



Full wwPDB X-ray Structure Validation Report

Mar 1, 2014 – 02:48 AM GMT

PDB ID : 2D39
Title : Trivalent Recognition Unit of Innate Immunity System; Crystal Structure of human M-ficolin Fibrinogen-like Domain
Authors : Tanio, M.; Kondo, S.; Sugio, S.; Kohno, T.
Deposited on : 2005-09-26
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>

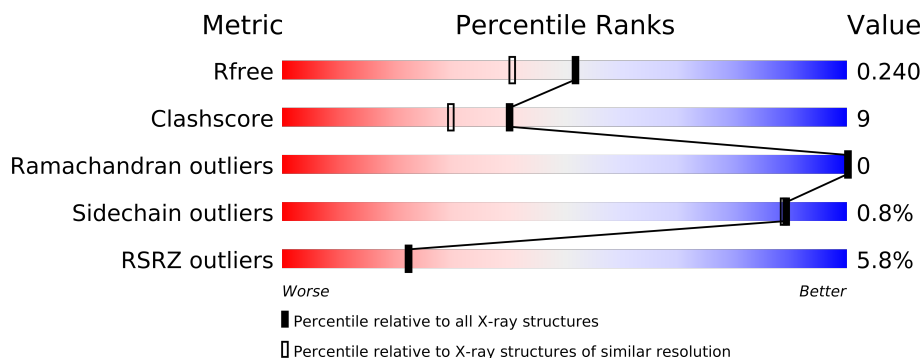
The following versions of software and data (see [references](#)) were used in the production of this report:

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	A	237	
1	B	237	
1	C	237	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5212 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 Ficolin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	209	Total	C	N	O	S	0	0	0
			1656	1049	284	314	9			
1	B	200	Total	C	N	O	S	0	0	0
			1591	1008	273	302	8			
1	C	212	Total	C	N	O	S	0	0	0
			1680	1063	289	319	9			

There are 75 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	113	GLU	-	CLONING ARTIFACT	UNP O00602
A	114	PHE	-	CLONING ARTIFACT	UNP O00602
A	327	PHE	-	CLONING ARTIFACT	UNP O00602
A	328	LEU	-	CLONING ARTIFACT	UNP O00602
A	329	GLU	-	SEE REMARK 999	UNP O00602
A	330	GLN	-	SEE REMARK 999	UNP O00602
A	331	LYS	-	SEE REMARK 999	UNP O00602
A	332	LEU	-	SEE REMARK 999	UNP O00602
A	333	ILE	-	SEE REMARK 999	UNP O00602
A	334	SER	-	SEE REMARK 999	UNP O00602
A	335	GLU	-	SEE REMARK 999	UNP O00602
A	336	GLU	-	SEE REMARK 999	UNP O00602
A	337	ASP	-	SEE REMARK 999	UNP O00602
A	338	LEU	-	SEE REMARK 999	UNP O00602
A	339	ASN	-	CLONING ARTIFACT	UNP O00602
A	340	SER	-	CLONING ARTIFACT	UNP O00602
A	341	ALA	-	CLONING ARTIFACT	UNP O00602
A	342	VAL	-	CLONING ARTIFACT	UNP O00602
A	343	ASP	-	CLONING ARTIFACT	UNP O00602
A	344	HIS	-	EXPRESSION TAG	UNP O00602
A	345	HIS	-	EXPRESSION TAG	UNP O00602
A	346	HIS	-	EXPRESSION TAG	UNP O00602
A	347	HIS	-	EXPRESSION TAG	UNP O00602

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Chain	Residue	Modelled	Actual	Comment	Reference
A	348	HIS	-	EXPRESSION TAG	UNP O00602
A	349	HIS	-	EXPRESSION TAG	UNP O00602
B	113	GLU	-	CLONING ARTIFACT	UNP O00602
B	114	PHE	-	CLONING ARTIFACT	UNP O00602
B	327	PHE	-	CLONING ARTIFACT	UNP O00602
B	328	LEU	-	CLONING ARTIFACT	UNP O00602
B	329	GLU	-	SEE REMARK 999	UNP O00602
B	330	GLN	-	SEE REMARK 999	UNP O00602
B	331	LYS	-	SEE REMARK 999	UNP O00602
B	332	LEU	-	SEE REMARK 999	UNP O00602
B	333	ILE	-	SEE REMARK 999	UNP O00602
B	334	SER	-	SEE REMARK 999	UNP O00602
B	335	GLU	-	SEE REMARK 999	UNP O00602
B	336	GLU	-	SEE REMARK 999	UNP O00602
B	337	ASP	-	SEE REMARK 999	UNP O00602
B	338	LEU	-	SEE REMARK 999	UNP O00602
B	339	ASN	-	CLONING ARTIFACT	UNP O00602
B	340	SER	-	CLONING ARTIFACT	UNP O00602
B	341	ALA	-	CLONING ARTIFACT	UNP O00602
B	342	VAL	-	CLONING ARTIFACT	UNP O00602
B	343	ASP	-	CLONING ARTIFACT	UNP O00602
B	344	HIS	-	EXPRESSION TAG	UNP O00602
B	345	HIS	-	EXPRESSION TAG	UNP O00602
B	346	HIS	-	EXPRESSION TAG	UNP O00602
B	347	HIS	-	EXPRESSION TAG	UNP O00602
B	348	HIS	-	EXPRESSION TAG	UNP O00602
B	349	HIS	-	EXPRESSION TAG	UNP O00602
C	113	GLU	-	CLONING ARTIFACT	UNP O00602
C	114	PHE	-	CLONING ARTIFACT	UNP O00602
C	327	PHE	-	CLONING ARTIFACT	UNP O00602
C	328	LEU	-	CLONING ARTIFACT	UNP O00602
C	329	GLU	-	SEE REMARK 999	UNP O00602
C	330	GLN	-	SEE REMARK 999	UNP O00602
C	331	LYS	-	SEE REMARK 999	UNP O00602
C	332	LEU	-	SEE REMARK 999	UNP O00602
C	333	ILE	-	SEE REMARK 999	UNP O00602
C	334	SER	-	SEE REMARK 999	UNP O00602
C	335	GLU	-	SEE REMARK 999	UNP O00602
C	336	GLU	-	SEE REMARK 999	UNP O00602
C	337	ASP	-	SEE REMARK 999	UNP O00602
C	338	LEU	-	SEE REMARK 999	UNP O00602
C	339	ASN	-	CLONING ARTIFACT	UNP O00602

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Chain	Residue	Modelled	Actual	Comment	Reference
C	340	SER	-	CLONING ARTIFACT	UNP O00602
C	341	ALA	-	CLONING ARTIFACT	UNP O00602
C	342	VAL	-	CLONING ARTIFACT	UNP O00602
C	343	ASP	-	CLONING ARTIFACT	UNP O00602
C	344	HIS	-	EXPRESSION TAG	UNP O00602
C	345	HIS	-	EXPRESSION TAG	UNP O00602
C	346	HIS	-	EXPRESSION TAG	UNP O00602
C	347	HIS	-	EXPRESSION TAG	UNP O00602
C	348	HIS	-	EXPRESSION TAG	UNP O00602
C	349	HIS	-	EXPRESSION TAG	UNP O00602

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Ca 1 1	0	0
2	C	1	Total Ca 1 1	0	0

- Molecule 3 is water.

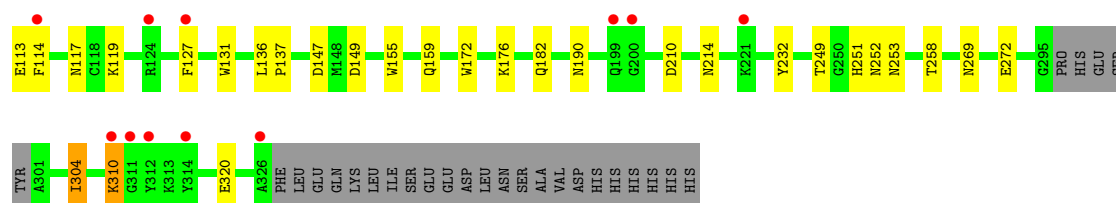
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	123	Total O 123 123	0	0
3	B	75	Total O 75 75	0	0
3	C	85	Total O 85 85	0	0

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.

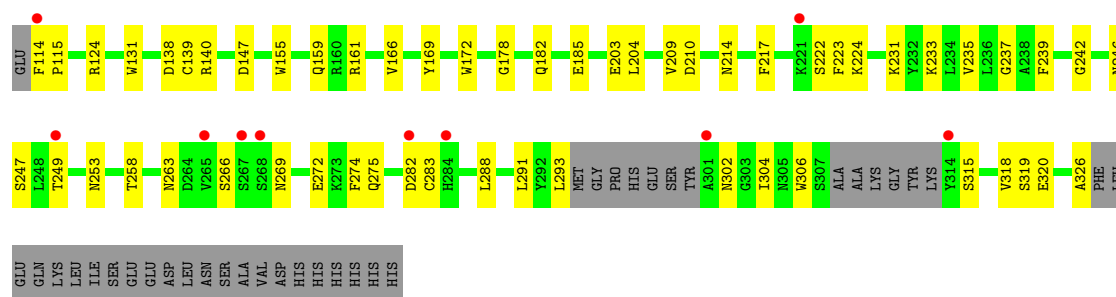
• Molecule 1: Ficolin-1

Chain A: 



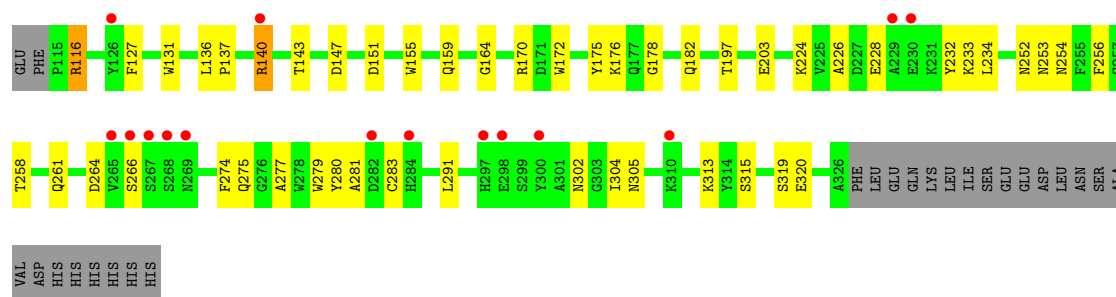
• Molecule 1: Ficolin-1

Chain B: 



• Molecule 1: Ficolin-1

Chain C: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	55.16Å 117.45Å 55.19Å 90.00° 99.88° 90.00°	Depositor
Resolution (Å)	30.00 – 1.90 29.36 – 1.90	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-1.90) 98.8 (29.36-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.86 (at 1.91Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.209 , 0.240 0.209 , 0.240	Depositor DCC
R_{free} test set	2717 reflections (5.06%)	DCC
Wilson B-factor (Å ²)	21.1	Xtriage
Anisotropy	0.105	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 33.0	EDS
Estimated twinning fraction	0.022 for l,-k,h	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 53715 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5212	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.65% of the height of the origin peak. No significant pseudotranslation is detected.*

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: 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	0.36	0/1701	0.63	0/2297
1	B	0.35	0/1634	0.60	0/2208
1	C	0.34	0/1728	0.64	1/2336 (0.0%)
All	All	0.35	0/5063	0.62	1/6841 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	151	ASP	CB-CG-OD1	5.85	123.57	118.30

There are no chirality outliers.

There are no planarity outliers.

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	1656	0	1532	23	0
1	B	1591	0	1465	36	0
1	C	1680	0	1553	33	0
2	A	1	0	0	0	0
2	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	123	0	0	0	0
3	B	75	0	0	0	0
3	C	85	0	0	1	0
All	All	5212	0	4550	89	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 9.

All (89) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:136:LEU:HB3	1:C:137:PRO:HD2	1.64	0.78
1:B:239:PHE:HB2	1:B:246:ASN:ND2	1.98	0.77
1:C:254:ASN:HD21	1:C:281:ALA:HB2	1.50	0.75
1:B:239:PHE:HB2	1:B:246:ASN:HD22	1.51	0.74
1:C:176:LYS:HE2	1:C:228:GLU:OE2	1.93	0.69
1:B:114:PHE:N	1:B:115:PRO:HD2	2.09	0.67
1:A:310:LYS:HD3	1:A:310:LYS:H	1.60	0.66
1:B:210:ASP:OD1	1:B:214:ASN:HB2	1.96	0.65
1:B:275:GLN:NE2	1:B:291:LEU:HD11	2.12	0.64
1:C:305:ASN:OD1	1:C:313:LYS:HB2	2.00	0.61
1:C:254:ASN:ND2	1:C:281:ALA:HB2	2.15	0.60
1:C:226:ALA:O	1:C:232:TYR:HA	2.02	0.60
1:B:138:ASP:OD2	1:B:140:ARG:HG2	2.03	0.58
1:C:197:THR:O	1:C:224:LYS:HE2	2.05	0.57
1:B:222:SER:HB3	1:B:237:GLY:HA3	1.87	0.56
1:A:310:LYS:H	1:A:310:LYS:CD	2.19	0.56
1:A:269:ASN:CG	1:A:272:GLU:HG3	2.25	0.56
1:A:310:LYS:HD3	1:A:310:LYS:N	2.20	0.55
1:C:136:LEU:HD12	1:C:140:ARG:HD2	1.88	0.55
1:B:266:SER:HB2	1:B:282:ASP:HA	1.87	0.55
1:C:302:ASN:O	1:C:315:SER:HB3	2.07	0.55
1:A:113:GLU:CG	1:A:114:PHE:H	2.19	0.54
1:B:169:TYR:CE1	1:B:275:GLN:HA	2.42	0.54
1:B:233:LYS:HD3	1:B:253:ASN:HA	1.89	0.53
1:A:113:GLU:HG3	1:A:114:PHE:H	1.73	0.53
1:C:280:TYR:CD2	1:C:283:CYS:HB3	2.43	0.53
1:C:116:ARG:HH11	1:C:116:ARG:HG2	1.73	0.53
1:B:302:ASN:O	1:B:315:SER:HB2	2.10	0.52
1:A:113:GLU:HG3	1:A:114:PHE:N	2.26	0.51
1:B:293:LEU:HB2	1:B:302:ASN:HA	1.92	0.51
1:B:274:PHE:CE2	1:B:283:CYS:HB2	2.47	0.50
1:A:136:LEU:HB3	1:A:137:PRO:HD2	1.94	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:164:GLY:HA2	3:C:2426:HOH:O	2.11	0.50
1:B:269:ASN:OD1	1:B:272:GLU:HG3	2.12	0.49
1:A:131:TRP:CZ2	1:A:182:GLN:HA	2.48	0.49
1:C:172:TRP:CE3	1:C:261:GLN:HB3	2.47	0.49
1:A:249:THR:O	1:A:251:HIS:HD2	1.97	0.48
1:B:247:SER:HB3	1:B:306:TRP:CE2	2.48	0.48
1:B:114:PHE:N	1:B:115:PRO:CD	2.75	0.48
1:B:131:TRP:CZ2	1:B:182:GLN:HA	2.49	0.48
1:B:239:PHE:CB	1:B:246:ASN:HD22	2.21	0.48
1:C:264:ASP:OD1	1:C:266:SER:HB3	2.14	0.48
1:C:275:GLN:HB2	1:C:291:LEU:HG	1.95	0.47
1:B:269:ASN:CG	1:B:272:GLU:HG3	2.34	0.47
1:B:224:LYS:HB3	1:B:235:VAL:HB	1.96	0.47
1:C:159:GLN:O	1:C:320:GLU:HA	2.15	0.47
1:C:131:TRP:CZ2	1:C:182:GLN:HA	2.51	0.46
1:C:176:LYS:HG3	1:C:232:TYR:OH	2.16	0.46
1:B:209:VAL:HB	1:B:318:VAL:HB	1.97	0.46
1:C:304:ILE:HD11	1:C:319:SER:HB3	1.98	0.45
1:B:231:LYS:HD3	1:B:263:ASN:CG	2.37	0.45
1:C:256:PHE:CE2	1:C:277:ALA:HB1	2.51	0.45
1:A:304:ILE:H	1:A:304:ILE:HD13	1.81	0.45
1:A:269:ASN:ND2	1:A:272:GLU:HG3	2.32	0.45
1:B:203:GLU:HG3	1:B:326:ALA:HB2	1.99	0.45
1:B:147:ASP:HB3	1:B:155:TRP:HB2	1.98	0.45
1:B:115:PRO:HD3	1:B:124:ARG:HH12	1.82	0.45
1:A:210:ASP:OD2	1:A:214:ASN:HB2	2.16	0.45
1:A:117:ASN:OD1	1:A:119:LYS:HB3	2.17	0.44
1:C:175:TYR:CZ	1:C:277:ALA:HB3	2.53	0.44
1:C:252:ASN:O	1:C:253:ASN:HB2	2.17	0.44
1:C:233:LYS:HD3	1:C:253:ASN:HA	1.98	0.44
1:A:252:ASN:O	1:A:253:ASN:HB2	2.18	0.44
1:C:172:TRP:CE3	1:C:261:GLN:HG2	2.53	0.43
1:A:127:PHE:CE2	1:C:178:GLY:HA3	2.53	0.43
1:B:204:LEU:HB2	1:B:223:PHE:CB	2.47	0.43
1:C:234:LEU:HB2	1:C:279:TRP:CD1	2.53	0.43
1:A:176:LYS:HG3	1:A:232:TYR:OH	2.18	0.43
1:C:172:TRP:HA	1:C:258:THR:HG21	2.01	0.43
1:A:136:LEU:HB3	1:A:137:PRO:CD	2.49	0.43
1:C:131:TRP:HE3	1:C:143:THR:HG22	1.84	0.43
1:C:274:PHE:CE2	1:C:283:CYS:HB2	2.55	0.42
1:B:246:ASN:OD1	1:B:249:THR:N	2.52	0.42
1:B:210:ASP:CG	1:B:214:ASN:HB2	2.39	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:138:ASP:O	1:B:139:CYS:HB2	2.19	0.42
1:B:166:VAL:CG2	1:B:185:GLU:HB2	2.50	0.42
1:A:149:ASP:CG	1:C:170:ARG:HH22	2.23	0.42
1:A:190:ASN:HB3	1:A:232:TYR:CD1	2.55	0.41
1:A:159:GLN:O	1:A:320:GLU:HA	2.19	0.41
1:C:147:ASP:HB3	1:C:155:TRP:HB2	2.02	0.41
1:A:147:ASP:HB3	1:A:155:TRP:HB2	2.03	0.41
1:B:159:GLN:O	1:B:320:GLU:HA	2.20	0.41
1:B:172:TRP:HA	1:B:258:THR:HG21	2.03	0.41
1:B:161:ARG:NH1	1:B:288:LEU:O	2.54	0.41
1:A:172:TRP:HA	1:A:258:THR:HG21	2.02	0.41
1:B:304:ILE:HD11	1:B:319:SER:HB3	2.02	0.41
1:B:178:GLY:HA3	1:C:127:PHE:CE2	2.56	0.41
1:C:155:TRP:CZ3	1:C:203:GLU:HG3	2.56	0.40
1:B:217:PHE:CE1	1:B:242:GLY:HA2	2.57	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	A	205/237 (86%)	198 (97%)	7 (3%)	0	100	100
1	B	194/237 (82%)	185 (95%)	9 (5%)	0	100	100
1	C	210/237 (89%)	197 (94%)	13 (6%)	0	100	100
All	All	609/711 (86%)	580 (95%)	29 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	170/197 (86%)	168 (99%)	2 (1%)	82	80
1	B	165/197 (84%)	165 (100%)	0	100	100
1	C	173/197 (88%)	171 (99%)	2 (1%)	82	80
All	All	508/591 (86%)	504 (99%)	4 (1%)	89	89

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	304	ILE
1	A	310	LYS
1	C	116	ARG
1	C	140	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	251	HIS
1	B	182	GLN
1	B	261	GLN
1	B	275	GLN
1	C	251	HIS
1	C	254	ASN
1	C	261	GLN
1	C	302	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 ⓘ

Of 2 ligands modelled in this entry, 2 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	209/237 (88%)	0.14	11 (5%) 25 26	12, 21, 42, 53	0
1	B	200/237 (84%)	0.30	10 (5%) 28 28	12, 26, 42, 49	0
1	C	212/237 (89%)	0.39	15 (7%) 16 15	12, 26, 48, 54	0
All	All	621/711 (87%)	0.28	36 (5%) 22 22	12, 24, 46, 54	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	114	PHE	6.6
1	B	267	SER	5.9
1	C	267	SER	4.7
1	B	284	HIS	4.0
1	A	310	LYS	3.9
1	B	314	TYR	3.6
1	A	314	TYR	3.6
1	B	301	ALA	3.6
1	C	265	VAL	3.5
1	A	114	PHE	3.5
1	A	199	GLN	3.4
1	B	249	THR	3.3
1	C	269	ASN	3.2
1	C	310	LYS	3.2
1	C	268	SER	3.2
1	C	284	HIS	3.1
1	A	124	ARG	3.0
1	C	229	ALA	3.0
1	A	326	ALA	3.0
1	C	140	ARG	2.6
1	B	282	ASP	2.6
1	B	265	VAL	2.5
1	C	230	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	268	SER	2.4
1	A	221	LYS	2.3
1	B	221	LYS	2.3
1	A	312	TYR	2.2
1	A	200	GLY	2.2
1	C	297	HIS	2.2
1	C	266	SER	2.2
1	C	298	GLU	2.1
1	C	126	TYR	2.1
1	A	127	PHE	2.1
1	C	300	TYR	2.0
1	C	282	ASP	2.0
1	A	311	GLY	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
2	CA	C	2401	1/1	0.08	-1.16	22,22,22,22	1
2	CA	A	1401	1/1	0.05	-2.60	20,20,20,20	0

6.5 Other polymers ⓘ

There are no such residues in this entry.