Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 08:37 am BST

PDB ID	:	5W2J
Title	:	Crystal structure of dimeric form of mouse Glutaminase C
Authors	:	Cerione, R.A.; Li, Y.
Deposited on	:	2017-06-06
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
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:

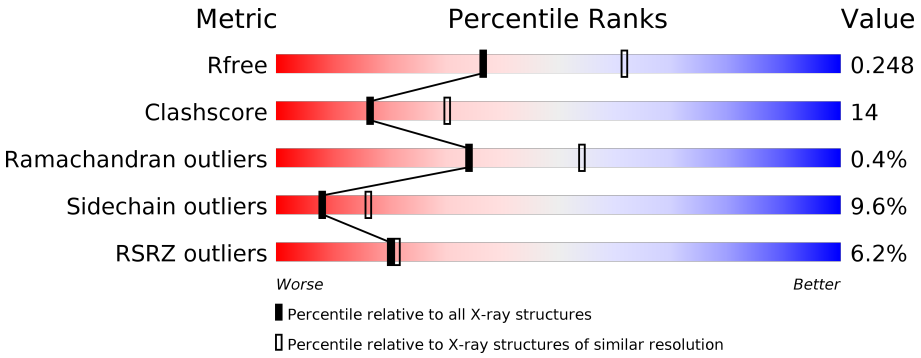
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (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 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	411	2% 78% 18%
1	B	411	9% 77% 19%
2	F	14	36% 50% 36% 14%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	CL	B	601	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6666 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 Glutaminase kidney isoform, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	408	Total	C	N	O	S	0	0	0
			3190	2036	539	587	28			
1	B	411	Total	C	N	O	S	0	1	0
			3215	2053	543	591	28			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	391	LYS	ASP	engineered mutation	UNP D3Z7P3
B	391	LYS	ASP	engineered mutation	UNP D3Z7P3

- Molecule 2 is a protein called unidentified peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	F	14	Total	C	N	O	0	0	0
			90	56	16	18			

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Cl	0	0
			1	1		
3	A	1	Total	Cl	0	0
			1	1		

- Molecule 4 is water.

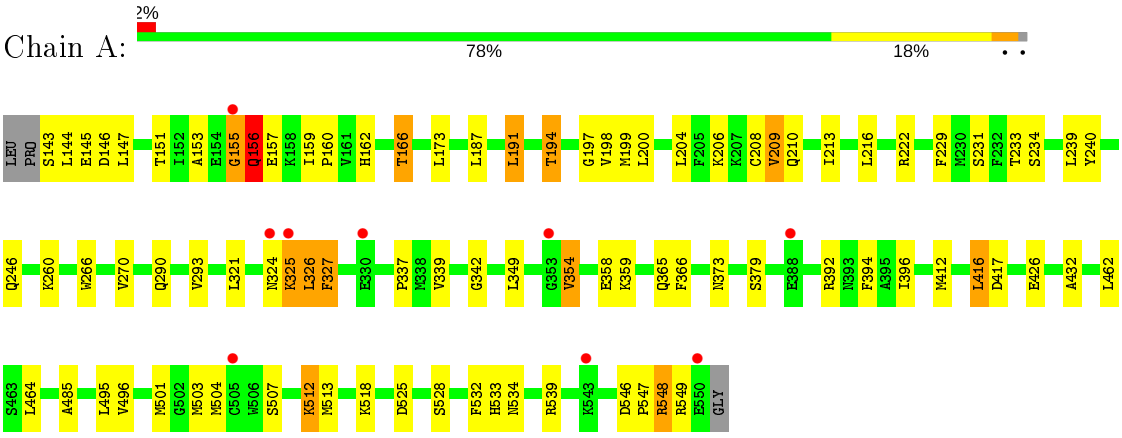
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	82	Total	O	0	0
			82	82		
4	B	87	Total	O	0	0
			87	87		

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.

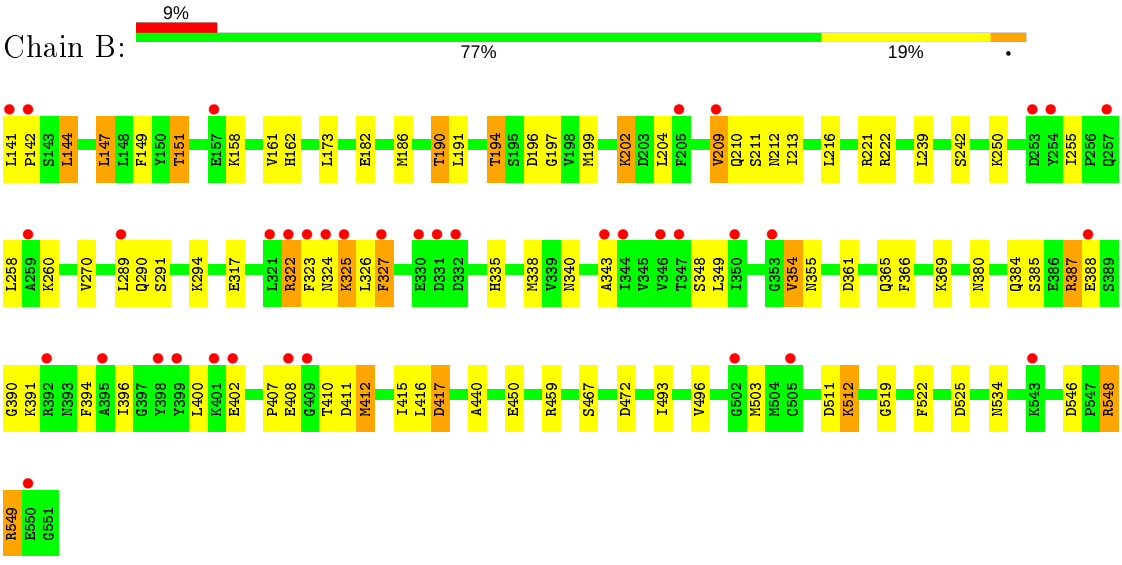
- Molecule 1: Glutaminase kidney isoform, mitochondrial

Chain A:



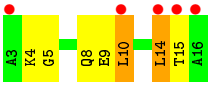
- Molecule 1: Glutaminase kidney isoform, mitochondrial

Chain B:



- Molecule 2: unidentified peptide

Chain F:


A3
K4
G5
Q8
E9
L10
L14
T15
A16

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	84.94Å 100.88Å 145.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.50 24.85 – 2.30	Depositor EDS
% Data completeness (in resolution range)	92.0 (50.00-2.50) 93.1 (24.85-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.92 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.196 , 0.228 0.223 , 0.248	Depositor DCC
R_{free} test set	1070 reflections (2.05%)	wwPDB-VP
Wilson B-factor (Å^2)	32.6	Xtriage
Anisotropy	0.103	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 39.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.52$, $< L^2 > = 0.36$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	6666	wwPDB-VP
Average B, all atoms (Å^2)	56.0	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.*

[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: CL

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	0.96	0/3261	0.89	0/4400
1	B	0.91	0/3290	0.86	0/4440
2	F	0.45	0/89	0.54	0/118
All	All	0.93	0/6640	0.87	0/8958

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

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	3190	0	3178	93	0
1	B	3215	0	3207	86	0
2	F	90	0	95	11	0
3	A	1	0	0	0	0
3	B	1	0	0	2	0
4	A	82	0	0	2	0
4	B	87	0	0	3	0
All	All	6666	0	6480	184	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 (184) 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:A:325:LYS:HB3	1:A:326:LEU:CA	1.40	1.46
1:A:325:LYS:CB	1:A:326:LEU:HA	1.38	1.41
1:A:325:LYS:CE	1:A:325:LYS:HA	1.44	1.26
1:A:324:ASN:O	1:A:325:LYS:HD2	1.43	1.15
1:A:325:LYS:NZ	1:A:325:LYS:HA	1.64	1.11
1:A:325:LYS:HA	1:A:325:LYS:HE3	1.28	1.09
1:B:194:THR:CG2	1:B:197:GLY:H	1.66	1.07
1:A:194:THR:HG22	1:A:197:GLY:H	1.19	1.07
1:A:325:LYS:CE	1:A:325:LYS:CA	2.30	1.07
1:A:354:VAL:HG13	1:A:358:GLU:CG	1.85	1.06
1:A:354:VAL:CG1	1:A:358:GLU:HG3	1.88	1.03
1:A:325:LYS:HE3	1:A:325:LYS:CA	1.85	1.02
1:B:194:THR:HG22	1:B:197:GLY:H	1.21	1.01
1:B:412:MET:CE	1:B:416:LEU:HG	1.94	0.98
1:A:194:THR:CG2	1:A:197:GLY:H	1.76	0.97
1:A:326:LEU:CD2	1:A:396:ILE:HG12	2.01	0.91
1:A:354:VAL:HG11	1:A:358:GLU:HG3	1.54	0.88
1:A:155:GLY:HA2	1:A:156:GLN:O	1.73	0.88
1:A:512:LYS:H	1:A:512:LYS:HD2	1.37	0.88
1:B:412:MET:HE3	1:B:416:LEU:HG	1.53	0.87
1:A:354:VAL:HG13	1:A:358:GLU:HG2	1.58	0.85
1:B:384:GLN:O	1:B:388:GLU:HG3	1.74	0.84
1:B:194:THR:HG22	1:B:197:GLY:N	1.92	0.83
1:A:325:LYS:HE2	1:A:327:PHE:CD1	2.13	0.83
1:A:191:LEU:HD13	1:A:200:LEU:HD21	1.60	0.83
1:B:194:THR:CG2	1:B:197:GLY:N	2.43	0.82
1:A:354:VAL:HG13	1:A:358:GLU:HG3	1.54	0.82
1:A:326:LEU:HD23	1:A:396:ILE:HG12	1.59	0.82
1:A:501:MET:CE	1:A:503:MET:CE	2.58	0.82
1:A:194:THR:HG22	1:A:197:GLY:N	1.95	0.81
1:A:546:ASP:OD1	1:A:548:ARG:HD2	1.80	0.81
1:A:512:LYS:H	1:A:512:LYS:CD	1.94	0.79
1:A:324:ASN:O	1:A:325:LYS:CD	2.30	0.79
1:B:239:LEU:HD22	1:B:525:ASP:HB3	1.63	0.78
1:B:385:SER:HA	1:B:388:GLU:HG3	1.66	0.77
2:F:10:LEU:HD12	2:F:10:LEU:O	1.84	0.76
1:A:501:MET:CE	1:A:503:MET:HE2	2.18	0.74
1:B:384:GLN:O	1:B:388:GLU:CG	2.36	0.73
1:A:501:MET:HE3	1:A:503:MET:HE2	1.72	0.71
1:A:501:MET:HE3	1:A:503:MET:CE	2.21	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:182:GLU:HG3	1:B:211:SER:OG	1.90	0.70
1:A:209:VAL:HG13	1:A:213:ILE:HD13	1.72	0.70
1:A:325:LYS:HD3	1:A:327:PHE:HE1	1.57	0.69
1:B:294:LYS:HE2	1:B:338:MET:O	1.93	0.68
1:B:348:SER:HA	1:B:415:ILE:HD12	1.75	0.68
1:B:270:VAL:HG22	1:B:503:MET:HG2	1.76	0.67
1:A:539:ARG:HG3	4:B:782:HOH:O	1.94	0.67
1:B:390:GLY:O	1:B:394:PHE:HD2	1.77	0.67
2:F:14:LEU:HD23	2:F:15:THR:N	2.10	0.66
1:A:209:VAL:HG22	1:A:216:LEU:CD1	2.26	0.66
1:A:325:LYS:HZ1	1:A:325:LYS:HA	1.60	0.66
1:B:325:LYS:O	1:B:327:PHE:CD1	2.49	0.65
1:A:155:GLY:HA2	1:A:156:GLN:CB	2.26	0.65
1:A:160:PRO:HA	1:A:199:MET:HE2	1.78	0.65
1:B:291:SER:HB2	3:B:601:CL:CL	2.33	0.65
1:B:546:ASP:OD1	1:B:548:ARG:HD2	1.98	0.64
2:F:14:LEU:HD23	2:F:14:LEU:C	2.18	0.64
1:A:501:MET:HE1	1:A:503:MET:CE	2.27	0.64
1:A:325:LYS:HD3	1:A:327:PHE:CE1	2.33	0.63
1:B:325:LYS:HB3	1:B:327:PHE:CE1	2.34	0.63
1:B:327:PHE:CE2	1:B:335:HIS:CE1	2.86	0.63
1:A:324:ASN:O	1:A:325:LYS:NZ	2.30	0.62
1:B:142:PRO:O	2:F:8:GLN:NE2	2.28	0.62
1:A:191:LEU:CD1	1:A:200:LEU:HD21	2.30	0.62
1:B:354:VAL:HG13	1:B:355:ASN:N	2.12	0.62
1:A:354:VAL:CG1	1:A:358:GLU:CG	2.54	0.62
1:B:394:PHE:CD1	1:B:412:MET:HE1	2.35	0.62
1:B:394:PHE:HD1	1:B:412:MET:HE1	1.65	0.61
1:B:141:LEU:N	1:B:142:PRO:CD	2.63	0.61
1:B:186:MET:O	1:B:190:THR:HB	2.00	0.61
1:B:325:LYS:O	1:B:327:PHE:HD1	1.83	0.60
1:A:546:ASP:OD1	1:A:548:ARG:CD	2.50	0.60
1:A:145:GLU:HG3	1:A:206:LYS:HG3	1.83	0.60
1:A:533:HIS:CD2	1:B:459:ARG:HD2	2.37	0.60
1:A:325:LYS:HB3	1:A:326:LEU:CB	2.27	0.60
1:B:369:LYS:HD3	1:B:450:GLU:OE2	2.01	0.60
1:A:270:VAL:HG22	1:A:503:MET:HG2	1.84	0.59
1:B:209:VAL:HG13	1:B:213:ILE:HD13	1.85	0.59
1:A:324:ASN:C	1:A:325:LYS:HD2	2.21	0.58
1:A:143:SER:HA	1:A:146:ASP:HB2	1.86	0.58
1:B:396:ILE:HG22	1:B:400:LEU:CD1	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:10:LEU:C	2:F:10:LEU:HD12	2.24	0.57
1:A:359:LYS:HE2	4:A:720:HOH:O	2.05	0.57
1:A:512:LYS:HD2	1:A:512:LYS:N	2.11	0.57
1:B:291:SER:CB	3:B:601:CL:CL	2.90	0.57
1:A:240:TYR:CE1	1:A:266:TRP:CD1	2.93	0.57
1:B:407:PRO:O	1:B:410:THR:OG1	2.22	0.56
1:B:209:VAL:HG22	1:B:216:LEU:CD1	2.36	0.56
4:B:736:HOH:O	2:F:15:THR:HG21	2.06	0.56
1:A:198:VAL:HG12	1:A:199:MET:HE2	1.86	0.56
1:B:385:SER:CA	1:B:388:GLU:HG3	2.35	0.56
1:B:144:LEU:CD2	2:F:4:LYS:HD2	2.37	0.55
1:B:412:MET:HE3	1:B:416:LEU:CG	2.31	0.55
1:B:412:MET:CE	1:B:416:LEU:CG	2.76	0.55
1:A:209:VAL:HG22	1:A:216:LEU:HD13	1.87	0.55
1:B:385:SER:HA	1:B:388:GLU:CG	2.37	0.55
1:A:394:PHE:CD1	1:A:416:LEU:HD22	2.42	0.54
1:B:512:LYS:CD	1:B:512:LYS:H	2.19	0.54
1:A:147:LEU:O	1:A:151:THR:HG23	2.07	0.54
1:A:155:GLY:CA	1:A:156:GLN:O	2.53	0.54
1:B:512:LYS:H	1:B:512:LYS:HD2	1.73	0.53
1:B:380:ASN:O	1:B:384:GLN:HG2	2.09	0.53
1:B:390:GLY:O	1:B:394:PHE:CD2	2.61	0.53
1:A:239:LEU:HD22	1:A:525:ASP:HB3	1.90	0.52
1:A:432:ALA:HB1	1:A:504:MET:HE2	1.92	0.52
1:A:194:THR:CG2	1:A:197:GLY:N	2.58	0.52
1:A:325:LYS:CE	1:A:327:PHE:CD1	2.89	0.52
1:B:141:LEU:N	1:B:142:PRO:HD3	2.24	0.52
2:F:5:GLY:O	2:F:9:GLU:HG3	2.09	0.52
1:A:501:MET:HE1	1:A:503:MET:HE1	1.91	0.52
1:A:394:PHE:CE1	1:A:416:LEU:HD22	2.45	0.52
1:B:396:ILE:HG22	1:B:400:LEU:HD12	1.92	0.51
1:A:160:PRO:CA	1:A:199:MET:HE2	2.40	0.51
1:B:511:ASP:HA	1:B:512:LYS:HZ2	1.76	0.51
1:A:162:HIS:O	1:A:166:THR:CG2	2.59	0.51
1:B:387:ARG:CD	1:B:417:ASP:OD1	2.59	0.50
1:A:321:LEU:HD12	1:A:327:PHE:CZ	2.47	0.50
1:B:354:VAL:CG1	1:B:355:ASN:N	2.74	0.50
1:A:155:GLY:CA	1:A:156:GLN:CB	2.89	0.50
1:B:194:THR:HG22	1:B:197:GLY:CA	2.42	0.49
1:A:159:ILE:HG22	1:A:160:PRO:O	2.12	0.49
1:A:325:LYS:HE2	1:A:327:PHE:CE1	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:255:ILE:HG12	1:B:258:LEU:HD12	1.95	0.49
1:B:209:VAL:HG22	1:B:216:LEU:HD13	1.94	0.49
1:A:532:PHE:CZ	1:A:547:PRO:HG2	2.48	0.49
1:A:412:MET:SD	1:A:416:LEU:CD1	3.01	0.49
1:B:294:LYS:HG2	1:B:343:ALA:HB2	1.95	0.48
1:B:387:ARG:HD3	1:B:417:ASP:OD1	2.13	0.48
1:B:493:ILE:HD12	1:B:519:GLY:HA3	1.96	0.48
1:A:191:LEU:O	1:A:194:THR:HB	2.13	0.48
1:A:373:ASN:ND2	4:A:701:HOH:O	2.35	0.48
1:B:546:ASP:HB3	1:B:549:ARG:HD2	1.96	0.48
1:A:155:GLY:CA	1:A:156:GLN:HB2	2.44	0.48
1:A:155:GLY:HA2	1:A:156:GLN:C	2.22	0.48
1:B:412:MET:HE2	1:B:416:LEU:HG	1.90	0.48
1:A:143:SER:CA	1:A:146:ASP:HB2	2.43	0.47
1:B:503:MET:HE1	1:B:522:PHE:CE1	2.49	0.47
1:A:462:LEU:HD21	1:A:496:VAL:HG11	1.96	0.47
1:A:325:LYS:C	1:A:325:LYS:HE3	2.34	0.47
1:B:144:LEU:HD22	2:F:4:LYS:HD2	1.97	0.47
1:B:289:LEU:O	1:B:290:GLN:C	2.52	0.47
1:B:294:LYS:HE3	1:B:343:ALA:HB2	1.97	0.47
1:A:266:TRP:CE3	1:A:507:SER:HB2	2.51	0.46
1:B:327:PHE:CD2	1:B:335:HIS:HE1	2.33	0.46
1:B:503:MET:HE3	1:B:503:MET:HB3	1.61	0.46
1:B:323:PHE:C	1:B:325:LYS:H	2.19	0.46
1:B:327:PHE:CD2	1:B:335:HIS:CE1	3.04	0.46
1:B:270:VAL:HG22	1:B:503:MET:CG	2.46	0.46
1:A:240:TYR:CZ	1:A:266:TRP:CD1	3.04	0.46
1:A:209:VAL:CG1	1:A:213:ILE:HD13	2.43	0.45
1:B:149:PHE:CG	1:B:202:LYS:HG2	2.51	0.45
1:B:144:LEU:HD23	2:F:4:LYS:HD2	1.98	0.45
1:A:153:ALA:O	1:A:156:GLN:CB	2.65	0.45
1:B:294:LYS:NZ	1:B:340:ASN:OD1	2.47	0.45
1:B:384:GLN:O	1:B:388:GLU:HG2	2.15	0.44
1:A:325:LYS:NZ	1:A:325:LYS:CA	2.58	0.44
1:A:229:PHE:O	1:A:233:THR:HG23	2.17	0.44
1:A:162:HIS:O	1:A:166:THR:HG22	2.17	0.44
1:B:196:ASP:OD2	1:B:199:MET:HG2	2.17	0.44
1:A:339:VAL:HG23	1:A:342:GLY:H	1.82	0.44
1:B:327:PHE:CD1	1:B:327:PHE:N	2.86	0.44
1:B:144:LEU:HA	1:B:144:LEU:HD12	1.85	0.43
1:B:194:THR:CG2	1:B:197:GLY:CA	2.95	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:147:LEU:O	1:B:151:THR:CG2	2.66	0.43
1:B:325:LYS:O	1:B:327:PHE:CE1	2.71	0.43
1:B:161:VAL:HG13	1:B:162:HIS:N	2.34	0.43
1:B:147:LEU:O	1:B:151:THR:HG22	2.18	0.42
1:B:396:ILE:HG22	1:B:400:LEU:HD11	2.00	0.42
1:A:187:LEU:HD23	1:A:208:CYS:SG	2.59	0.42
1:B:222:ARG:HA	4:B:757:HOH:O	2.19	0.42
1:B:144:LEU:HB2	2:F:4:LYS:HZ2	1.84	0.42
1:A:290:GLN:O	1:A:293:VAL:HG12	2.20	0.42
1:B:411:ASP:C	1:B:411:ASP:OD1	2.58	0.42
1:A:325:LYS:CE	1:A:327:PHE:HD1	2.29	0.41
1:A:337:PRO:HG2	1:A:464:LEU:HD13	2.01	0.41
1:B:182:GLU:HG2	1:B:212:ASN:OD1	2.21	0.41
1:B:322:ARG:HG2	1:B:472:ASP:OD2	2.20	0.41
1:A:246:GLN:O	1:A:518:LYS:HE3	2.20	0.41
1:A:532:PHE:CZ	1:A:547:PRO:CG	3.03	0.41
1:B:387:ARG:HD2	1:B:417:ASP:OD1	2.21	0.41
1:A:485:ALA:HB2	1:A:495:LEU:HD12	2.03	0.41
1:B:322:ARG:HB3	1:B:322:ARG:HH11	1.85	0.41
1:A:379:SER:HB2	1:A:426:GLU:OE2	2.22	0.40
1:B:440:ALA:HB2	1:B:496:VAL:HG13	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	406/411 (99%)	392 (97%)	12 (3%)	2 (0%)	29 48
1	B	410/411 (100%)	396 (97%)	13 (3%)	1 (0%)	47 68
2	F	12/14 (86%)	12 (100%)	0	0	100 100
All	All	828/836 (99%)	800 (97%)	25 (3%)	3 (0%)	34 54

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	155	GLY
1	B	324	ASN
1	A	156	GLN

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	354/356 (99%)	324 (92%)	30 (8%)	10 21
1	B	357/356 (100%)	320 (90%)	37 (10%)	7 13
2	F	7/7 (100%)	5 (71%)	2 (29%)	0 0
All	All	718/719 (100%)	649 (90%)	69 (10%)	8 16

All (69) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	144	LEU
1	A	156	GLN
1	A	157	GLU
1	A	166	THR
1	A	173	LEU
1	A	191	LEU
1	A	194	THR
1	A	204	LEU
1	A	209	VAL
1	A	210	GLN
1	A	222	ARG
1	A	231	SER
1	A	234	SER
1	A	260	LYS
1	A	325	LYS
1	A	326	LEU
1	A	327	PHE
1	A	349	LEU

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Mol	Chain	Res	Type
1	A	354	VAL
1	A	365	GLN
1	A	366	PHE
1	A	392	ARG
1	A	416	LEU
1	A	417	ASP
1	A	512	LYS
1	A	513	MET
1	A	528	SER
1	A	534	ASN
1	A	548	ARG
1	A	549	ARG
1	B	144	LEU
1	B	147	LEU
1	B	151	THR
1	B	158	LYS
1	B	173	LEU
1	B	190	THR
1	B	191	LEU
1	B	194	THR
1	B	202	LYS
1	B	204	LEU
1	B	209	VAL
1	B	210	GLN
1	B	221	ARG
1	B	242	SER
1	B	250	LYS
1	B	260	LYS
1	B	317	GLU
1	B	322	ARG
1	B	325	LYS
1	B	326	LEU
1	B	327	PHE
1	B	349	LEU
1	B	354	VAL
1	B	361	ASP
1	B	365	GLN
1	B	366	PHE
1	B	387	ARG
1	B	391	LYS
1	B	402	GLU
1	B	408	GLU

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Mol	Chain	Res	Type
1	B	412	MET
1	B	417	ASP
1	B	467	SER
1	B	512	LYS
1	B	534	ASN
1	B	548	ARG
1	B	549	ARG
2	F	10	LEU
2	F	14	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	393	ASN
1	B	335	HIS
1	B	466	HIS
1	B	534	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 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.

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, 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	408/411 (99%)	-0.22	9 (2%) 62 65	30, 49, 85, 122	0
1	B	411/411 (100%)	0.37	38 (9%) 9 9	31, 52, 100, 119	0
2	F	14/14 (100%)	1.60	5 (35%) 0 0	77, 108, 123, 126	0
All	All	833/836 (99%)	0.10	52 (6%) 20 21	30, 50, 98, 126	0

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	327	PHE	5.5
1	B	353	GLY	5.0
1	B	324	ASN	5.0
1	B	543	LYS	5.0
1	B	408	GLU	4.2
1	B	322	ARG	3.8
1	B	398	TYR	3.8
1	A	353	GLY	3.7
1	B	409	GLY	3.7
1	B	392	ARG	3.7
1	B	332	ASP	3.7
1	A	325	LYS	3.6
1	B	346	VAL	3.6
1	B	402	GLU	3.6
1	B	550	GLU	3.5
1	B	325	LYS	3.5
1	B	505	CYS	3.5
1	B	141	LEU	3.4
1	A	543	LYS	3.4
1	A	324	ASN	3.3
1	A	155	GLY	3.3
1	B	330	GLU	3.2
1	B	142	PRO	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	254	TYR	3.2
1	B	323	PHE	3.2
1	B	350	ILE	3.1
1	B	253	ASP	3.0
1	B	343	ALA	3.0
2	F	14	LEU	3.0
2	F	3	ALA	2.8
2	F	16	ALA	2.8
1	B	399	TYR	2.8
1	B	205	PHE	2.7
1	B	347	THR	2.6
1	B	157	GLU	2.6
1	A	550	GLU	2.6
1	B	388	GLU	2.6
1	A	330	GLU	2.6
2	F	15	THR	2.6
1	B	209	VAL	2.3
1	B	259	ALA	2.3
1	B	257	GLN	2.3
1	A	505	CYS	2.2
1	B	502	GLY	2.2
1	B	344	ILE	2.2
1	B	289	LEU	2.2
1	A	388	GLU	2.1
1	B	395	ALA	2.1
1	B	401	LYS	2.1
1	B	321	LEU	2.1
2	F	10	LEU	2.0
1	B	331	ASP	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

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
3	CL	B	601	1/1	0.95	0.06	81,81,81,81	0
3	CL	A	601	1/1	0.96	0.21	62,62,62,62	0

6.5 Other polymers

There are no such residues in this entry.