Full wwPDB X-ray Structure Validation Report (i)

Jun 23, 2024 – 03:13 AM EDT

PDB ID	:	4QEX
Title	:	Crystal structure of PfEBA-175 RII in complex with a Fab fragment from inhibitory antibody R217
Authors	:	Chen, E.; Paing, M.M.; Salinas, N.; Sim, B.K.; Tolia, N.H.
Deposited on	:	2014-05-19
Resolution	:	4.50 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 (i) 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 (1)) were used in the production of this report:

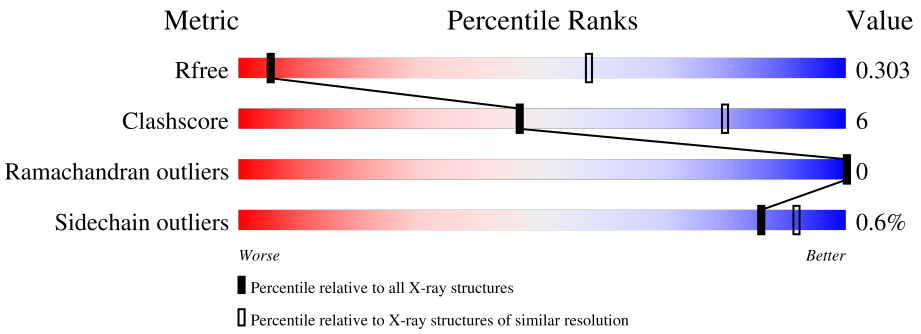
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 4.50 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}	130704	1055 (5.20-3.80)
Clashscore	141614	1123 (5.20-3.80)
Ramachandran outliers	138981	1069 (5.20-3.80)
Sidechain outliers	138945	1050 (5.20-3.80)

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	602	81% 12% 7%
1	B	602	83% 13% •
2	L	214	79% 21% •
2	M	214	77% 22%
3	H	215	78% 18% •
3	I	215	78% 20% •

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 31624 atoms, of which 15595 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 Erythrocyte-binding antigen-175.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	561	9393	2994	4660	826	880	33	0	0	0
1	B	580	9696	3088	4810	851	913	34	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	3	GLN	ASN	ENGINEERED MUTATION	UNP Q05644
A	50	ALA	SER	ENGINEERED MUTATION	UNP Q05644
A	195	ALA	SER	ENGINEERED MUTATION	UNP Q05644
A	206	ALA	THR	ENGINEERED MUTATION	UNP Q05644
B	3	GLN	ASN	ENGINEERED MUTATION	UNP Q05644
B	50	ALA	SER	ENGINEERED MUTATION	UNP Q05644
B	195	ALA	SER	ENGINEERED MUTATION	UNP Q05644
B	206	ALA	THR	ENGINEERED MUTATION	UNP Q05644

- Molecule 2 is a protein called Antibody Light Chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
2	L	212	3201	1024	1557	284	330	6	0	0	0
2	M	213	3212	1027	1562	285	332	6	0	0	0

- Molecule 3 is a protein called Antibody Heavy Chain.

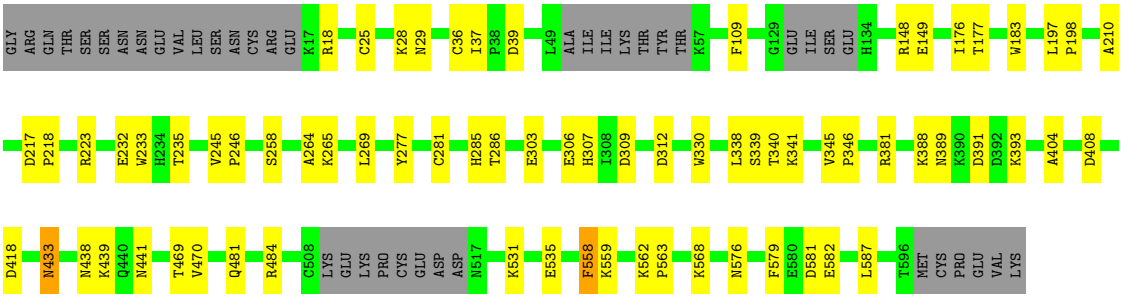
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
3	H	206	3040	973	1493	248	318	8	0	0	0
3	I	210	3082	986	1513	252	323	8	0	0	0

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. 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. 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.

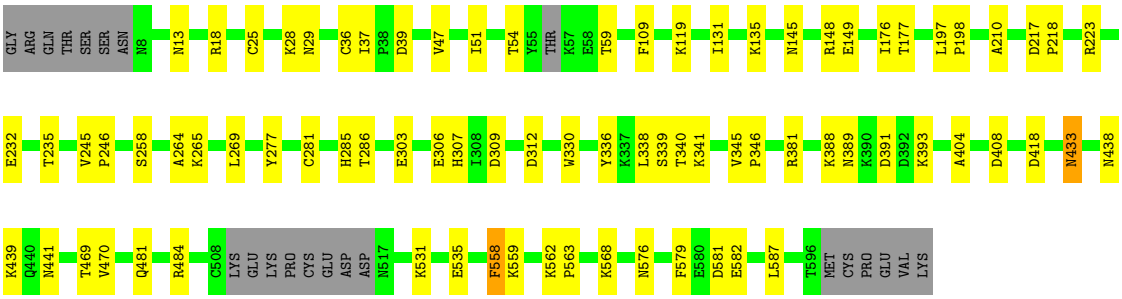
• Molecule 1: Erythrocyte-binding antigen-175

Chain A:



• Molecule 1: Erythrocyte-binding antigen-175

Chain B:



• Molecule 2: Antibody Light Chain

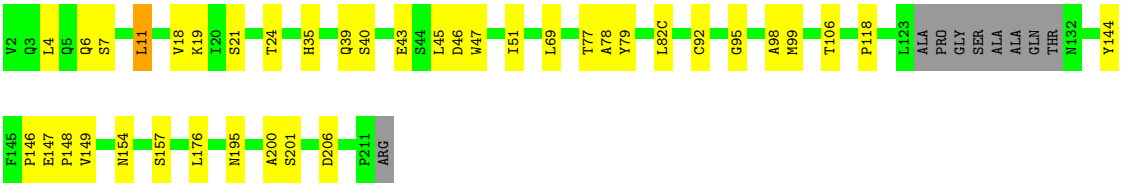
Chain L:

• Molecule 2: Antibody Light Chain

Chain M:

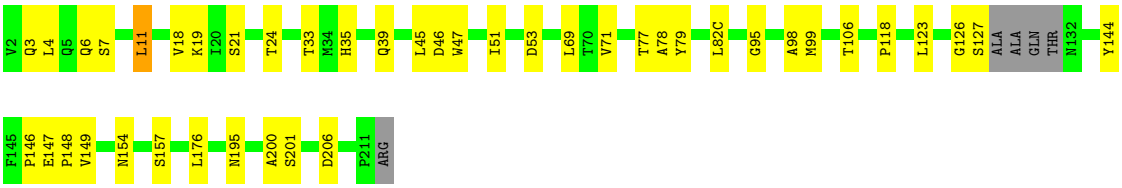
• Molecule 3: Antibody Heavy Chain

Chain H:



• Molecule 3: Antibody Heavy Chain

Chain I:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	208.10Å 101.26Å 117.59Å 90.00° 102.86° 90.00°	Depositor
Resolution (Å)	19.84 – 4.50 19.84 – 4.50	Depositor EDS
% Data completeness (in resolution range)	94.0 (19.84-4.50) 94.0 (19.84-4.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.59 (at 4.54Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.232 , 0.285 0.241 , 0.303	Depositor DCC
R_{free} test set	667 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	118.4	Xtriage
Anisotropy	0.345	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.25 , 72.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.44$, $< L^2 > = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.86	EDS
Total number of atoms	31624	wwPDB-VP
Average B, all atoms (Å^2)	146.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.23% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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	0.23	0/4831	0.37	0/6468
1	B	0.23	0/4986	0.37	0/6679
2	L	0.23	0/1683	0.43	0/2284
2	M	0.23	0/1690	0.42	0/2295
3	H	0.24	0/1585	0.45	0/2166
3	I	0.24	0/1608	0.45	0/2198
All	All	0.23	0/16383	0.40	0/22090

There are no bond length outliers.

There are no bond angle outliers.

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	4733	4660	4670	41	0
1	B	4886	4810	4820	53	0
2	L	1644	1557	1562	28	0
2	M	1650	1562	1568	31	0
3	H	1547	1493	1497	25	0
3	I	1569	1513	1517	31	0
All	All	16029	15595	15634	198	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 6.

All (198) 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)
3:I:6:GLN:HG3	3:I:106:THR:OG1	1.86	0.76
3:H:6:GLN:HG3	3:H:106:THR:OG1	1.86	0.76
2:M:34:HIS:CD2	3:I:98:ALA:HB2	2.22	0.73
1:B:433:ASN:N	1:B:433:ASN:OD1	2.23	0.71
3:I:147:GLU:HB2	3:I:148:PRO:HA	1.72	0.71
3:H:147:GLU:HB2	3:H:148:PRO:HA	1.72	0.70
1:A:433:ASN:OD1	1:A:433:ASN:N	2.24	0.69
1:B:51:ILE:O	1:B:119:LYS:NZ	2.27	0.68
2:L:76:ASP:HB3	2:L:77:PRO:HD3	1.82	0.61
2:M:76:ASP:HB3	2:M:77:PRO:HD3	1.83	0.60
3:H:154:ASN:HB2	3:H:157:SER:HB3	1.84	0.60
1:A:18:ARG:NH1	1:A:39:ASP:OD1	2.34	0.60
1:A:28:LYS:HG2	1:A:29:ASN:N	2.16	0.60
1:B:18:ARG:NH1	1:B:39:ASP:OD1	2.35	0.59
3:I:154:ASN:HB2	3:I:157:SER:HB3	1.83	0.59
1:B:28:LYS:HG2	1:B:29:ASN:N	2.17	0.58
3:I:6:GLN:CG	3:I:106:THR:OG1	2.51	0.57
3:H:6:GLN:CG	3:H:106:THR:OG1	2.52	0.57
1:B:469:THR:HG23	1:B:470:VAL:N	2.21	0.56
2:M:36:TYR:CE2	2:M:46:LEU:HD23	2.41	0.56
2:L:34:HIS:CD2	3:H:98:ALA:HB2	2.41	0.56
2:M:126:THR:N	2:M:127:PRO:HD2	2.21	0.56
1:B:28:LYS:HA	1:B:109:PHE:CE1	2.41	0.55
1:A:28:LYS:HA	1:A:109:PHE:CE1	2.41	0.55
2:L:126:THR:N	2:L:127:PRO:HD2	2.21	0.55
1:A:258:SER:CB	1:A:264:ALA:HB2	2.36	0.55
1:B:18:ARG:HD2	1:B:39:ASP:OD2	2.07	0.55
1:A:469:THR:HG23	1:A:470:VAL:N	2.21	0.55
3:H:6:GLN:HG3	3:H:7:SER:H	1.72	0.55
1:B:562:LYS:HB3	1:B:563:PRO:HD2	1.89	0.55
1:B:258:SER:CB	1:B:264:ALA:HB2	2.37	0.54
2:L:36:TYR:CE2	2:L:46:LEU:HD23	2.42	0.54
1:A:18:ARG:HD2	1:A:39:ASP:OD2	2.07	0.54
1:A:562:LYS:HB3	1:A:563:PRO:HD2	1.89	0.53
2:L:198:HIS:ND1	2:L:199:LYS:HG2	2.24	0.53
1:B:340:THR:HG21	3:I:53:ASP:CB	2.39	0.53
1:B:340:THR:HG21	3:I:53:ASP:HB3	1.90	0.53
1:B:245:VAL:N	1:B:246:PRO:CD	2.72	0.52
3:I:195:ASN:HA	3:I:206:ASP:HB3	1.91	0.52
3:I:6:GLN:HG3	3:I:7:SER:H	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:338:LEU:HD13	3:H:35:HIS:CD2	2.44	0.52
2:M:198:HIS:ND1	2:M:199:LYS:HG2	2.24	0.52
1:A:558:PHE:CG	1:A:559:LYS:N	2.78	0.52
1:A:245:VAL:N	1:A:246:PRO:CD	2.72	0.51
1:A:579:PHE:HA	1:A:582:GLU:HB2	1.93	0.51
1:B:558:PHE:CG	1:B:559:LYS:N	2.78	0.51
3:I:200:ALA:O	3:I:201:SER:HB3	2.10	0.51
3:H:195:ASN:HA	3:H:206:ASP:HB3	1.92	0.51
1:B:131:ILE:HB	1:B:135:LYS:HD2	1.92	0.50
1:A:36:CYS:SG	1:A:235:THR:HB	2.51	0.50
1:B:579:PHE:HA	1:B:582:GLU:HB2	1.93	0.50
2:M:2:ILE:HD12	2:M:2:ILE:N	2.27	0.50
2:L:133:VAL:HG11	2:L:135:PHE:CZ	2.46	0.50
1:B:36:CYS:SG	1:B:235:THR:HB	2.52	0.50
2:M:37:GLN:HB2	2:M:47:LEU:HD11	1.93	0.50
3:I:18:VAL:HG12	3:I:19:LYS:N	2.26	0.50
2:L:2:ILE:HD12	2:L:2:ILE:N	2.27	0.50
3:H:200:ALA:O	3:H:201:SER:HB3	2.12	0.50
3:H:18:VAL:HG12	3:H:19:LYS:N	2.26	0.50
2:M:133:VAL:HG11	2:M:135:PHE:CZ	2.46	0.49
2:M:6:GLN:OE1	2:M:102:THR:HG23	2.12	0.49
3:I:126:GLY:O	3:I:127:SER:C	2.49	0.49
2:L:37:GLN:HB2	2:L:47:LEU:HD11	1.93	0.49
2:L:6:GLN:OE1	2:L:102:THR:HG23	2.12	0.49
1:B:303:GLU:O	1:B:307:HIS:HB3	2.14	0.48
1:B:336:TYR:CE2	1:B:339:SER:HB2	2.49	0.48
1:A:303:GLU:O	1:A:307:HIS:HB3	2.14	0.48
1:A:418:ASP:N	1:A:418:ASP:OD1	2.46	0.47
3:H:21:SER:HB3	3:H:79:TYR:CE1	2.49	0.47
3:H:118:PRO:HB3	3:H:144:TYR:HB3	1.97	0.47
1:B:339:SER:O	1:B:340:THR:C	2.52	0.47
2:M:118:PHE:CD2	3:I:123:LEU:HB3	2.49	0.47
1:B:418:ASP:OD1	1:B:418:ASP:N	2.47	0.47
3:I:21:SER:HB3	3:I:79:TYR:CE1	2.48	0.47
3:I:77:THR:HG22	3:I:78:ALA:N	2.30	0.47
2:L:96:PHE:HB2	3:H:47:TRP:CG	2.50	0.47
2:L:11:LEU:O	2:L:11:LEU:HD12	2.15	0.46
2:L:83:ALA:HB2	2:L:106:ILE:HG12	1.98	0.46
2:M:4:LEU:HD12	2:M:4:LEU:N	2.30	0.46
2:L:155:ARG:NE	2:L:181:LEU:HD21	2.30	0.46
1:B:438:ASN:ND2	1:B:441:ASN:OD1	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:531:LYS:HE2	1:B:535:GLU:OE2	2.16	0.46
3:I:118:PRO:HB3	3:I:144:TYR:HB3	1.98	0.46
1:B:217:ASP:N	1:B:218:PRO:HD2	2.31	0.46
2:M:11:LEU:HD12	2:M:11:LEU:O	2.15	0.46
3:H:77:THR:HG22	3:H:78:ALA:N	2.30	0.46
1:A:391:ASP:OD2	1:A:393:LYS:HB3	2.16	0.45
1:A:217:ASP:N	1:A:218:PRO:HD2	2.31	0.45
1:A:531:LYS:HE2	1:A:535:GLU:OE2	2.15	0.45
1:B:265:LYS:O	1:B:269:LEU:HG	2.16	0.45
1:B:210:ALA:HB1	1:B:281:CYS:O	2.17	0.45
1:A:388:LYS:HG3	1:A:389:ASN:N	2.32	0.45
2:L:4:LEU:HD12	2:L:4:LEU:N	2.31	0.45
1:A:469:THR:CG2	1:A:470:VAL:N	2.79	0.45
2:M:155:ARG:NE	2:M:181:LEU:HD21	2.30	0.45
1:A:265:LYS:O	1:A:269:LEU:HG	2.17	0.45
2:L:33:MET:C	2:L:34:HIS:CG	2.90	0.45
2:M:35:TRP:CD2	2:M:73:LEU:HB2	2.51	0.45
1:B:336:TYR:CZ	1:B:339:SER:HB2	2.52	0.45
2:M:33:MET:C	2:M:34:HIS:CG	2.90	0.45
1:A:210:ALA:HB1	1:A:281:CYS:O	2.17	0.45
1:B:54:THR:HG23	1:B:59:THR:HB	1.98	0.45
2:L:35:TRP:CD2	2:L:73:LEU:HB2	2.52	0.44
1:B:469:THR:CG2	1:B:470:VAL:N	2.80	0.44
2:L:202:GLU:N	2:L:202:GLU:OE1	2.50	0.44
3:H:11:LEU:HD22	3:H:146:PRO:CG	2.47	0.44
2:M:136:LEU:HD12	2:M:136:LEU:N	2.32	0.44
1:B:391:ASP:OD2	1:B:393:LYS:HB3	2.17	0.44
2:M:202:GLU:N	2:M:202:GLU:OE1	2.50	0.44
1:A:438:ASN:ND2	1:A:441:ASN:OD1	2.49	0.44
3:H:51:ILE:HD12	3:H:51:ILE:O	2.18	0.44
3:I:11:LEU:HD22	3:I:146:PRO:CG	2.47	0.44
1:B:338:LEU:HB3	3:I:33:THR:OG1	2.18	0.44
1:B:340:THR:CG2	3:I:53:ASP:HB3	2.48	0.44
2:M:39:ARG:HG2	2:M:84:ALA:HB2	2.00	0.44
2:M:132:VAL:CG2	2:M:179:LEU:HB3	2.48	0.44
2:L:35:TRP:CZ3	2:L:88:CYS:HB3	2.53	0.44
2:M:140:TYR:CG	2:M:141:PRO:HA	2.52	0.44
1:B:388:LYS:HG3	1:B:389:ASN:N	2.32	0.44
1:B:285:HIS:CE1	1:B:286:THR:HG1	2.36	0.43
1:B:340:THR:HG22	1:B:341:LYS:N	2.32	0.43
1:A:285:HIS:CE1	1:A:286:THR:HG1	2.36	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:136:LEU:HD12	2:L:136:LEU:N	2.33	0.43
2:M:83:ALA:HB2	2:M:106:ILE:HG12	1.98	0.43
1:A:481:GLN:HA	1:A:484:ARG:NH1	2.34	0.43
3:H:176:LEU:HD12	3:H:176:LEU:C	2.39	0.43
1:B:481:GLN:HA	1:B:484:ARG:NH1	2.33	0.43
1:A:330:TRP:CZ2	1:A:346:PRO:HB3	2.54	0.43
2:L:39:ARG:HG2	2:L:84:ALA:HB2	2.00	0.43
1:B:197:LEU:N	1:B:198:PRO:HD2	2.34	0.43
1:B:223:ARG:HB2	1:B:277:TYR:CE1	2.54	0.43
1:A:37:ILE:N	1:A:37:ILE:HD12	2.34	0.43
1:A:197:LEU:N	1:A:198:PRO:HD2	2.34	0.43
2:L:132:VAL:CG2	2:L:179:LEU:HB3	2.49	0.43
1:B:37:ILE:HD12	1:B:37:ILE:N	2.34	0.43
2:M:35:TRP:CZ3	2:M:88:CYS:HB3	2.53	0.43
2:M:96:PHE:HB2	3:I:47:TRP:CG	2.54	0.43
2:L:117:ILE:O	2:L:117:ILE:HG13	2.18	0.42
3:I:176:LEU:C	3:I:176:LEU:HD12	2.39	0.42
1:B:330:TRP:CZ2	1:B:346:PRO:HB3	2.54	0.42
1:A:345:VAL:HG23	1:A:346:PRO:HD2	2.01	0.42
1:A:340:THR:HG22	1:A:341:LYS:N	2.35	0.42
1:A:404:ALA:O	1:A:408:ASP:OD2	2.37	0.42
1:A:581:ASP:OD1	1:A:587:LEU:HD21	2.19	0.42
1:B:345:VAL:HG23	1:B:346:PRO:HD2	2.00	0.42
1:B:404:ALA:O	1:B:408:ASP:OD2	2.37	0.42
1:A:223:ARG:HB2	1:A:277:TYR:CE1	2.55	0.42
1:A:339:SER:O	1:A:340:THR:C	2.58	0.42
1:A:568:LYS:NZ	1:A:576:ASN:HA	2.34	0.42
1:A:148:ARG:HG3	1:A:149:GLU:N	2.35	0.42
1:B:568:LYS:NZ	1:B:576:ASN:HA	2.34	0.42
3:I:18:VAL:HG23	3:I:82(C):LEU:HD11	2.02	0.42
1:B:309:ASP:HB3	1:B:312:ASP:OD2	2.20	0.42
3:I:149:VAL:CG2	3:I:176:LEU:HD21	2.50	0.42
1:B:338:LEU:HD11	3:I:35:HIS:CD2	2.55	0.42
2:L:48:ILE:HA	2:L:53:HIS:O	2.20	0.42
1:B:148:ARG:HG3	1:B:149:GLU:N	2.35	0.42
3:H:18:VAL:HG23	3:H:82(C):LEU:HD11	2.02	0.41
1:B:581:ASP:OD1	1:B:587:LEU:HD21	2.19	0.41
3:I:51:ILE:CG2	3:I:69:LEU:HB2	2.50	0.41
1:B:13:ASN:HB2	1:B:47:VAL:HG21	2.01	0.41
2:M:116:SER:HA	2:M:205:HIS:ND1	2.35	0.41
2:L:21:ILE:O	2:L:72:THR:HA	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:151:ASP:HA	2:M:191:SER:HB3	2.03	0.41
3:I:51:ILE:HD11	3:I:71:VAL:CG1	2.50	0.41
3:H:51:ILE:CG2	3:H:69:LEU:HB2	2.50	0.41
3:H:149:VAL:CG2	3:H:176:LEU:HD21	2.50	0.41
1:B:28:LYS:CG	1:B:29:ASN:N	2.82	0.41
1:B:145:ASN:HA	1:B:148:ARG:HD2	2.03	0.41
3:I:51:ILE:HD12	3:I:51:ILE:O	2.20	0.41
2:L:7:SER:CB	2:L:8:PRO:CD	2.98	0.41
1:B:306:GLU:O	1:B:381:ARG:HD3	2.21	0.41
2:M:21:ILE:O	2:M:72:THR:HA	2.20	0.41
2:M:7:SER:CB	2:M:8:PRO:CD	2.98	0.41
1:A:25:CYS:SG	1:A:232:GLU:HG2	2.61	0.41
1:A:306:GLU:O	1:A:381:ARG:HD3	2.21	0.41
1:A:309:ASP:HB3	1:A:312:ASP:OD2	2.20	0.41
2:L:83:ALA:O	2:L:84:ALA:HB2	2.19	0.41
3:H:39:GLN:HB2	3:H:45:LEU:HD23	2.01	0.41
2:M:48:ILE:HA	2:M:53:HIS:O	2.20	0.41
2:M:159:VAL:C	2:M:160:LEU:HD12	2.41	0.41
1:A:183:TRP:CH2	1:A:233:TRP:HB2	2.56	0.41
3:H:4:LEU:HG	3:H:24:THR:HG22	2.03	0.41
3:H:95:GLY:HA3	3:H:99:MET:HA	2.03	0.41
1:B:25:CYS:SG	1:B:232:GLU:HG2	2.61	0.41
1:B:176:ILE:HG23	1:B:177:THR:N	2.36	0.41
1:B:336:TYR:CD2	1:B:339:SER:HB2	2.55	0.41
3:I:39:GLN:HB2	3:I:45:LEU:HD23	2.02	0.41
2:L:116:SER:HA	2:L:205:HIS:ND1	2.36	0.40
2:M:83:ALA:O	2:M:84:ALA:HB2	2.21	0.40
2:M:116:SER:HA	2:M:205:HIS:CE1	2.56	0.40
3:I:4:LEU:HG	3:I:24:THR:HG22	2.03	0.40
1:A:176:ILE:HG23	1:A:177:THR:N	2.37	0.40
2:L:162:SER:O	2:L:175:MET:HB2	2.21	0.40
3:H:40:SER:HB2	3:H:43:GLU:HB2	2.03	0.40
3:H:92:CYS:SG	3:H:92:CYS:O	2.79	0.40
3:I:3:GLN:C	3:I:4:LEU:HD12	2.41	0.40
3:I:95:GLY:HA3	3:I:99:MET:HA	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	553/602 (92%)	526 (95%)	27 (5%)	0	100	100
1	B	574/602 (95%)	546 (95%)	28 (5%)	0	100	100
2	L	208/214 (97%)	192 (92%)	16 (8%)	0	100	100
2	M	211/214 (99%)	195 (92%)	16 (8%)	0	100	100
3	H	202/215 (94%)	185 (92%)	17 (8%)	0	100	100
3	I	206/215 (96%)	188 (91%)	18 (9%)	0	100	100
All	All	1954/2062 (95%)	1832 (94%)	122 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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	530/569 (93%)	527 (99%)	3 (1%)	86	92
1	B	548/569 (96%)	545 (100%)	3 (0%)	88	93
2	L	182/184 (99%)	182 (100%)	0	100	100
2	M	183/184 (100%)	183 (100%)	0	100	100
3	H	182/187 (97%)	180 (99%)	2 (1%)	73	85
3	I	184/187 (98%)	182 (99%)	2 (1%)	73	85
All	All	1809/1880 (96%)	1799 (99%)	10 (1%)	86	92

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	433	ASN
1	A	439	LYS
1	A	558	PHE
3	H	11	LEU
3	H	46	ASP
1	B	433	ASN
1	B	439	LYS
1	B	558	PHE
3	I	11	LEU
3	I	46	ASP

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	436	HIS
2	L	34	HIS
1	B	371	HIS
1	B	436	HIS
2	M	34	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.