



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 12:56 am GMT

PDB ID : 4MDV
Title : Crystal structure of calcium-bound annexin (Sm)1
Authors : Hofmann, A.
Deposited on : 2013-08-23
Resolution : 2.50 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

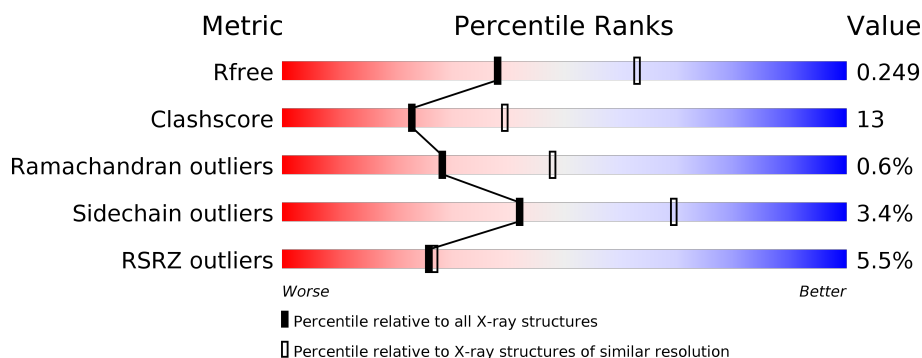
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	100719	3846 (2.50-2.50)
Clashscore	112137	4554 (2.50-2.50)
Ramachandran outliers	110173	4463 (2.50-2.50)
Sidechain outliers	110143	4465 (2.50-2.50)
RSRZ outliers	101464	3876 (2.50-2.50)

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. 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 $\leq 5\%$. 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	375	<div> <div>6%</div> <div> <div></div> <div>70%</div> <div>23%</div> <div>• 6%</div> </div> </div>
1	B	375	<div> <div>5%</div> <div> <div></div> <div>65%</div> <div>27%</div> <div>• 7%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5780 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 Annexin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	351	Total	C	N	O	S	125	4	0
			2831	1789	477	546	19			
1	B	349	Total	C	N	O	S	166	3	0
			2815	1781	474	542	18			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	EXPRESSION TAG	UNP C4QH88
A	2	ALA	-	EXPRESSION TAG	UNP C4QH88
A	8	GLU	GLY	CONFLICT	UNP C4QH88
A	368	LEU	-	EXPRESSION TAG	UNP C4QH88
A	369	GLU	-	EXPRESSION TAG	UNP C4QH88
A	370	HIS	-	EXPRESSION TAG	UNP C4QH88
A	371	HIS	-	EXPRESSION TAG	UNP C4QH88
A	372	HIS	-	EXPRESSION TAG	UNP C4QH88
A	373	HIS	-	EXPRESSION TAG	UNP C4QH88
A	374	HIS	-	EXPRESSION TAG	UNP C4QH88
A	375	HIS	-	EXPRESSION TAG	UNP C4QH88
B	1	MET	-	EXPRESSION TAG	UNP C4QH88
B	2	ALA	-	EXPRESSION TAG	UNP C4QH88
B	8	GLU	GLY	CONFLICT	UNP C4QH88
B	368	LEU	-	EXPRESSION TAG	UNP C4QH88
B	369	GLU	-	EXPRESSION TAG	UNP C4QH88
B	370	HIS	-	EXPRESSION TAG	UNP C4QH88
B	371	HIS	-	EXPRESSION TAG	UNP C4QH88
B	372	HIS	-	EXPRESSION TAG	UNP C4QH88
B	373	HIS	-	EXPRESSION TAG	UNP C4QH88
B	374	HIS	-	EXPRESSION TAG	UNP C4QH88
B	375	HIS	-	EXPRESSION TAG	UNP C4QH88

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	7	Total 7	Ca 7	0	2
2	A	6	Total 6	Ca 6	0	0

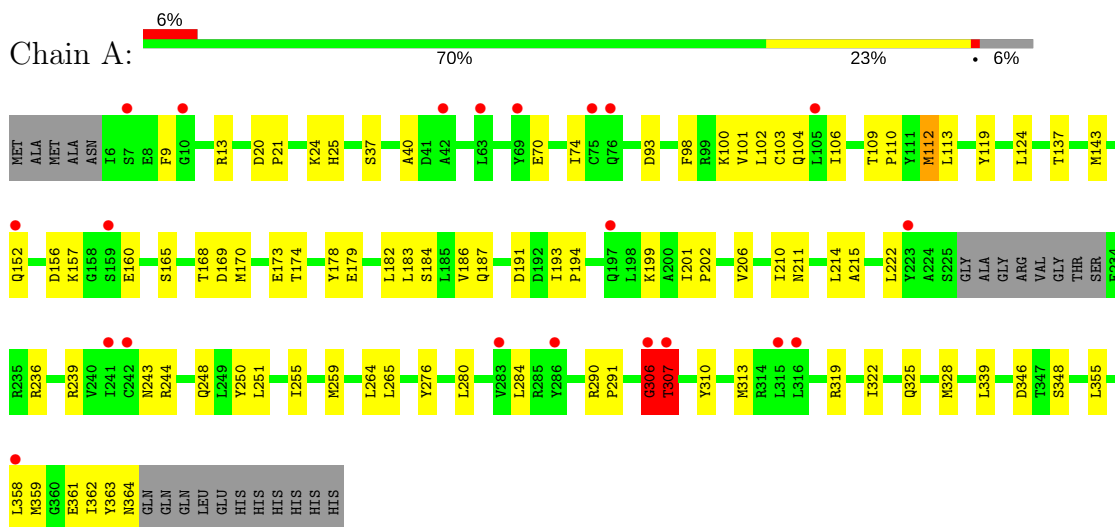
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	62	Total 64	O 64	0	2
3	B	55	Total 57	O 57	0	2

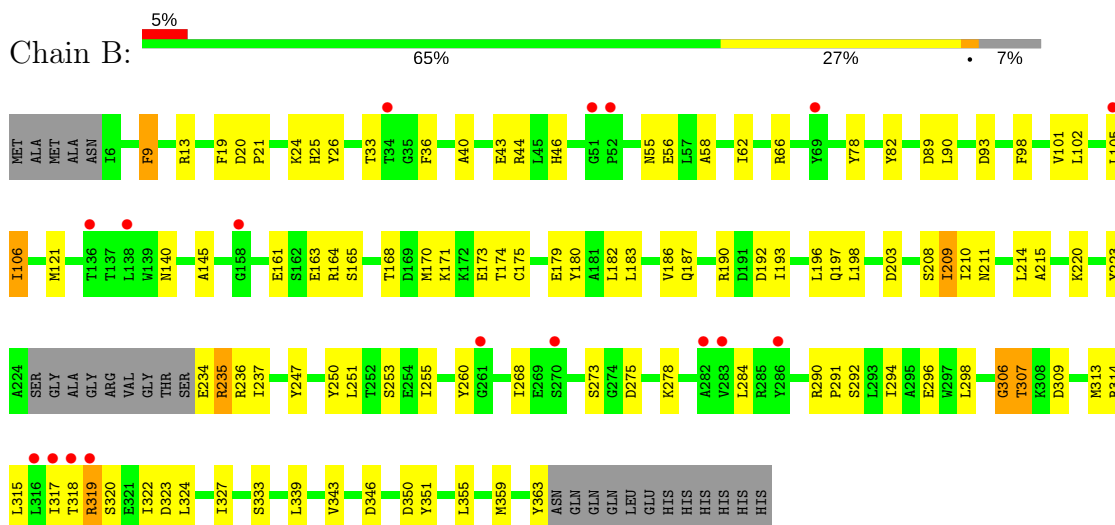
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Annexin



• Molecule 1: Annexin



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	67.82Å 88.49Å 68.47Å 90.00° 111.18° 90.00°	Depositor
Resolution (Å)	24.10 – 2.50 24.13 – 2.42	Depositor EDS
% Data completeness (in resolution range)	99.6 (24.10-2.50) 98.0 (24.13-2.42)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.29 (at 2.41Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.190 , 0.257 0.177 , 0.249	Depositor DCC
R_{free} test set	1333 reflections (5.10%)	DCC
Wilson B-factor (Å ²)	61.0	Xtriage
Anisotropy	0.142	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 62.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.014 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5780	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.01% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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

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	0.45	0/2890	0.63	1/3895 (0.0%)
1	B	0.43	0/2870	0.60	0/3868
All	All	0.44	0/5760	0.62	1/7763 (0.0%)

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	A	0	2
1	B	0	2
All	All	0	4

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	306	GLY	N-CA-C	5.07	125.78	113.10

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	306	GLY	Peptide
1	A	307	THR	Peptide
1	B	306	GLY	Peptide
1	B	307	THR	Peptide

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	2831	0	2850	56	0
1	B	2815	0	2838	81	0
2	A	6	0	0	0	0
2	B	7	0	0	0	0
3	A	64	0	0	1	0
3	B	57	0	0	0	0
All	All	5780	0	5688	136	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 13.

All (136) 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)
1:B:174:THR:HG22	1:B:179:GLU:HB2	1.55	0.87
1:B:210:ILE:HD12	1:B:251:LEU:HD22	1.58	0.84
1:A:170:MET:HE1	1:A:182:LEU:HB3	1.69	0.74
1:B:121:MET:HG2	1:B:173:GLU:HG2	1.70	0.74
1:B:294:ILE:HG21	1:B:327:ILE:HD13	1.69	0.74
1:A:170:MET:O	1:A:174:THR:HG22	1.90	0.72
1:B:292:SER:O	1:B:296:GLU:HG3	1.92	0.70
1:A:206:VAL:O	1:A:210:ILE:HG12	1.93	0.69
1:A:112:MET:HE2	1:A:113:LEU:HD23	1.75	0.69
1:A:102:LEU:O	1:A:106:ILE:HG13	1.94	0.68
1:B:180:TYR:CZ	1:B:235:ARG:HD3	2.30	0.66
1:B:90:LEU:HD22	1:B:102:LEU:HD13	1.78	0.66
1:B:165:SER:H	1:B:168:THR:HB	1.60	0.65
1:B:209:ILE:HG13	1:B:209:ILE:O	1.97	0.65
1:B:183:LEU:O	1:B:187:GLN:HG2	1.97	0.64
1:A:290:ARG:HB3	1:A:291:PRO:HD3	1.80	0.62
1:A:165:SER:H	1:A:168:THR:HB	1.64	0.62
1:B:170:MET:SD	1:B:186:VAL:HG21	2.40	0.62
1:A:355:LEU:O	1:A:359[B]:MET:HG3	2.00	0.62
1:B:55:ASN:ND2	1:B:58:ALA:HB2	2.16	0.61
1:A:20:ASP:HB2	1:A:21:PRO:HD2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:143[A]:MET:SD	1:A:186:VAL:HA	2.41	0.60
1:B:197:GLN:HE21	1:B:209:ILE:HG22	1.66	0.60
1:A:244:ARG:HD2	1:A:248:GLN:HG2	1.83	0.59
1:A:276:TYR:CZ	1:A:280:LEU:HD11	2.38	0.59
1:A:20:ASP:HB2	1:A:21:PRO:CD	2.33	0.59
1:B:56:GLU:HG2	1:B:350:ASP:OD2	2.02	0.58
1:B:174:THR:HG21	1:B:182:LEU:HD12	1.85	0.57
1:B:182:LEU:O	1:B:186:VAL:HG23	2.04	0.57
1:A:170:MET:CE	1:A:182:LEU:HB3	2.35	0.57
1:A:170:MET:SD	1:A:186:VAL:HG21	2.45	0.56
1:B:211:ASN:ND2	1:B:214:LEU:HB2	2.21	0.56
1:B:309:ASP:O	1:B:313[A]:MET:HG2	2.06	0.55
1:B:355:LEU:O	1:B:359[B]:MET:HG3	2.06	0.55
1:B:40:ALA:O	1:B:44:ARG:HG3	2.05	0.55
1:A:265:LEU:HD13	1:A:284:LEU:HD23	1.88	0.55
1:B:339:LEU:HG	1:B:359[B]:MET:HE1	1.88	0.54
1:A:13:ARG:HG3	1:A:322:ILE:HD11	1.90	0.54
1:B:170:MET:CE	1:B:182:LEU:HB3	2.37	0.54
1:B:171:LYS:HE2	1:B:183:LEU:CD1	2.38	0.54
1:B:174:THR:HG21	1:B:179:GLU:HA	1.89	0.53
1:A:191:ASP:OD2	1:A:244:ARG:HD3	2.08	0.53
1:B:290:ARG:HB3	1:B:291:PRO:HD3	1.89	0.53
1:A:325:GLN:HA	1:A:328[B]:MET:HE2	1.91	0.53
1:A:361:GLU:C	1:A:362:ILE:HD13	2.29	0.53
1:B:275:ASP:HA	1:B:278:LYS:HG3	1.90	0.53
1:A:109:THR:N	1:A:110:PRO:HD2	2.23	0.52
1:A:178:TYR:CZ	1:A:182:LEU:HD11	2.44	0.52
1:B:98:PHE:O	1:B:101:VAL:HG12	2.09	0.52
1:B:268:ILE:HD12	1:B:284:LEU:HD22	1.91	0.52
1:B:250:TYR:O	1:B:253:SER:HB3	2.10	0.52
1:A:179:GLU:O	1:A:183:LEU:HG	2.10	0.51
1:A:310:TYR:HA	1:A:313:MET:HE3	1.92	0.51
1:A:363:TYR:HB2	3:A:516:HOH:O	2.10	0.51
1:A:20:ASP:OD2	1:A:24:LYS:HB3	2.11	0.51
1:A:214:LEU:HD11	1:A:244:ARG:HH21	1.75	0.51
1:B:351:TYR:CZ	1:B:355:LEU:HD11	2.46	0.51
1:A:306:GLY:HA3	1:A:307:THR:CB	2.41	0.51
1:A:143[A]:MET:HE1	1:A:186:VAL:HG13	1.94	0.50
1:A:21:PRO:HB3	1:A:250:TYR:CG	2.46	0.50
1:A:239:ARG:O	1:A:243:ASN:HB2	2.12	0.50
1:B:174:THR:HG22	1:B:175:CYS:N	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:174:THR:HG22	1:B:179:GLU:CB	2.33	0.50
1:B:197:GLN:NE2	1:B:209:ILE:HG22	2.27	0.50
1:B:165:SER:O	1:B:168:THR:HB	2.12	0.49
1:B:234:GLU:HG2	1:B:236:ARG:HG3	1.94	0.49
1:A:124:LEU:CD1	1:B:237:ILE:HD12	2.42	0.49
1:A:362:ILE:HD13	1:A:362:ILE:N	2.27	0.49
1:B:294:ILE:CG2	1:B:327:ILE:HD13	2.41	0.49
1:A:37:SER:HB3	1:A:40:ALA:HB3	1.93	0.49
1:B:197:GLN:HE22	1:B:208:SER:HB2	1.76	0.49
1:A:174:THR:HG23	1:A:179:GLU:HG3	1.95	0.49
1:B:234:GLU:CG	1:B:236:ARG:HG3	2.42	0.49
1:A:201:ILE:N	1:A:202:PRO:CD	2.76	0.49
1:B:62:ILE:O	1:B:66:ARG:HG2	2.12	0.48
1:B:174:THR:CG2	1:B:179:GLU:HA	2.43	0.48
1:B:20:ASP:HB2	1:B:21:PRO:CD	2.43	0.48
1:A:137:THR:HB	1:A:319:ARG:NH2	2.28	0.48
1:A:222:LEU:HD13	1:A:264:LEU:HD11	1.96	0.48
1:B:171:LYS:HE2	1:B:183:LEU:HD11	1.96	0.48
1:A:103:CYS:HA	1:A:106:ILE:HD11	1.94	0.48
1:B:197:GLN:NE2	1:B:208:SER:HB2	2.28	0.48
1:B:13:ARG:HG3	1:B:322:ILE:HD11	1.96	0.47
1:B:209:ILE:HD11	1:B:247:TYR:CD2	2.49	0.47
1:B:20:ASP:OD2	1:B:24:LYS:HB3	2.15	0.47
1:A:169:ASP:O	1:A:173:GLU:HB2	2.15	0.47
1:B:21:PRO:HB3	1:B:250:TYR:CG	2.48	0.47
1:A:328[B]:MET:HG2	1:A:339:LEU:HD23	1.96	0.47
1:B:220:LYS:HA	1:B:260:TYR:OH	2.15	0.47
1:B:26:TYR:HB3	1:B:323:ASP:HB3	1.96	0.47
1:B:78:TYR:OH	1:B:89:ASP:OD2	2.33	0.47
1:B:215:ALA:CB	1:B:255:ILE:HD12	2.44	0.46
1:B:9:PHE:HE1	1:B:145:ALA:HB3	1.80	0.46
1:A:199:LYS:O	1:A:202:PRO:HD2	2.15	0.46
1:A:259:MET:HB3	1:A:259:MET:HE2	1.73	0.46
1:A:70:GLU:O	1:A:74:ILE:HG13	2.15	0.46
1:B:102:LEU:O	1:B:106:ILE:HG13	2.15	0.46
1:B:351:TYR:CE1	1:B:355:LEU:HD11	2.51	0.46
1:B:197:GLN:HA	1:B:197:GLN:OE1	2.16	0.45
1:A:362:ILE:HG22	1:A:363:TYR:N	2.31	0.45
1:B:193:ILE:HG22	1:B:198:LEU:HG	1.99	0.45
1:A:184:SER:O	1:A:187:GLN:HB2	2.17	0.44
1:B:20:ASP:HB2	1:B:21:PRO:HD2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:33:THR:HB	1:B:36:PHE:HB2	1.98	0.44
1:B:339:LEU:O	1:B:343:VAL:HG23	2.18	0.43
1:B:315:LEU:O	1:B:319:ARG:HB2	2.19	0.43
1:A:98:PHE:O	1:A:101:VAL:HG12	2.19	0.43
1:A:355:LEU:HA	1:A:358:LEU:HD12	2.01	0.43
1:B:105:LEU:HD13	1:B:317:ILE:HG12	2.01	0.43
1:A:210:ILE:HD12	1:A:251:LEU:HD22	2.01	0.42
1:B:196:LEU:HA	1:B:196:LEU:HD23	1.77	0.42
1:B:19:PHE:HE1	1:B:25:HIS:CE1	2.37	0.42
1:B:46:HIS:CG	1:B:82:TYR:CE2	3.07	0.42
1:B:314:ARG:O	1:B:318:THR:HG23	2.20	0.42
1:A:119:TYR:OH	1:A:157:LYS:HE3	2.18	0.42
1:B:170:MET:HE1	1:B:182:LEU:HB3	2.02	0.42
1:B:171:LYS:HG2	1:B:183:LEU:HD11	2.01	0.42
1:B:320:SER:HA	1:B:324:LEU:HB2	2.01	0.42
1:A:211:ASN:OD1	1:A:211:ASN:C	2.57	0.42
1:A:100:LYS:O	1:A:104:GLN:HG2	2.21	0.41
1:B:215:ALA:HB1	1:B:255:ILE:HD12	2.03	0.41
1:B:323:ASP:N	1:B:323:ASP:OD1	2.53	0.41
1:B:43:GLU:HA	1:B:82:TYR:OH	2.19	0.41
1:B:106:ILE:C	1:B:106:ILE:CD1	2.89	0.41
1:B:183:LEU:HD23	1:B:183:LEU:HA	1.97	0.41
1:A:152:GLN:HG3	1:A:156:ASP:OD2	2.21	0.41
1:A:101:VAL:HG23	1:A:313:MET:HG2	2.02	0.41
1:A:215:ALA:CB	1:A:255:ILE:HD12	2.50	0.41
1:B:298:LEU:HD23	1:B:298:LEU:HA	1.84	0.40
1:B:161:GLU:OE1	1:B:164:ARG:HD2	2.22	0.40
1:B:339:LEU:HD23	1:B:359[B]:MET:HE3	2.04	0.40
1:B:171:LYS:HE2	1:B:183:LEU:HD13	2.03	0.40
1:B:363:TYR:N	1:B:363:TYR:CD1	2.88	0.40
1:A:193:ILE:HA	1:A:194:PRO:HD3	1.91	0.40
1:B:140:ASN:OD1	1:B:190:ARG:HG3	2.22	0.40
1:B:223:TYR:CD1	1:B:223:TYR:C	2.95	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	351/375 (94%)	335 (95%)	14 (4%)	2 (1%)	28	48
1	B	348/375 (93%)	333 (96%)	13 (4%)	2 (1%)	28	48
All	All	699/750 (93%)	668 (96%)	27 (4%)	4 (1%)	28	48

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	306	GLY
1	B	306	GLY
1	A	307	THR
1	B	307	THR

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	313/327 (96%)	304 (97%)	9 (3%)	48	75
1	B	310/327 (95%)	298 (96%)	12 (4%)	37	63
All	All	623/654 (95%)	602 (97%)	21 (3%)	42	69

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	PHE
1	A	25	HIS

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Mol	Chain	Res	Type
1	A	93	ASP
1	A	112	MET
1	A	160	GLU
1	A	236	ARG
1	A	346	ASP
1	A	348	SER
1	A	364	ASN
1	B	9	PHE
1	B	93	ASP
1	B	106	ILE
1	B	163	GLU
1	B	192	ASP
1	B	203	ASP
1	B	209	ILE
1	B	235	ARG
1	B	273	SER
1	B	319	ARG
1	B	333	SER
1	B	346	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	364	ASN
1	B	197	GLN
1	B	243	ASN

5.3.3 RNA ⓘ

There are no RNA molecules 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 13 ligands modelled in this entry, 13 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

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	350/375 (93%)	0.21	21 (6%) 23 23	41, 66, 104, 127	32 (9%)
1	B	345/375 (92%)	0.18	17 (4%) 30 32	43, 67, 103, 127	35 (10%)
All	All	695/750 (92%)	0.19	38 (5%) 26 27	41, 66, 104, 127	67 (9%)

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	51	GLY	4.2
1	A	42	ALA	4.0
1	B	158	GLY	3.8
1	A	7	SER	3.4
1	A	75[A]	CYS	3.4
1	B	283	VAL	3.3
1	A	306	GLY	3.2
1	A	105	LEU	3.2
1	A	307	THR	3.1
1	B	286	TYR	3.0
1	A	223	TYR	2.8
1	B	52	PRO	2.8
1	A	159	SER	2.8
1	B	316	LEU	2.7
1	A	197	GLN	2.6
1	B	34	THR	2.6
1	A	358	LEU	2.6
1	A	286	TYR	2.5
1	A	63	LEU	2.5
1	B	282	ALA	2.5
1	B	136	THR	2.5
1	A	69	TYR	2.4
1	B	318	THR	2.4
1	A	241	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	105	LEU	2.3
1	B	270	SER	2.3
1	B	317	ILE	2.3
1	A	76	GLN	2.2
1	A	283	VAL	2.2
1	A	10	GLY	2.2
1	A	316	LEU	2.2
1	B	261	GLY	2.2
1	A	315	LEU	2.1
1	A	152	GLN	2.1
1	A	242	CYS	2.1
1	B	319	ARG	2.1
1	B	69	TYR	2.1
1	B	138	LEU	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 carbohydrates 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. 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	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	CA	A	406	1/1	0.44	0.19	0.33	118,118,118,118	0
2	CA	B	403	1/1	0.97	0.11	-0.90	70,70,70,70	0
2	CA	A	405	1/1	0.78	0.11	-1.02	99,99,99,99	0
2	CA	B	402	1/1	0.92	0.13	-1.03	91,91,91,91	0
2	CA	A	402	1/1	0.91	0.07	-1.07	72,72,72,72	0
2	CA	A	401	1/1	0.92	0.07	-2.19	104,104,104,104	0
2	CA	A	404	1/1	0.99	0.02	-2.33	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	CA	B	401[A]	1/1	0.64	0.28	-	61,61,61,61	1
2	CA	B	405[B]	1/1	0.94	0.40	-	64,64,64,64	1
2	CA	A	403	1/1	0.91	0.07	-	120,120,120,120	0
2	CA	B	404	1/1	0.95	0.04	-	86,86,86,86	0
2	CA	B	406	1/1	0.91	0.05	-	93,93,93,93	0
2	CA	B	407	1/1	0.91	0.27	-	135,135,135,135	0

6.5 Other polymers [i](#)

There are no such residues in this entry.