Full wwPDB X-ray Structure Validation Report ⓘ

Feb 17, 2024 – 03:53 PM EST

PDB ID	:	3TS5
Title	:	Crystal Structure of a Light Chain Domain of Scallop Smooth Muscle Myosin
Authors	:	Kumar, V.S.S.; O'Neall-Hennessey, E.; Reshetnikova, L.; Brown, J.H.; Robinson, H.; Szent-Gyorgyi, A.G.; Cohen, C.
Deposited on	:	2011-09-12
Resolution	:	2.39 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:

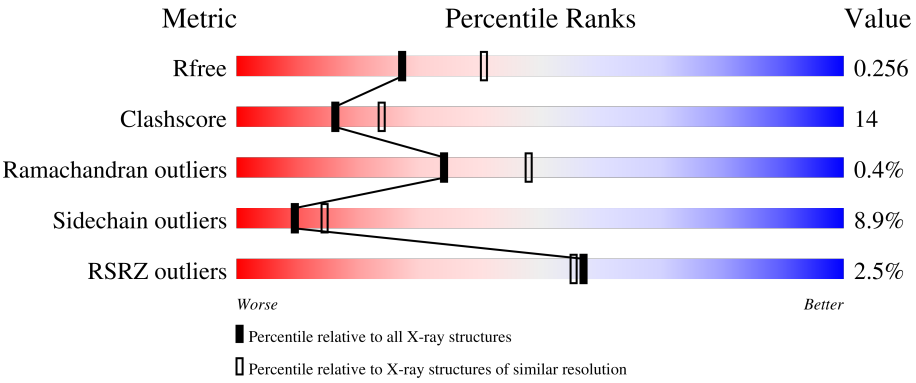
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.39 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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% 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	69	70% 25%
1	D	69	75% 22%
2	B	161	66% 18% 12%
2	E	161	7% 60% 25% 5% 9%
3	C	156	74% 22%

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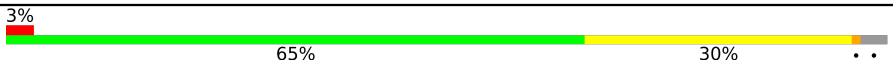
Mol	Chain	Length	Quality of chain
3	F	156	

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 6145 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 Myosin heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	68	Total	C	N	O	S	0	0	0
			598	392	113	91	2			
1	D	69	Total	C	N	O	S	0	0	0
			606	396	115	93	2			

- Molecule 2 is a protein called Myosin regulatory light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	142	Total	C	N	O	S	0	0	0
			1140	721	184	224	11			
2	E	146	Total	C	N	O	S	0	0	0
			1172	742	189	230	11			

- Molecule 3 is a protein called Myosin essential light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	152	Total	C	N	O	S	0	0	0
			1210	764	192	247	7			
3	F	151	Total	C	N	O	S	0	0	0
			1198	755	191	245	7			

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Mg	0	0
			1	1		
4	E	1	Total	Mg	0	0
			1	1		

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	C	1	Total Ca 1 1	0	0
5	F	1	Total Ca 1 1	0	0

- Molecule 6 is water.

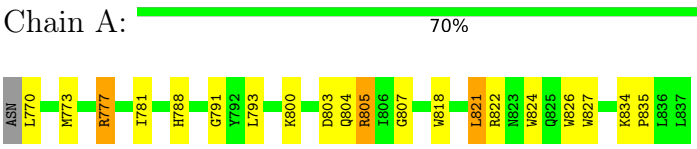
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	24	Total O 24 24	0	0
6	B	58	Total O 58 58	0	0
6	C	65	Total O 65 65	0	0
6	D	16	Total O 16 16	0	0
6	E	20	Total O 20 20	0	0
6	F	34	Total O 34 34	0	0

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.

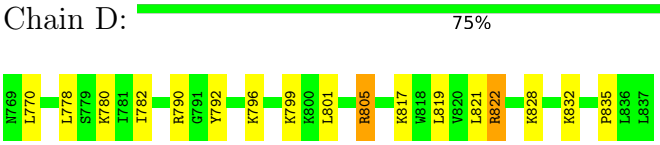
• Molecule 1: Myosin heavy chain

Chain A:



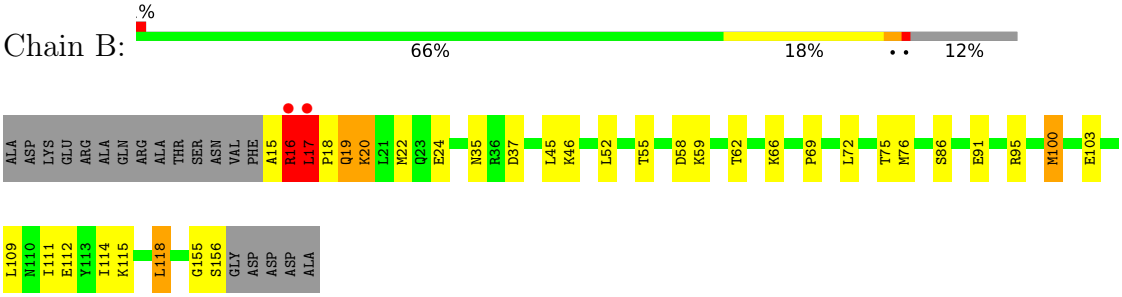
• Molecule 1: Myosin heavy chain

Chain D:



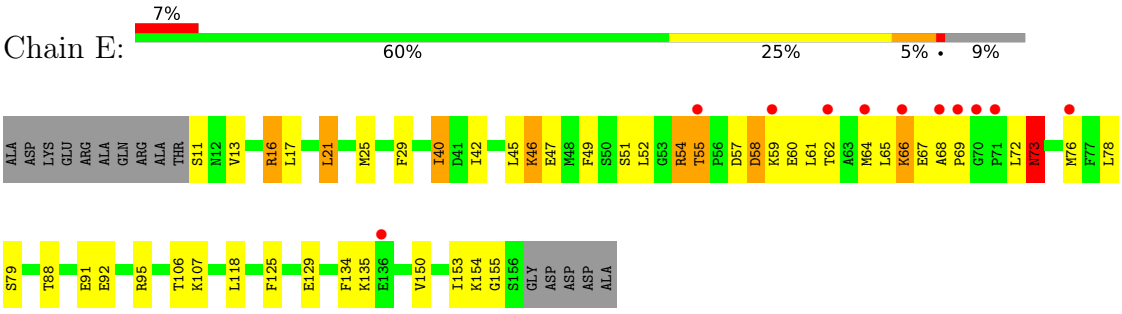
• Molecule 2: Myosin regulatory light chain

Chain B:



• Molecule 2: Myosin regulatory light chain

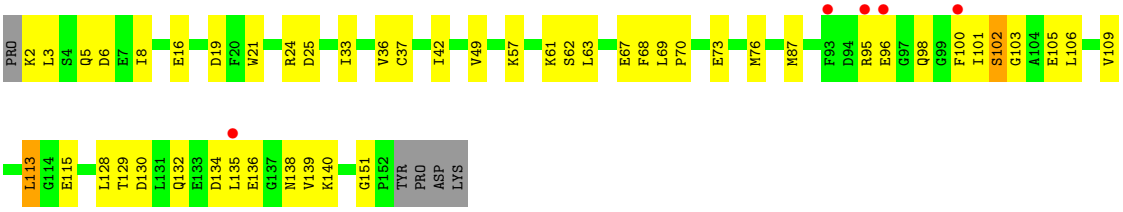
Chain E:



• Molecule 3: Myosin essential light chain

Chain C:

• Molecule 3: Myosin essential light chain



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	50.81Å 68.78Å 79.42Å 77.33° 85.99° 73.65°	Depositor
Resolution (Å)	48.75 – 2.39 48.75 – 2.39	Depositor EDS
% Data completeness (in resolution range)	99.0 (48.75-2.39) 94.6 (48.75-2.39)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.59 (at 2.39Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, R_{free}	0.191 , 0.241 0.202 , 0.256	Depositor DCC
R_{free} test set	2000 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å^2)	45.2	Xtriage
Anisotropy	0.168	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 45.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	6145	wwPDB-VP
Average B, all atoms (Å^2)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.67% 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

5.1 Standard geometry

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

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	0.50	0/611	0.58	0/818
1	D	0.39	0/619	0.51	0/829
2	B	0.48	0/1158	0.62	1/1547 (0.1%)
2	E	0.45	1/1191 (0.1%)	0.54	0/1592
3	C	0.53	0/1233	0.60	0/1658
3	F	0.47	0/1220	0.58	0/1640
All	All	0.47	1/6032 (0.0%)	0.58	1/8084 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	73	ASN	C-N	-5.59	1.21	1.34

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	17	LEU	N-CA-C	-5.43	96.35	111.00

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	598	0	643	23	0
1	D	606	0	649	14	0
2	B	1140	0	1123	37	0
2	E	1172	0	1152	46	0
3	C	1210	0	1134	28	0
3	F	1198	0	1125	40	0
4	B	1	0	0	0	0
4	E	1	0	0	0	0
5	C	1	0	0	0	0
5	F	1	0	0	0	0
6	A	24	0	0	5	0
6	B	58	0	0	1	0
6	C	65	0	0	2	0
6	D	16	0	0	1	0
6	E	20	0	0	2	0
6	F	34	0	0	0	0
All	All	6145	0	5826	169	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 14.

All (169) 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)
2:B:16:ARG:CB	2:B:17:LEU:HA	1.74	1.17
2:B:16:ARG:HG2	2:B:18:PRO:HD3	1.30	1.13
2:B:16:ARG:HB3	2:B:17:LEU:HA	1.05	1.03
2:E:61:LEU:O	2:E:65:LEU:HD23	1.59	1.00
2:B:16:ARG:HB3	2:B:17:LEU:CA	1.92	0.97
2:B:16:ARG:CG	2:B:18:PRO:HD3	1.96	0.95
2:B:15:ALA:O	2:B:16:ARG:HB2	1.67	0.94
2:B:16:ARG:HG2	2:B:18:PRO:CD	2.00	0.93
2:E:45:LEU:HD22	2:E:65:LEU:HD21	1.52	0.92
3:C:146:LYS:O	3:C:150:THR:HG23	1.72	0.89
2:B:58:ASP:O	2:B:62:THR:HG23	1.75	0.87
2:B:35:ASN:HB3	2:B:37:ASP:HB2	1.57	0.85
2:B:19:GLN:NE2	2:B:19:GLN:HA	1.89	0.85
2:E:40:ILE:HD13	2:E:45:LEU:HD13	1.58	0.85
2:E:40:ILE:HD11	2:E:65:LEU:HD11	1.60	0.81
2:E:42:ILE:HD12	2:E:42:ILE:H	1.45	0.80
2:E:61:LEU:O	2:E:65:LEU:CD2	2.29	0.80
1:A:821:LEU:C	1:A:821:LEU:HD23	2.01	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:73:ASN:HD22	2:E:73:ASN:H	1.27	0.79
1:A:821:LEU:O	1:A:827:TRP:CD1	2.38	0.77
2:E:64:MET:O	2:E:67:GLU:HG3	1.85	0.77
3:F:5:GLN:HA	3:F:8:ILE:HD12	1.68	0.75
1:A:791:GLY:HA2	3:C:38:ARG:HG2	1.67	0.75
2:B:17:LEU:HD23	2:B:17:LEU:N	2.01	0.75
1:D:778:LEU:O	1:D:782:ILE:HG12	1.87	0.75
3:F:106:LEU:O	3:F:109:VAL:HG22	1.86	0.75
2:B:91:GLU:HG2	2:B:95:ARG:HH21	1.52	0.74
2:B:16:ARG:CB	2:B:17:LEU:CA	2.57	0.74
3:F:134:ASP:OD1	3:F:135:LEU:N	2.22	0.71
3:C:150:THR:HG22	6:C:208:HOH:O	1.91	0.70
2:B:16:ARG:CD	2:B:18:PRO:HD3	2.21	0.70
2:B:16:ARG:HD3	2:B:18:PRO:HD3	1.74	0.69
3:C:100:PHE:CE1	3:C:140:LYS:HD3	2.27	0.69
2:E:68:ALA:HB1	2:E:76:MET:SD	2.33	0.69
1:D:819:LEU:HA	1:D:822:ARG:HD2	1.73	0.69
2:B:62:THR:O	2:B:66:LYS:HG3	1.94	0.68
1:D:790:ARG:NH2	3:F:115:GLU:O	2.25	0.67
2:E:66:LYS:CB	2:E:66:LYS:NZ	2.58	0.66
2:E:45:LEU:HD22	2:E:65:LEU:CD2	2.26	0.64
2:E:62:THR:N	6:E:183:HOH:O	2.30	0.64
2:E:16:ARG:HG3	2:E:17:LEU:HD12	1.80	0.64
3:C:100:PHE:CZ	3:C:140:LYS:HD3	2.34	0.62
2:E:40:ILE:CD1	2:E:65:LEU:HD11	2.30	0.62
3:F:109:VAL:HA	3:F:113:LEU:HD12	1.81	0.61
2:B:16:ARG:CG	2:B:17:LEU:HA	2.31	0.60
2:E:66:LYS:NZ	2:E:66:LYS:HB2	2.15	0.60
1:A:770:LEU:HD12	6:A:112:HOH:O	2.02	0.60
2:E:11:SER:O	2:E:16:ARG:NH1	2.35	0.59
3:C:132:GLN:HG2	6:C:197:HOH:O	2.02	0.59
3:F:105:GLU:O	3:F:109:VAL:HG13	2.02	0.59
2:E:59:LYS:C	6:E:183:HOH:O	2.41	0.58
3:F:100:PHE:HE2	3:F:140:LYS:HE2	1.68	0.58
3:F:73:GLU:HA	3:F:76:MET:HE2	1.84	0.58
3:F:134:ASP:HB3	3:F:138:ASN:H	1.67	0.58
1:A:805:ARG:HD2	6:A:226:HOH:O	2.04	0.57
3:C:102:SER:OG	3:C:105:GLU:HG3	2.05	0.57
2:E:91:GLU:HG2	2:E:150:VAL:HG12	1.85	0.57
1:A:821:LEU:HG	1:A:827:TRP:CG	2.40	0.56
3:C:69:LEU:HB3	3:C:70:PRO:HD3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:796:LYS:HG2	3:F:128:LEU:HD13	1.88	0.56
3:C:4:SER:HB3	3:C:7:GLU:HG3	1.87	0.55
1:D:801:LEU:HD22	3:F:21:TRP:NE1	2.22	0.55
2:B:35:ASN:CB	2:B:37:ASP:HB2	2.34	0.55
3:F:136:GLU:OE1	3:F:136:GLU:N	2.39	0.55
2:B:69:PRO:HD2	2:B:76:MET:SD	2.47	0.54
2:E:76:MET:HA	2:E:76:MET:HE2	1.88	0.54
2:E:73:ASN:HD22	2:E:73:ASN:N	1.95	0.54
3:F:69:LEU:HB3	3:F:70:PRO:HD3	1.90	0.54
1:A:821:LEU:C	1:A:821:LEU:CD2	2.73	0.54
2:E:153:ILE:O	2:E:154:LYS:HB2	2.08	0.53
1:D:832:LYS:HB3	2:E:52:LEU:HD13	1.92	0.52
3:C:4:SER:HB3	3:C:7:GLU:OE2	2.10	0.52
1:A:803:ASP:O	2:B:100:MET:HE1	2.09	0.52
3:F:101:ILE:HG23	3:F:103:GLY:H	1.73	0.51
2:B:19:GLN:NE2	2:B:19:GLN:CA	2.70	0.51
2:E:42:ILE:HG22	2:E:46:LYS:HD3	1.92	0.51
2:E:66:LYS:HB2	2:E:66:LYS:HZ1	1.76	0.51
3:C:61:LYS:HD2	3:C:63:LEU:HD21	1.93	0.51
3:F:61:LYS:HE2	3:F:63:LEU:HD21	1.92	0.50
1:A:770:LEU:HD21	6:A:149:HOH:O	2.12	0.50
1:D:801:LEU:HD22	3:F:21:TRP:CD1	2.46	0.50
2:E:62:THR:O	2:E:66:LYS:N	2.43	0.50
3:F:36:VAL:HG11	3:F:68:PHE:CE2	2.47	0.49
1:A:807:GLY:HA3	2:B:100:MET:CE	2.42	0.49
1:A:800:LYS:NZ	2:B:103:GLU:OE2	2.41	0.48
1:A:821:LEU:HD23	1:A:822:ARG:N	2.28	0.48
2:E:118:LEU:HD12	2:E:134:PHE:HZ	1.78	0.48
3:F:101:ILE:O	3:F:103:GLY:N	2.46	0.48
3:F:134:ASP:N	3:F:138:ASN:O	2.39	0.48
3:F:102:SER:HB2	3:F:105:GLU:HB2	1.96	0.48
3:C:2:LYS:HG3	3:C:3:LEU:N	2.29	0.48
3:C:73:GLU:HA	3:C:76:MET:HE2	1.96	0.48
2:B:19:GLN:HA	2:B:19:GLN:HE21	1.76	0.47
3:F:2:LYS:HE2	3:F:76:MET:HE1	1.96	0.47
3:C:133:GLU:HB3	3:C:137:GLY:HA2	1.96	0.47
1:A:824:TRP:CE2	1:A:826:TRP:HB2	2.49	0.47
2:B:156:SER:N	6:B:168:HOH:O	2.47	0.47
3:C:2:LYS:HG3	3:C:3:LEU:H	1.80	0.47
1:D:792:TYR:CD2	3:F:151:GLY:HA2	2.50	0.47
1:D:822:ARG:O	1:D:828:LYS:HD2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:29:PHE:CE1	2:E:40:ILE:HG23	2.49	0.47
3:F:2:LYS:HE2	3:F:76:MET:CE	2.44	0.47
1:A:834:LYS:HE2	2:B:24:GLU:OE1	2.16	0.46
3:C:57:LYS:HG2	3:C:60:GLU:OE1	2.16	0.46
2:E:40:ILE:HG13	2:E:72:LEU:HD13	1.97	0.46
2:E:58:ASP:N	2:E:58:ASP:OD1	2.49	0.46
2:E:118:LEU:HD12	2:E:134:PHE:CZ	2.50	0.46
1:A:781:ILE:HG21	3:C:89:ALA:HB2	1.97	0.46
1:D:805:ARG:NH2	3:F:16:GLU:CD	2.69	0.46
2:E:54:ARG:H	2:E:54:ARG:NE	2.14	0.46
1:D:790:ARG:NH2	3:F:115:GLU:HB3	2.32	0.45
1:A:821:LEU:HG	1:A:827:TRP:CD2	2.51	0.45
2:E:21:LEU:O	2:E:25:MET:HG3	2.16	0.45
1:A:834:LYS:N	1:A:835:PRO:CD	2.80	0.45
2:B:114:ILE:HG13	2:B:118:LEU:HD22	1.99	0.45
3:F:96:GLU:O	3:F:98:GLN:N	2.47	0.45
3:C:5:GLN:HA	3:C:8:ILE:HD12	1.99	0.45
1:D:805:ARG:NE	6:D:190:HOH:O	2.21	0.45
2:E:106:THR:O	2:E:107:LYS:HB2	2.17	0.45
1:A:773:MET:HG2	6:A:140:HOH:O	2.16	0.44
3:F:101:ILE:HD12	3:F:101:ILE:HA	1.79	0.44
2:E:125:PHE:HA	2:E:129:GLU:OE1	2.18	0.44
2:B:46:LYS:CE	2:B:58:ASP:OD2	2.66	0.44
3:F:19:ASP:OD2	3:F:25:ASP:O	2.36	0.44
3:F:101:ILE:HG22	3:F:139:VAL:HG23	1.99	0.44
3:C:25:ASP:N	3:C:25:ASP:OD1	2.51	0.43
2:E:46:LYS:H	2:E:46:LYS:HG2	1.54	0.43
3:F:37:CYS:HB3	3:F:42:ILE:HD11	2.01	0.43
2:E:73:ASN:H	2:E:73:ASN:ND2	2.04	0.43
2:E:60:GLU:O	2:E:64:MET:HG3	2.19	0.43
1:D:805:ARG:NH2	3:F:16:GLU:OE1	2.52	0.43
3:F:24:ARG:HG2	3:F:24:ARG:HH11	1.83	0.43
2:E:78:LEU:HD12	2:E:78:LEU:HA	1.85	0.43
3:F:129:THR:O	3:F:130:ASP:HB3	2.18	0.43
3:F:102:SER:HB2	3:F:105:GLU:H	1.83	0.43
2:B:16:ARG:HD2	2:B:86:SER:O	2.19	0.42
2:B:17:LEU:N	2:B:17:LEU:CD2	2.76	0.42
3:C:45:ARG:O	3:C:48:ASP:HB2	2.19	0.42
1:A:804:GLN:HA	2:B:100:MET:HE3	2.02	0.42
3:F:87:MET:HA	3:F:87:MET:CE	2.49	0.42
2:B:20:LYS:HB2	2:B:20:LYS:HE3	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:781:ILE:CG2	3:C:89:ALA:HB2	2.50	0.41
2:B:111:ILE:O	2:B:115:LYS:HG3	2.20	0.41
2:E:66:LYS:CB	2:E:66:LYS:HZ1	2.30	0.41
2:E:76:MET:HE3	2:E:76:MET:HB2	1.90	0.41
2:E:88:THR:HG23	2:E:155:GLY:O	2.20	0.41
3:C:101:ILE:HG12	3:C:105:GLU:HB2	2.01	0.41
1:D:832:LYS:O	1:D:835:PRO:HD2	2.21	0.41
2:E:40:ILE:CD1	2:E:45:LEU:HD13	2.40	0.41
3:F:33:ILE:HD11	3:F:63:LEU:HD11	2.03	0.41
3:F:67:GLU:O	3:F:70:PRO:HD2	2.19	0.41
2:E:40:ILE:C	2:E:40:ILE:HD12	2.40	0.41
3:C:69:LEU:N	3:C:70:PRO:CD	2.83	0.41
3:C:77:ASP:N	3:C:77:ASP:OD1	2.47	0.41
1:A:818:TRP:HA	1:A:821:LEU:HD22	2.02	0.41
2:B:100:MET:HE2	2:B:100:MET:HB2	1.85	0.41
3:C:3:LEU:HD12	3:C:3:LEU:HA	1.79	0.41
6:A:224:HOH:O	2:B:155:GLY:HA2	2.20	0.41
2:E:73:ASN:N	2:E:73:ASN:ND2	2.66	0.41
3:C:4:SER:HB3	3:C:7:GLU:CG	2.51	0.40
1:A:777:ARG:NH1	3:C:88:GLU:OE1	2.54	0.40
1:A:807:GLY:HA3	2:B:100:MET:HE1	2.04	0.40
2:B:59:LYS:HA	2:B:59:LYS:HD2	1.64	0.40
3:F:130:ASP:OD1	3:F:132:GLN:NE2	2.47	0.40
2:E:92:GLU:OE1	2:E:95:ARG:NH1	2.52	0.40
3:F:102:SER:HB2	3:F:105:GLU:CB	2.51	0.40
2:E:49:PHE:HB3	2:E:55:THR:HB	2.03	0.40
3:C:76:MET:HE2	3:C:76:MET:HB2	1.94	0.40
3:F:61:LYS:HE2	3:F:63:LEU:CD2	2.52	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	66/69 (96%)	66 (100%)	0	0	100	100
1	D	67/69 (97%)	65 (97%)	2 (3%)	0	100	100
2	B	140/161 (87%)	135 (96%)	4 (3%)	1 (1%)	22	32
2	E	144/161 (89%)	138 (96%)	5 (4%)	1 (1%)	22	32
3	C	150/156 (96%)	147 (98%)	3 (2%)	0	100	100
3	F	149/156 (96%)	141 (95%)	7 (5%)	1 (1%)	22	32
All	All	716/772 (93%)	692 (97%)	21 (3%)	3 (0%)	34	48

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	16	ARG
3	F	102	SER
2	E	69	PRO

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	63/64 (98%)	58 (92%)	5 (8%)	12	19
1	D	64/64 (100%)	57 (89%)	7 (11%)	6	8
2	B	126/140 (90%)	112 (89%)	14 (11%)	6	8
2	E	130/140 (93%)	115 (88%)	15 (12%)	5	7
3	C	129/133 (97%)	120 (93%)	9 (7%)	15	24
3	F	128/133 (96%)	121 (94%)	7 (6%)	21	35
All	All	640/674 (95%)	583 (91%)	57 (9%)	9	14

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	777	ARG
1	A	788	HIS

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Mol	Chain	Res	Type
1	A	793	LEU
1	A	805	ARG
1	A	821	LEU
2	B	16	ARG
2	B	17	LEU
2	B	19	GLN
2	B	20	LYS
2	B	22	MET
2	B	45	LEU
2	B	52	LEU
2	B	55	THR
2	B	72	LEU
2	B	75	THR
2	B	100	MET
2	B	109	LEU
2	B	112	GLU
2	B	118	LEU
3	C	6	ASP
3	C	12	LYS
3	C	16	GLU
3	C	80	GLN
3	C	91	LYS
3	C	101	ILE
3	C	132	GLN
3	C	150	THR
3	C	153	TYR
1	D	770	LEU
1	D	780	LYS
1	D	799	LYS
1	D	805	ARG
1	D	817	LYS
1	D	821	LEU
1	D	822	ARG
2	E	13	VAL
2	E	16	ARG
2	E	21	LEU
2	E	40	ILE
2	E	46	LYS
2	E	47	GLU
2	E	51	SER
2	E	54	ARG
2	E	55	THR

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Mol	Chain	Res	Type
2	E	57	ASP
2	E	58	ASP
2	E	66	LYS
2	E	73	ASN
2	E	79	SER
2	E	135	LYS
3	F	3	LEU
3	F	6	ASP
3	F	49	VAL
3	F	57	LYS
3	F	62	SER
3	F	95	ARG
3	F	113	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	19	GLN
2	E	73	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 4 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, 95^{th} 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	68/69 (98%)	0.03	0 100 100	32, 42, 66, 76	0
1	D	69/69 (100%)	0.05	0 100 100	39, 49, 88, 94	0
2	B	142/161 (88%)	0.08	2 (1%) 75 73	20, 46, 69, 87	0
2	E	146/161 (90%)	0.32	11 (7%) 14 13	25, 60, 88, 103	0
3	C	152/156 (97%)	0.01	0 100 100	32, 46, 65, 75	0
3	F	151/156 (96%)	0.07	5 (3%) 46 45	37, 56, 96, 107	0
All	All	728/772 (94%)	0.11	18 (2%) 57 55	20, 50, 85, 107	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	69	PRO	7.0
2	B	16	ARG	5.2
2	B	17	LEU	4.6
2	E	66	LYS	3.5
3	F	135	LEU	3.0
2	E	68	ALA	3.0
2	E	70	GLY	2.7
3	F	100	PHE	2.3
2	E	59	LYS	2.2
2	E	76	MET	2.2
2	E	55	THR	2.2
2	E	136	GLU	2.1
3	F	95	ARG	2.1
3	F	93	PHE	2.1
2	E	71	PRO	2.1
3	F	96	GLU	2.1
2	E	62	THR	2.1
2	E	64	MET	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 monosaccharides 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, 95^{th} 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
4	MG	E	162	1/1	0.94	0.12	71,71,71,71	0
5	CA	C	157	1/1	0.95	0.12	43,43,43,43	0
4	MG	B	162	1/1	0.98	0.34	42,42,42,42	0
5	CA	F	157	1/1	0.99	0.14	44,44,44,44	0

6.5 Other polymers (i)

There are no such residues in this entry.