



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 10, 2021 – 06:07 PM EDT

PDB ID : 3DF0
Title : Calcium-dependent complex between m-calpain and calpastatin
Authors : Moldoveanu, T.; Gehring, K.; Green, D.R.
Deposited on : 2008-06-11
Resolution : 2.95 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 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	:	2.23.2
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)	:	2.23.2

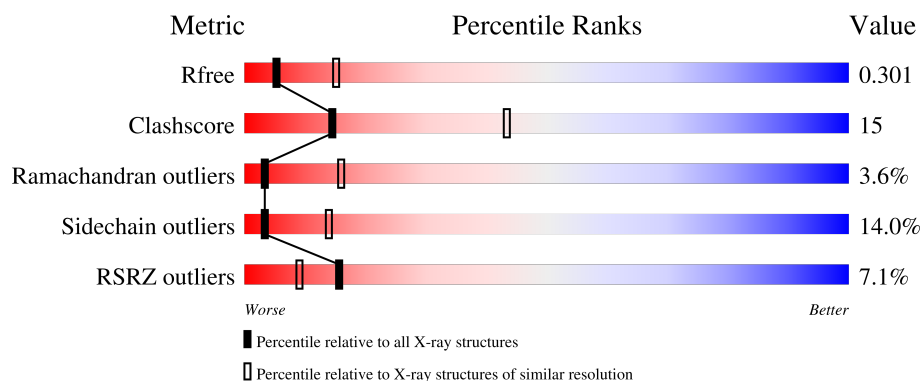
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.95 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	3104 (3.00-2.92)
Clashscore	141614	3462 (3.00-2.92)
Ramachandran outliers	138981	3340 (3.00-2.92)
Sidechain outliers	138945	3343 (3.00-2.92)
RSRZ outliers	127900	2986 (3.00-2.92)

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 $\leq 5\%$. 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	714	<div> <div>7%</div> <div> <div></div> <div>58%</div> <div>30%</div> <div>6%</div> <div>5%</div> </div> </div>
2	B	184	<div> <div>5%</div> <div> <div></div> <div>59%</div> <div>30%</div> <div>• • 5%</div> </div> </div>
3	C	86	<div> <div>8%</div> <div> <div></div> <div>43%</div> <div>17%</div> <div>5%</div> <div>35%</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7300 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 Calpain-2 catalytic subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	676	Total	C	N	O	S	0	0	0
			5453	3468	915	1047	23			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	105	SER	CYS	engineered mutation	UNP Q07009
A	701	GLY	-	expression tag	UNP Q07009
A	702	LYS	-	expression tag	UNP Q07009
A	703	LEU	-	expression tag	UNP Q07009
A	704	ALA	-	expression tag	UNP Q07009
A	705	ALA	-	expression tag	UNP Q07009
A	706	ALA	-	expression tag	UNP Q07009
A	707	LEU	-	expression tag	UNP Q07009
A	708	GLU	-	expression tag	UNP Q07009
A	709	HIS	-	expression tag	UNP Q07009
A	710	HIS	-	expression tag	UNP Q07009
A	711	HIS	-	expression tag	UNP Q07009
A	712	HIS	-	expression tag	UNP Q07009
A	713	HIS	-	expression tag	UNP Q07009
A	714	HIS	-	expression tag	UNP Q07009

- Molecule 2 is a protein called Calpain small subunit 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	174	Total	C	N	O	S	0	0	0
			1411	888	243	270	10			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	87	MET	SER	variant	UNP Q64537

- Molecule 3 is a protein called Calpastatin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	56	Total	C	N	O	S	0	0	0
			426	270	64	90	2			

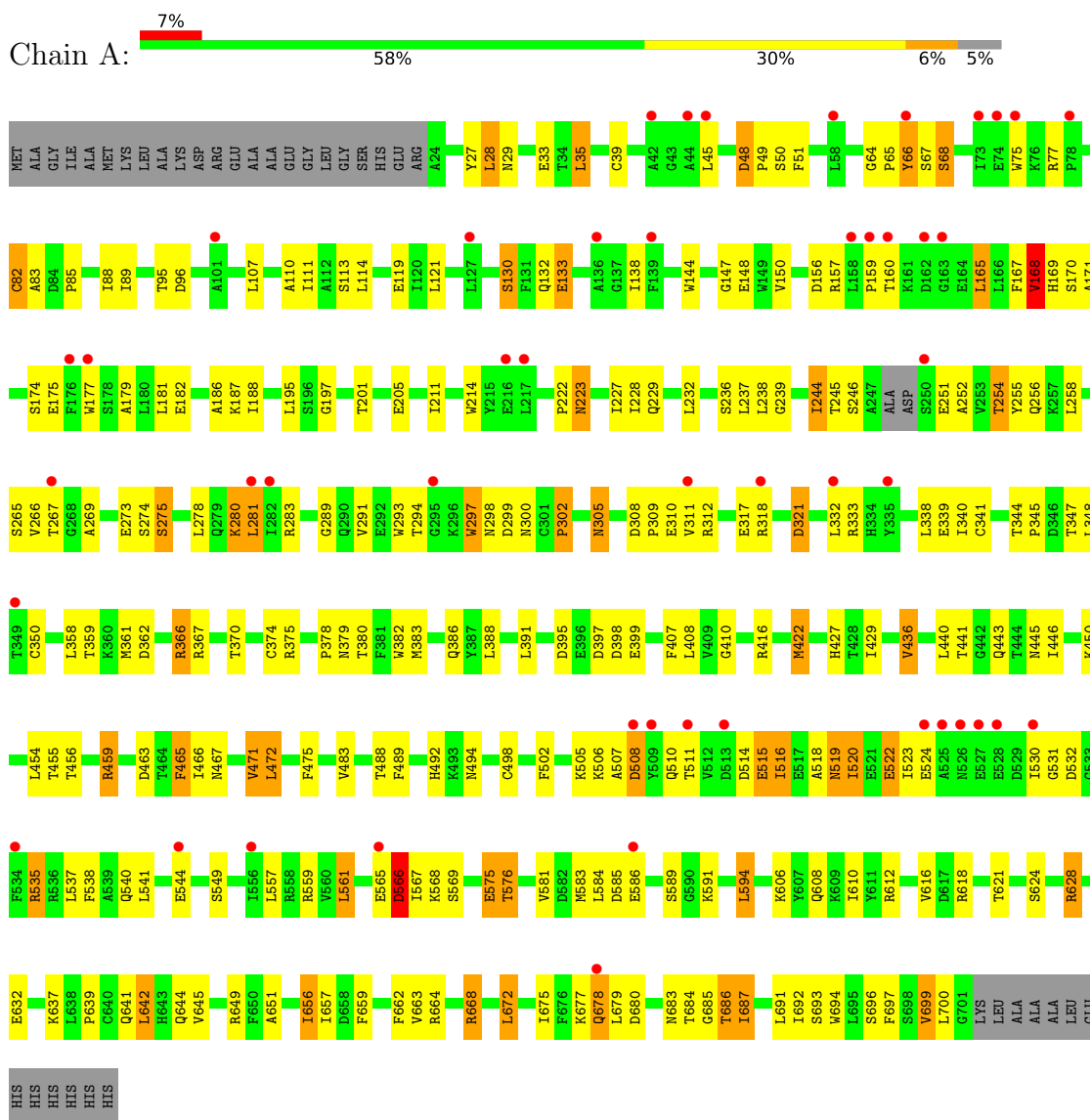
- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	6	Total	Ca	0	0
			6	6		
4	B	4	Total	Ca	0	0
			4	4		

3 Residue-property plots

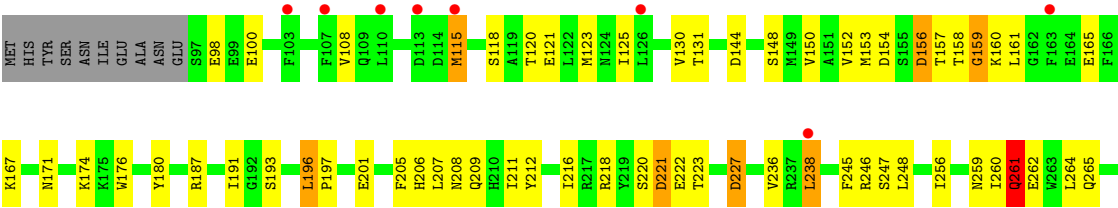
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Calpain-2 catalytic subunit



• Molecule 2: Calpain small subunit 1





● Molecule 3: Calpastatin



4 Data and refinement statistics

Property	Value	Source
Space group	P 42	Depositor
Cell constants a, b, c, α , β , γ	147.39Å 147.39Å 47.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.15 – 2.95 46.61 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.15-2.95) 99.8 (46.61-2.90)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.229 , 0.299 0.223 , 0.301	Depositor DCC
R_{free} test set	1164 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	83.8	Xtriage
Anisotropy	0.028	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 89.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.031 for h,-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7300	wwPDB-VP
Average B, all atoms (Å ²)	96.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.48% 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	0.79	7/5575 (0.1%)	0.75	2/7536 (0.0%)
2	B	0.61	0/1438	0.72	0/1932
3	C	0.75	2/430 (0.5%)	0.77	0/580
All	All	0.76	9/7443 (0.1%)	0.74	2/10048 (0.0%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	310	GLU	CD-OE1	21.07	1.48	1.25
1	A	305	ASN	CG-OD1	15.23	1.57	1.24
1	A	305	ASN	CG-ND2	13.95	1.67	1.32
3	C	188	LYS	CE-NZ	8.16	1.69	1.49
1	A	544	GLU	CD-OE1	8.01	1.34	1.25
1	A	544	GLU	CD-OE2	6.83	1.33	1.25
1	A	310	GLU	CD-OE2	-6.05	1.19	1.25
3	C	188	LYS	CD-CE	5.88	1.66	1.51
1	A	374	CYS	CB-SG	-5.83	1.72	1.81

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	305	ASN	CB-CG-OD1	5.37	132.34	121.60
1	A	375	ARG	NE-CZ-NH2	-5.09	117.76	120.30

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	5453	0	5294	181	0
2	B	1411	0	1362	42	0
3	C	426	0	413	14	0
4	A	6	0	0	0	0
4	B	4	0	0	0	0
All	All	7300	0	7069	221	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 15.

All (221) 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:C:188:LYS:NZ	3:C:188:LYS:CE	1.69	1.55
1:A:305:ASN:CG	1:A:305:ASN:ND2	1.67	1.45
1:A:668:ARG:HG3	1:A:668:ARG:HH11	1.15	1.08
1:A:679:LEU:HD23	1:A:687:ILE:HD11	1.07	1.06
2:B:268:MET:CE	2:B:268:MET:HA	1.88	1.01
3:C:176:GLY:HA2	3:C:181:THR:HG21	1.38	1.01
1:A:679:LEU:CD2	1:A:687:ILE:HD11	1.93	0.99
1:A:679:LEU:HD23	1:A:687:ILE:CD1	1.96	0.94
1:A:168:VAL:HB	1:A:182:GLU:OE1	1.67	0.94
2:B:268:MET:HA	2:B:268:MET:HE2	1.52	0.92
1:A:668:ARG:HG3	1:A:668:ARG:NH1	1.85	0.89
1:A:668:ARG:HH21	2:B:270:SER:HB3	1.38	0.86
1:A:516:ILE:H	1:A:516:ILE:HD12	1.42	0.85
1:A:621:THR:HB	1:A:656:ILE:HD12	1.57	0.85
1:A:317:GLU:HG2	1:A:318:ARG:H	1.43	0.83
1:A:675:ILE:HD13	1:A:697:PHE:CD2	2.18	0.79
1:A:523:ILE:HG13	1:A:524:GLU:H	1.49	0.78
2:B:268:MET:HA	2:B:268:MET:HE3	1.68	0.74
1:A:651:ALA:HB2	1:A:657:ILE:HD11	1.68	0.74
1:A:144:TRP:CH2	1:A:147:GLY:HA2	2.23	0.73
1:A:82:CYS:SG	1:A:174:SER:HB2	2.27	0.73
1:A:621:THR:CB	1:A:656:ILE:HD12	2.19	0.73

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:559:ARG:HG2	3:C:138:LEU:HD22	1.72	0.72
1:A:668:ARG:NH2	2:B:270:SER:HB3	2.05	0.72
1:A:566:ASP:OD1	1:A:566:ASP:N	2.23	0.72
3:C:176:GLY:CA	3:C:181:THR:HG21	2.19	0.72
1:A:197:GLY:HA2	3:C:175:LEU:O	1.89	0.71
1:A:168:VAL:CG1	1:A:179:ALA:HA	2.22	0.70
2:B:259:ASN:ND2	2:B:262:GLU:OE1	2.25	0.70
1:A:668:ARG:HH11	1:A:668:ARG:CG	2.00	0.68
1:A:532:ASP:HA	1:A:535:ARG:HB2	1.75	0.68
1:A:96:ASP:O	1:A:170:SER:HA	1.94	0.68
1:A:510:GLN:O	1:A:511:THR:HB	1.93	0.67
1:A:397:ASP:OD2	1:A:399:GLU:HB2	1.95	0.67
1:A:523:ILE:HG23	1:A:524:GLU:HG3	1.77	0.66
1:A:201:THR:HG23	1:A:339:GLU:HB3	1.77	0.66
1:A:549:SER:HA	1:A:591:LYS:HG2	1.77	0.66
1:A:488:THR:HG22	1:A:489:PHE:N	2.11	0.65
1:A:201:THR:CG2	1:A:339:GLU:HB3	2.26	0.65
1:A:567:ILE:O	1:A:567:ILE:HG22	1.97	0.64
1:A:167:PHE:O	1:A:168:VAL:O	2.16	0.63
1:A:239:GLY:O	1:A:338:LEU:HD12	1.99	0.63
2:B:150:VAL:HA	2:B:161:LEU:HD21	1.80	0.63
2:B:201:GLU:HA	2:B:205:PHE:O	1.98	0.62
2:B:171:ASN:O	2:B:174:LYS:HG2	2.00	0.62
2:B:121:GLU:O	2:B:125:ILE:HG12	2.00	0.62
1:A:668:ARG:HD3	2:B:268:MET:HE1	1.81	0.62
1:A:691:LEU:HD23	2:B:245:PHE:CD2	2.35	0.62
1:A:201:THR:HG21	1:A:214:TRP:HE1	1.65	0.61
1:A:107:LEU:O	1:A:110:ALA:HB3	2.00	0.61
1:A:302:PRO:HA	1:A:305:ASN:OD1	2.00	0.61
1:A:228:ILE:HG22	1:A:232:LEU:HD12	1.83	0.61
2:B:221:ASP:O	2:B:223:THR:N	2.33	0.61
2:B:196:LEU:HB3	2:B:197:PRO:HD3	1.83	0.60
1:A:684:THR:O	1:A:686:THR:N	2.34	0.60
1:A:684:THR:C	1:A:686:THR:H	2.03	0.60
1:A:305:ASN:ND2	1:A:305:ASN:CB	2.61	0.60
1:A:436:VAL:HG12	1:A:483:VAL:HG23	1.82	0.60
1:A:201:THR:O	1:A:205:GLU:HG3	2.02	0.59
1:A:422:MET:HG3	1:A:422:MET:O	1.97	0.59
2:B:268:MET:HE2	2:B:268:MET:CA	2.30	0.59
1:A:581:VAL:O	1:A:583:MET:N	2.30	0.59
1:A:641:GLN:O	1:A:645:VAL:HG23	2.03	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:516:ILE:HD12	1:A:516:ILE:N	2.16	0.58
1:A:317:GLU:CG	1:A:318:ARG:H	2.14	0.58
1:A:651:ALA:HB2	1:A:657:ILE:CD1	2.33	0.58
1:A:111:ILE:HD13	1:A:181:LEU:HD23	1.86	0.57
1:A:516:ILE:HG21	2:B:260:ILE:HG13	1.86	0.57
1:A:113:SER:HB3	1:A:265:SER:OG	2.05	0.57
1:A:317:GLU:HG2	1:A:318:ARG:N	2.16	0.57
1:A:114:LEU:HD23	1:A:121:LEU:HD12	1.86	0.57
1:A:358:LEU:HD13	1:A:502:PHE:CE1	2.40	0.57
1:A:407:PHE:C	1:A:408:LEU:HD12	2.25	0.56
2:B:154:ASP:HA	2:B:165:GLU:OE1	2.05	0.56
1:A:488:THR:HG22	1:A:489:PHE:H	1.69	0.55
1:A:668:ARG:HE	2:B:270:SER:C	2.09	0.55
2:B:207:LEU:HD12	2:B:212:TYR:CE1	2.42	0.55
1:A:699:VAL:HG13	1:A:700:LEU:HG	1.88	0.54
2:B:153:MET:O	2:B:165:GLU:HG2	2.06	0.54
2:B:260:ILE:HG23	2:B:261:GLN:N	2.22	0.54
1:A:541:LEU:HD21	3:C:138:LEU:HG	1.90	0.54
1:A:606:LYS:O	1:A:610:ILE:HG12	2.07	0.54
1:A:75:TRP:CZ3	1:A:159:PRO:HD3	2.43	0.54
1:A:395:ASP:OD2	1:A:505:LYS:HD2	2.08	0.53
1:A:130:SER:HB3	1:A:132:GLN:H	1.72	0.53
1:A:523:ILE:HG13	1:A:524:GLU:N	2.19	0.53
1:A:576:THR:HG23	1:A:664:ARG:HD3	1.91	0.53
1:A:309:PRO:HA	1:A:312:ARG:HB3	1.91	0.53
1:A:382:TRP:CE3	1:A:382:TRP:O	2.62	0.53
1:A:366:ARG:HA	1:A:494:ASN:OD1	2.09	0.53
1:A:585:ASP:OD2	1:A:589:SER:O	2.26	0.53
1:A:347:THR:HG23	1:A:350:CYS:HB3	1.90	0.53
2:B:268:MET:O	2:B:269:TYR:HD2	1.92	0.52
1:A:144:TRP:CZ2	1:A:147:GLY:HA2	2.44	0.52
1:A:692:ILE:HD12	1:A:693:SER:N	2.25	0.52
1:A:699:VAL:CG1	1:A:700:LEU:HG	2.38	0.52
1:A:659:PHE:O	1:A:662:PHE:HB3	2.10	0.52
1:A:82:CYS:SG	1:A:174:SER:CB	2.98	0.51
2:B:260:ILE:HG23	2:B:261:GLN:H	1.74	0.51
1:A:96:ASP:OD1	1:A:175:GLU:OE1	2.28	0.51
1:A:510:GLN:O	1:A:511:THR:CB	2.59	0.51
1:A:280:LYS:HE2	1:A:280:LYS:H	1.75	0.51
1:A:675:ILE:HD13	1:A:697:PHE:HD2	1.72	0.51
3:C:192:LYS:O	3:C:193:ASN:CB	2.59	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:380:THR:O	1:A:383:MET:HG2	2.11	0.50
1:A:229:GLN:HG3	1:A:269:ALA:HB1	1.93	0.50
1:A:561:LEU:HD11	1:A:569:SER:HB2	1.94	0.50
1:A:114:LEU:CD2	1:A:121:LEU:HD12	2.42	0.50
1:A:440:LEU:HD13	1:A:446:ILE:HG13	1.93	0.50
1:A:523:ILE:CG1	1:A:524:GLU:H	2.22	0.50
1:A:167:PHE:HB3	1:A:182:GLU:OE2	2.11	0.50
1:A:83:ALA:O	1:A:85:PRO:HD3	2.12	0.49
1:A:379:ASN:HA	1:A:450:LYS:HE3	1.94	0.49
1:A:677:LYS:O	1:A:678:GLN:HB2	2.12	0.49
1:A:466:ILE:HD11	3:C:172:LEU:HD23	1.94	0.49
1:A:691:LEU:HD23	2:B:245:PHE:CG	2.48	0.49
1:A:186:ALA:HA	1:A:195:LEU:HD21	1.95	0.49
2:B:216:ILE:O	2:B:220:SER:HB2	2.12	0.49
1:A:289:GLY:HA2	1:A:321:ASP:O	2.12	0.48
1:A:186:ALA:HB2	1:A:195:LEU:HD11	1.95	0.48
1:A:358:LEU:HD13	1:A:502:PHE:CZ	2.48	0.48
2:B:157:THR:C	2:B:159:GLY:H	2.16	0.48
1:A:77:ARG:NE	1:A:156:ASP:OD2	2.47	0.48
1:A:201:THR:HG23	1:A:339:GLU:OE2	2.14	0.48
2:B:205:PHE:CE1	2:B:238:LEU:HB3	2.48	0.48
1:A:410:GLY:HA2	1:A:472:LEU:HB2	1.95	0.48
1:A:668:ARG:HD3	2:B:268:MET:CE	2.42	0.48
1:A:159:PRO:CG	1:A:167:PHE:HD2	2.27	0.47
1:A:160:THR:HG22	1:A:165:LEU:HA	1.95	0.47
1:A:516:ILE:HG13	1:A:639:PRO:HD3	1.97	0.47
2:B:148:SER:O	2:B:152:VAL:HG22	2.14	0.47
1:A:159:PRO:HG2	1:A:167:PHE:HD2	1.80	0.47
3:C:188:LYS:NZ	3:C:188:LYS:CD	2.70	0.47
1:A:244:ILE:HG22	3:C:173:GLU:HG2	1.95	0.47
2:B:154:ASP:OD2	2:B:157:THR:HA	2.15	0.47
2:B:248:LEU:HD12	2:B:256:ILE:HD12	1.96	0.47
1:A:537:LEU:HD23	3:C:141:LEU:HD22	1.95	0.47
1:A:628:ARG:O	1:A:632:GLU:HG3	2.15	0.47
1:A:274:SER:O	1:A:275:SER:C	2.53	0.47
1:A:642:LEU:HD12	1:A:642:LEU:HA	1.57	0.47
1:A:236:SER:C	1:A:237:LEU:HD23	2.35	0.47
1:A:693:SER:HA	1:A:696:SER:OG	2.15	0.46
1:A:168:VAL:HG11	1:A:179:ALA:HA	1.97	0.46
1:A:35:LEU:O	1:A:39:CYS:SG	2.74	0.46
1:A:367:ARG:HG3	1:A:492:HIS:HB3	1.98	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:158:THR:C	2:B:160:LYS:H	2.19	0.46
1:A:211:ILE:HG13	1:A:345:PRO:HA	1.97	0.45
1:A:77:ARG:HG3	1:A:157:ARG:HG2	1.99	0.45
1:A:232:LEU:HG	1:A:238:LEU:HD13	1.99	0.45
1:A:538:PHE:CD2	1:A:594:LEU:HD12	2.51	0.45
1:A:561:LEU:HD11	1:A:569:SER:CB	2.46	0.45
1:A:488:THR:CG2	1:A:489:PHE:N	2.79	0.45
1:A:680:ASP:CG	1:A:680:ASP:O	2.54	0.45
2:B:100:GLU:OE2	2:B:167:LYS:HD2	2.17	0.45
1:A:256:GLN:O	1:A:294:THR:N	2.37	0.44
1:A:429:ILE:HG13	1:A:471:VAL:CG1	2.47	0.44
1:A:333:ARG:NH1	1:A:333:ARG:HB2	2.32	0.44
1:A:465:PHE:N	1:A:465:PHE:CD2	2.84	0.44
1:A:362:ASP:HB3	1:A:498:CYS:HB3	1.99	0.44
1:A:370:THR:HA	1:A:383:MET:O	2.17	0.44
1:A:168:VAL:HB	1:A:182:GLU:CD	2.36	0.44
1:A:386:GLN:HB3	1:A:483:VAL:CG1	2.47	0.44
2:B:118:SER:OG	2:B:121:GLU:HB2	2.17	0.44
2:B:208:ASN:OD1	2:B:211:ILE:HG12	2.18	0.44
1:A:518:ALA:O	1:A:519:ASN:OD1	2.35	0.44
1:A:378:PRO:HB2	1:A:454:LEU:HD21	2.00	0.44
1:A:530:ILE:HG22	1:A:531:GLY:N	2.33	0.44
1:A:175:GLU:HG2	1:A:177:TRP:CD1	2.53	0.43
1:A:663:VAL:O	1:A:664:ARG:C	2.57	0.43
1:A:684:THR:C	1:A:686:THR:N	2.70	0.43
1:A:362:ASP:HA	1:A:498:CYS:HA	1.99	0.43
2:B:176:TRP:HZ3	2:B:236:VAL:CG2	2.31	0.43
1:A:28:LEU:HD13	1:A:50:SER:HB2	2.00	0.43
1:A:238:LEU:HG	1:A:340:ILE:HG12	2.01	0.43
2:B:260:ILE:CG2	2:B:261:GLN:H	2.32	0.43
1:A:254:THR:HG23	1:A:258:LEU:O	2.19	0.43
1:A:581:VAL:C	1:A:583:MET:N	2.71	0.43
2:B:156:ASP:OD1	2:B:156:ASP:N	2.47	0.43
1:A:201:THR:HG21	1:A:214:TRP:NE1	2.33	0.43
1:A:472:LEU:C	1:A:472:LEU:HD12	2.39	0.43
1:A:95:THR:O	1:A:171:ALA:HB2	2.19	0.42
1:A:267:THR:OG1	1:A:283:ARG:HG2	2.19	0.42
1:A:386:GLN:HB3	1:A:483:VAL:HG11	2.01	0.42
1:A:51:PHE:HB2	1:A:187:LYS:HE3	2.01	0.42
1:A:169:HIS:NE2	3:C:186:TYR:CZ	2.88	0.42
1:A:238:LEU:HB3	1:A:266:VAL:HB	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:515:GLU:O	1:A:516:ILE:C	2.58	0.42
1:A:48:ASP:HA	1:A:49:PRO:HD2	1.92	0.42
1:A:427:HIS:O	1:A:467:ASN:HA	2.19	0.42
1:A:27:TYR:C	1:A:29:ASN:N	2.71	0.41
1:A:677:LYS:O	1:A:678:GLN:CB	2.67	0.41
2:B:108:VAL:HG13	2:B:115:MET:SD	2.60	0.41
1:A:236:SER:HB3	1:A:341:CYS:O	2.21	0.41
2:B:158:THR:O	2:B:160:LYS:N	2.53	0.41
1:A:223:ASN:O	1:A:227:ILE:N	2.52	0.41
1:A:557:LEU:O	1:A:561:LEU:HB2	2.20	0.41
3:C:183:PRO:HB2	3:C:186:TYR:HB2	2.03	0.41
1:A:27:TYR:C	1:A:29:ASN:H	2.24	0.41
1:A:27:TYR:HB2	1:A:150:VAL:HG13	2.02	0.41
1:A:321:ASP:OD1	1:A:321:ASP:N	2.53	0.41
2:B:180:TYR:CE2	2:B:191:ILE:HG12	2.55	0.41
1:A:175:GLU:HG2	1:A:177:TRP:HD1	1.84	0.41
1:A:668:ARG:CD	2:B:268:MET:HE1	2.47	0.41
3:C:191:GLU:HB3	3:C:192:LYS:H	1.66	0.41
1:A:459:ARG:HA	1:A:459:ARG:HD2	1.76	0.41
1:A:672:LEU:HD12	1:A:672:LEU:HA	1.82	0.41
1:A:398:ASP:OD2	1:A:398:ASP:N	2.51	0.41
1:A:407:PHE:CE1	1:A:475:PHE:HB2	2.55	0.41
1:A:516:ILE:HA	1:A:637:LYS:O	2.21	0.41
1:A:567:ILE:O	1:A:567:ILE:CG2	2.67	0.41
1:A:575:GLU:H	1:A:575:GLU:HG2	1.59	0.41
1:A:576:THR:HG23	1:A:664:ARG:CD	2.50	0.41
1:A:281:LEU:HD11	1:A:297:TRP:CZ3	2.56	0.41
1:A:465:PHE:N	1:A:465:PHE:HD2	2.19	0.41
1:A:67:SER:O	1:A:68:SER:C	2.59	0.40
1:A:64:GLY:O	1:A:66:TYR:N	2.54	0.40
1:A:308:ASP:HA	1:A:309:PRO:HD3	1.83	0.40
1:A:408:LEU:HB2	1:A:502:PHE:HB2	2.03	0.40
1:A:506:LYS:O	1:A:508:ASP:N	2.54	0.40
1:A:576:THR:CG2	1:A:664:ARG:HD3	2.51	0.40
1:A:699:VAL:O	1:A:700:LEU:HD23	2.22	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	672/714 (94%)	565 (84%)	84 (12%)	23 (3%)	3	17
2	B	172/184 (94%)	155 (90%)	10 (6%)	7 (4%)	3	13
3	C	50/86 (58%)	38 (76%)	10 (20%)	2 (4%)	3	14
All	All	894/984 (91%)	758 (85%)	104 (12%)	32 (4%)	3	16

All (32) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	65	PRO
1	A	168	VAL
1	A	252	ALA
1	A	298	ASN
1	A	441	THR
1	A	507	ALA
1	A	516	ILE
1	A	566	ASP
1	A	618	ARG
2	B	222	GLU
3	C	193	ASN
3	C	212	ALA
1	A	297	TRP
1	A	685	GLY
2	B	247	SER
2	B	261	GLN
1	A	275	SER
1	A	445	ASN
2	B	227	ASP
1	A	28	LEU
1	A	133	GLU
1	A	522	GLU
1	A	594	LEU
2	B	123	MET

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	159	GLY
1	A	68	SER
1	A	291	VAL
1	A	519	ASN
2	B	115	MET
1	A	520	ILE
1	A	222	PRO
1	A	302	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	A	587/613 (96%)	504 (86%)	83 (14%)	3	14
2	B	153/162 (94%)	133 (87%)	20 (13%)	4	16
3	C	47/74 (64%)	40 (85%)	7 (15%)	3	12
All	All	787/849 (93%)	677 (86%)	110 (14%)	3	14

All (110) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	GLU
1	A	35	LEU
1	A	45	LEU
1	A	48	ASP
1	A	66	TYR
1	A	82	CYS
1	A	88	ILE
1	A	89	ILE
1	A	119	GLU
1	A	130	SER
1	A	133	GLU
1	A	138	ILE
1	A	148	GLU
1	A	165	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	168	VAL
1	A	188	ILE
1	A	223	ASN
1	A	244	ILE
1	A	245	THR
1	A	246	SER
1	A	251	GLU
1	A	254	THR
1	A	255	TYR
1	A	273	GLU
1	A	278	LEU
1	A	280	LYS
1	A	281	LEU
1	A	293	TRP
1	A	299	ASP
1	A	300	ASN
1	A	311	VAL
1	A	321	ASP
1	A	332	LEU
1	A	344	THR
1	A	348	LEU
1	A	359	THR
1	A	361	MET
1	A	366	ARG
1	A	388	LEU
1	A	391	LEU
1	A	416	ARG
1	A	422	MET
1	A	436	VAL
1	A	443	GLN
1	A	455	THR
1	A	456	THR
1	A	459	ARG
1	A	463	ASP
1	A	465	PHE
1	A	471	VAL
1	A	472	LEU
1	A	508	ASP
1	A	514	ASP
1	A	515	GLU
1	A	520	ILE
1	A	522	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	535	ARG
1	A	540	GLN
1	A	561	LEU
1	A	565	GLU
1	A	566	ASP
1	A	568	LYS
1	A	575	GLU
1	A	576	THR
1	A	584	LEU
1	A	586	GLU
1	A	608	GLN
1	A	612	ARG
1	A	616	VAL
1	A	624	SER
1	A	628	ARG
1	A	642	LEU
1	A	644	GLN
1	A	649	ARG
1	A	656	ILE
1	A	668	ARG
1	A	672	LEU
1	A	678	GLN
1	A	683	ASN
1	A	686	THR
1	A	687	ILE
1	A	694	TRP
1	A	699	VAL
2	B	98	GLU
2	B	120	THR
2	B	130	VAL
2	B	131	THR
2	B	144	ASP
2	B	156	ASP
2	B	187	ARG
2	B	193	SER
2	B	196	LEU
2	B	206	HIS
2	B	209	GLN
2	B	218	ARG
2	B	221	ASP
2	B	227	ASP
2	B	238	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	246	ARG
2	B	261	GLN
2	B	264	LEU
2	B	265	GLN
2	B	268	MET
3	C	139	ASP
3	C	141	LEU
3	C	164	LEU
3	C	167	MET
3	C	181	THR
3	C	211	HIS
3	C	213	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	608	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 10 ligands modelled in this entry, 10 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	676/714 (94%)	0.42	48 (7%) 16 9	75, 97, 108, 127	0
2	B	174/184 (94%)	0.22	9 (5%) 27 17	73, 94, 106, 112	0
3	C	56/86 (65%)	0.81	7 (12%) 3 2	92, 103, 110, 117	0
All	All	906/984 (92%)	0.41	64 (7%) 16 9	73, 97, 108, 127	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	193	ASN	6.8
1	A	509	TYR	6.3
1	A	534	PHE	6.0
2	B	110	LEU	5.9
1	A	44	ALA	5.4
1	A	524	GLU	4.8
3	C	137	ALA	4.7
1	A	78	PRO	4.4
1	A	136	ALA	4.0
2	B	270	SER	3.9
1	A	159	PRO	3.9
1	A	526	ASN	3.8
1	A	160	THR	3.7
1	A	525	ALA	3.6
1	A	318	ARG	3.5
1	A	282	ILE	3.5
1	A	511	THR	3.3
2	B	115	MET	3.3
2	B	163	PHE	3.2
1	A	74	GLU	3.2
1	A	295	GLY	3.1
1	A	335	TYR	3.0
1	A	281	LEU	3.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	B	238	LEU	3.0
1	A	66	TYR	3.0
1	A	544	GLU	2.9
2	B	103	PHE	2.9
2	B	113	ASP	2.8
3	C	138	LEU	2.7
1	A	267	THR	2.7
2	B	126	LEU	2.6
1	A	58	LEU	2.6
1	A	163	GLY	2.6
1	A	158	LEU	2.5
1	A	586	GLU	2.5
1	A	139	PHE	2.5
1	A	311	VAL	2.4
3	C	192	LYS	2.4
1	A	530	ILE	2.4
1	A	216	GLU	2.4
1	A	101	ALA	2.3
3	C	139	ASP	2.3
1	A	177	TRP	2.3
1	A	45	LEU	2.3
1	A	528	GLU	2.3
1	A	508	ASP	2.3
1	A	349	THR	2.2
1	A	73	ILE	2.2
1	A	217	LEU	2.2
1	A	332	LEU	2.2
1	A	127	LEU	2.2
1	A	250	SER	2.2
1	A	162	ASP	2.2
1	A	527	GLU	2.2
3	C	164	LEU	2.1
1	A	42	ALA	2.1
1	A	176	PHE	2.1
1	A	678	GLN	2.1
1	A	513	ASP	2.1
1	A	565	GLU	2.1
1	A	75	TRP	2.1
1	A	556	ILE	2.1
3	C	194	GLU	2.0
2	B	107	PHE	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, 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	B-factors(\AA^2)	Q<0.9
4	CA	A	718	1/1	0.87	0.06	103,103,103,103	0
4	CA	A	720	1/1	0.91	0.07	72,72,72,72	0
4	CA	B	602	1/1	0.91	0.07	94,94,94,94	0
4	CA	B	601	1/1	0.92	0.07	105,105,105,105	0
4	CA	A	716	1/1	0.93	0.08	119,119,119,119	0
4	CA	B	604	1/1	0.93	0.06	87,87,87,87	0
4	CA	A	717	1/1	0.94	0.04	130,130,130,130	0
4	CA	A	715	1/1	0.97	0.03	96,96,96,96	0
4	CA	B	603	1/1	0.98	0.03	79,79,79,79	0
4	CA	A	719	1/1	0.99	0.03	71,71,71,71	0

6.5 Other polymers [i](#)

There are no such residues in this entry.