206:LYS:HE3	2.15	0.47
2:I:5:GLN:HB3	2:I:23:LYS:HB3	1.97	0.47
2:I:12:VAL:HG12	2:I:16:PRO:HG2	1.96	0.46
1:H:155:SER:HB3	2:I:17:SER:OG	2.16	0.46
3:M:136:LEU:CD2	3:M:196:ALA:HB2	2.45	0.46
2:I:35:HIS:ND1	2:I:47:TRP:NE1	2.32	0.46
1:H:127:ASP:O	1:H:128:THR:C	2.53	0.46
1:H:210:ARG:HG3	5:H:2054:HOH:O	2.16	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:I:43:GLN:HB3	2:I:44:GLY:H	1.53	0.46
1:H:12:VAL:O	1:H:108:VAL:HA	2.15	0.46
3:L:116:SER:O	3:L:134:CYS:HA	2.15	0.46
2:I:125:CYS:HA	2:I:211:VAL:CG1	2.42	0.45
1:H:82:LEU:HB3	1:H:82(C):LEU:HD21	1.99	0.45
3:M:191:SER:HB2	3:M:210:ASN:ND2	2.32	0.45
2:I:69:LEU:CD1	2:I:80:MET:HG3	2.47	0.45
1:H:185:TRP:CG	1:H:186:PRO:HA	2.52	0.44
2:I:185:TRP:CG	2:I:186:PRO:HA	2.52	0.44
3:M:85:PHE:CZ	3:M:101:GLY:HA3	2.52	0.44
3:M:18:ARG:CZ	5:M:2013:HOH:O	2.65	0.44
3:L:213:GLU:HB3	5:L:2130:HOH:O	2.18	0.44
1:H:164:PRO:HD2	3:L:162:SER:OG	2.18	0.44
3:M:107:LYS:HE3	5:M:2006:HOH:O	2.18	0.44
1:H:185:TRP:HA	1:H:186:PRO:C	2.38	0.44
2:I:157:SER:HB2	5:I:2050:HOH:O	2.17	0.44
3:L:150:ILE:O	3:L:151:ASP:HB2	2.18	0.44
3:M:33:LEU:HG	3:M:71:TYR:CB	2.48	0.43
2:I:66:LYS:O	2:I:82:LEU:HA	2.19	0.43
2:I:186:PRO:HG3	2:I:213:ILE:HD12	2.00	0.43
3:L:140:TYR:CG	3:L:141:PRO:HA	2.53	0.43
1:H:149:LEU:HD23	1:H:149:LEU:C	2.39	0.43
3:L:210:ASN:O	3:L:211:ARG:C	2.57	0.43
3:L:34:ASN:O	3:L:88:CYS:HA	2.19	0.43
3:M:34:ASN:O	3:M:88:CYS:HA	2.19	0.43
2:I:126:GLY:N	2:I:211:VAL:HG11	2.34	0.42
2:I:125:CYS:HB3	2:I:211:VAL:HG21	2.01	0.42
3:L:39:LYS:HB3	3:L:40:PRO:CD	2.50	0.42
2:I:211:VAL:HG13	2:I:211:VAL:O	2.18	0.42
3:M:118:PHE:HA	3:M:119:PRO:HD3	1.94	0.42
1:H:144:PRO:HD2	1:H:198:ALA:HB3	2.01	0.42
1:H:197:PRO:O	1:H:198:ALA:C	2.59	0.42
1:H:119:TYR:CE1	3:L:123:GLU:HG2	2.55	0.41
3:L:39:LYS:HB3	3:L:40:PRO:HD2	2.01	0.41
1:H:13:LYS:HD2	1:H:110:SER:HA	2.02	0.41
3:M:27:GLN:O	3:M:27:GLN:HG3	2.20	0.41
2:I:73:LYS:HG3	2:I:73:LYS:H	1.56	0.41
1:H:124:VAL:O	1:H:125:CYS:C	2.58	0.41
2:I:61:GLU:HA	2:I:64:LYS:NZ	2.36	0.40
3:M:18:ARG:CZ	3:M:76:SER:OG	2.69	0.40
1:H:167:LEU:HD13	1:H:172:TYR:CZ	2.56	0.40
3:M:61:ARG:HB2	3:M:76:SER:O	2.21	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:H:124:VAL:HG22	3:L:119:PRO:HG3	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	H	214/217 (99%)	191 (89%)	15 (7%)	8 (4%)	5	0
2	I	215/217 (99%)	199 (93%)	9 (4%)	7 (3%)	6	1
3	L	212/214 (99%)	205 (97%)	5 (2%)	2 (1%)	25	10
3	M	212/214 (99%)	206 (97%)	4 (2%)	2 (1%)	25	10
4	P	5/7 (71%)	5 (100%)	0	0	100	100
4	Q	5/7 (71%)	5 (100%)	0	0	100	100
All	All	863/876 (98%)	811 (94%)	33 (4%)	19 (2%)	10	2

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	126	GLY
1	H	129	THR
1	H	211	VAL
2	I	126	GLY
2	I	128	THR
3	L	211	ARG
3	L	212	ASN
1	H	43	GLN
2	I	125	CYS
3	M	28	ASP
1	H	169	SER
2	I	73	LYS
2	I	130	GLY
3	M	213	GLU

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Mol	Chain	Res	Type
1	H	113	THR
1	H	187	SER
2	I	43	GLN
2	I	96	PRO
1	H	96	PRO

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	H	188/189 (100%)	154 (82%)	34 (18%)	2	0
2	I	190/190 (100%)	163 (86%)	27 (14%)	5	1
3	L	190/190 (100%)	180 (95%)	10 (5%)	32	18
3	M	190/190 (100%)	172 (90%)	18 (10%)	12	4
4	P	7/7 (100%)	7 (100%)	0	100	100
4	Q	7/7 (100%)	7 (100%)	0	100	100
All	All	772/773 (100%)	683 (88%)	89 (12%)	8	3

All (89) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	1	GLN
1	H	4	LEU
1	H	10	GLU
1	H	11	LEU
1	H	29	PHE
1	H	41	PRO
1	H	43	GLN
1	H	45	LEU
1	H	64	LYS
1	H	65	THR
1	H	69	LEU
1	H	71	VAL
1	H	82	LEU
1	H	84	SER

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Mol	Chain	Res	Type
1	H	98	ASP
1	H	106	LEU
1	H	108	VAL
1	H	121	LEU
1	H	125	CYS
1	H	128	THR
1	H	129	THR
1	H	135	LEU
1	H	144	PRO
1	H	147	VAL
1	H	158	SER
1	H	168	GLN
1	H	174	LEU
1	H	178	VAL
1	H	181	THR
1	H	200	SER
1	H	205	LYS
1	H	208	GLU
1	H	210	ARG
1	H	211	VAL
2	I	4	LEU
2	I	10	GLU
2	I	13	LYS
2	I	25	SER
2	I	29	PHE
2	I	43	GLN
2	I	62	LYS
2	I	69	LEU
2	I	71	VAL
2	I	76	ASN
2	I	82	LEU
2	I	84	SER
2	I	98	ASP
2	I	102	GLN
2	I	106	LEU
2	I	108	VAL
2	I	112	LYS
2	I	121	LEU
2	I	127	ASP
2	I	128	THR
2	I	135	LEU
2	I	147	VAL

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Mol	Chain	Res	Type
2	I	168	GLN
2	I	178	VAL
2	I	193	ASN
2	I	205	LYS
2	I	213	ILE
3	L	15	LEU
3	L	69	THR
3	L	104	LEU
3	L	107	LYS
3	L	145	ASN
3	L	156	GLN
3	L	199	LYS
3	L	205	ILE
3	L	212	ASN
3	L	213	GLU
3	M	15	LEU
3	M	24	ARG
3	M	26	SER
3	M	31	HIS
3	M	63	SER
3	M	69	THR
3	M	70	ASP
3	M	72	SER
3	M	100	SER
3	M	104	LEU
3	M	147	LYS
3	M	156	GLN
3	M	168	SER
3	M	169	LYS
3	M	190	ASN
3	M	191	SER
3	M	206	VAL
3	M	212	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	1	GLN
1	H	43	GLN
1	H	76	ASN
1	H	161	HIS
1	H	168	GLN

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Mol	Chain	Res	Type
1	H	196	HIS
2	I	5	GLN
2	I	43	GLN
2	I	102	GLN
2	I	168	GLN
3	L	77	ASN
3	L	210	ASN
3	L	212	ASN
3	M	27	GLN
3	M	55	HIS
3	M	210	ASN

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 ⓘ

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 ⓘ

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	H	216/217 (99%)	0.58	24 (11%)	6 5	23, 38, 58, 79	0
2	I	217/217 (100%)	0.63	19 (8%)	10 9	21, 36, 59, 79	0
3	L	214/214 (100%)	0.38	14 (6%)	18 18	21, 35, 53, 69	0
3	M	214/214 (100%)	0.15	8 (3%)	39 41	21, 32, 47, 68	0
4	P	7/7 (100%)	-0.19	0	100 100	23, 25, 27, 27	0
4	Q	7/7 (100%)	0.42	0	100 100	34, 35, 38, 42	0
All	All	875/876 (99%)	0.43	65 (7%)	14 14	21, 35, 55, 79	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	I	126	GLY	11.5
3	L	214	CYS	10.5
2	I	128	THR	8.8
1	H	128	THR	7.2
1	H	129	THR	7.1
1	H	211	VAL	6.9
2	I	129	THR	6.5
3	M	212	ASN	5.6
3	M	214	CYS	5.5
1	H	65	THR	5.4
2	I	41	PRO	5.0
1	H	126	GLY	4.7
3	M	213	GLU	4.0
2	I	127	ASP	4.0
2	I	74	SER	4.0
2	I	75	SER	4.0
1	H	210	ARG	3.9
1	H	187	SER	3.8
3	L	212	ASN	3.8

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Mol	Chain	Res	Type	RSRZ
1	H	212	PRO	3.6
2	I	25	SER	3.6
2	I	169	SER	3.6
3	M	31	HIS	3.6
1	H	188	GLN	3.6
3	L	203	SER	3.5
1	H	127	ASP	3.5
3	L	156	GLN	3.2
3	L	157	ASN	3.2
1	H	183	SER	3.2
2	I	1	GLN	3.2
2	I	56	ARG	3.1
2	I	16	PRO	3.0
1	H	131	SER	3.0
3	L	155	ARG	2.9
2	I	130	GLY	2.8
2	I	125	CYS	2.8
2	I	43	GLN	2.8
1	H	170	ASP	2.7
3	L	213	GLU	2.7
1	H	42	GLY	2.6
3	M	24	ARG	2.6
2	I	168	GLN	2.5
2	I	211	VAL	2.4
3	L	194	CYS	2.4
1	H	184	THR	2.4
1	H	56	ARG	2.4
1	H	44	GLY	2.4
1	H	130	GLY	2.3
1	H	125	CYS	2.2
3	M	157	ASN	2.2
1	H	202	LYS	2.2
3	L	202	THR	2.2
1	H	43	GLN	2.2
2	I	28	THR	2.1
3	L	188	ARG	2.1
1	H	132	SER	2.1
1	H	185	TRP	2.1
3	M	27	GLN	2.1
3	L	126	THR	2.1
1	H	168	GLN	2.1
3	L	169	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
3	L	201	SER	2.0
2	I	42	GLY	2.0
3	L	160	LEU	2.0
3	M	3	GLN	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 ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.