Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 10:10 AM GMT

PDB ID	:	3L4Q
Title	:	Structural insights into phosphoinositide 3-kinase activation by the influenza A virus NS1 protein
Authors	:	Hale, B.G.; Kerry, P.S.; Jackson, D.; Precious, B.L.; Gray, A.; Killip, M.J.; Randall, R.E.; Russell, R.J.
Deposited on	:	2009-12-21
Resolution	:	2.30 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

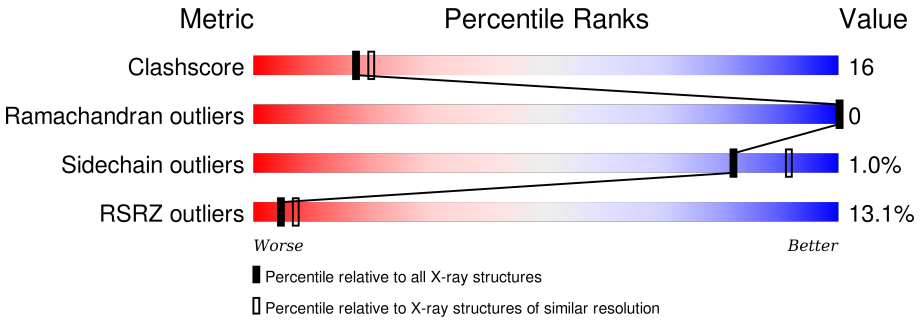
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 2.30 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))
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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 <=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	164	2% 60% 12% 27%
1	B	164	2% 53% 18% 27%
2	C	170	19% 79% 16%
2	D	170	21% 66% 30%

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	GOL	C	1	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4923 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 Non-structural protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	120	Total	C	N	O	S	0	0	0
			933	593	158	176	6			
1	B	119	Total	C	N	O	S	0	0	0
			927	590	157	174	6			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	67	HIS	-	EXPRESSION TAG	UNP P03496
A	68	HIS	-	EXPRESSION TAG	UNP P03496
A	69	HIS	-	EXPRESSION TAG	UNP P03496
A	70	HIS	-	EXPRESSION TAG	UNP P03496
A	71	HIS	-	EXPRESSION TAG	UNP P03496
A	72	HIS	-	EXPRESSION TAG	UNP P03496
B	67	HIS	-	EXPRESSION TAG	UNP P03496
B	68	HIS	-	EXPRESSION TAG	UNP P03496
B	69	HIS	-	EXPRESSION TAG	UNP P03496
B	70	HIS	-	EXPRESSION TAG	UNP P03496
B	71	HIS	-	EXPRESSION TAG	UNP P03496
B	72	HIS	-	EXPRESSION TAG	UNP P03496

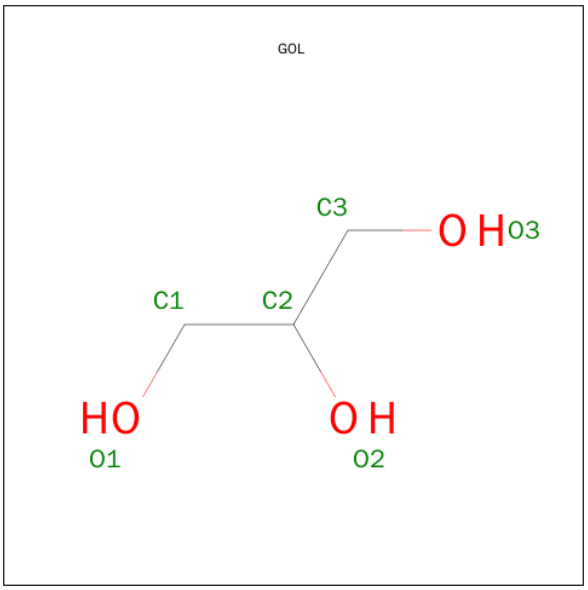
- Molecule 2 is a protein called Phosphatidylinositol 3-kinase regulatory subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	163	Total	C	N	O	S	0	0	0
			1385	855	256	270	4			
2	D	163	Total	C	N	O	S	0	0	0
			1385	855	256	270	4			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	495	SER	CYS	ENGINEERED	UNP P23726
D	495	SER	CYS	ENGINEERED	UNP P23726

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	1	Total C O 6 3 3	0	0
3	D	1	Total C O 6 3 3	0	0

- Molecule 4 is water.

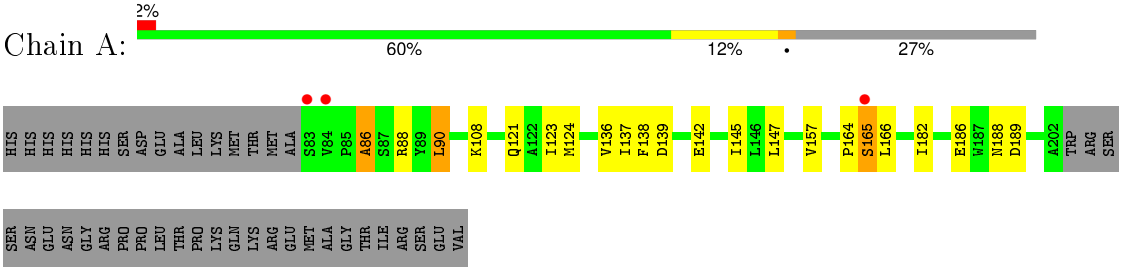
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	72	Total O 72 72	0	0
4	C	76	Total O 76 76	0	0
4	B	68	Total O 68 68	0	0
4	D	65	Total O 65 65	0	0

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 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.

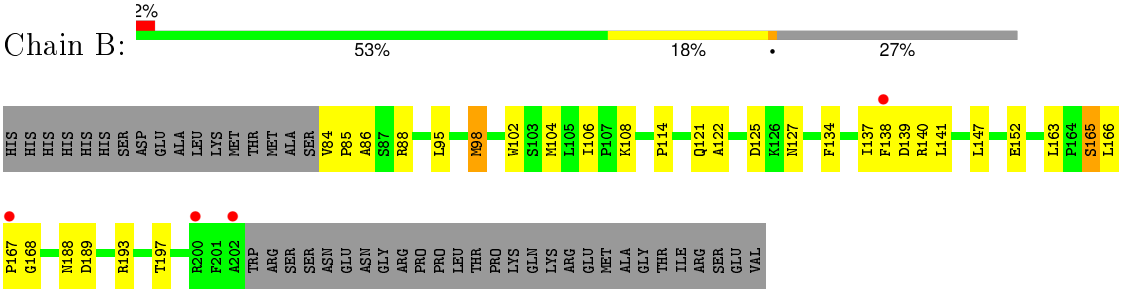
- Molecule 1: Non-structural protein 1

Chain A:



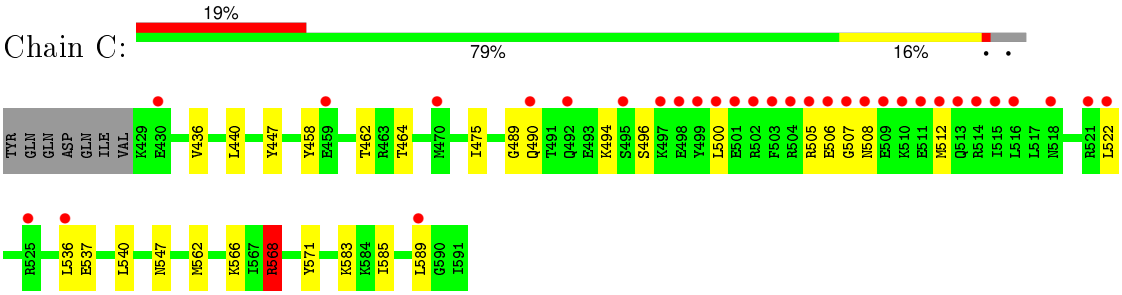
- Molecule 1: Non-structural protein 1

Chain B:



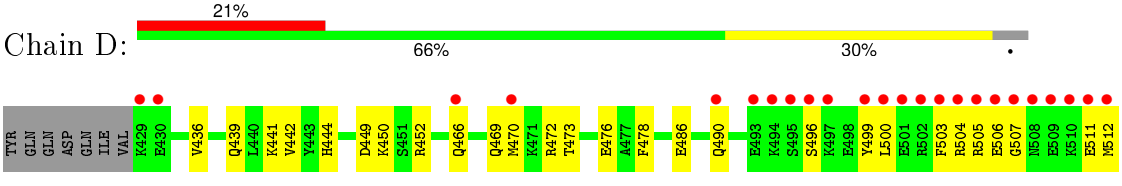
- Molecule 2: Phosphatidylinositol 3-kinase regulatory subunit beta

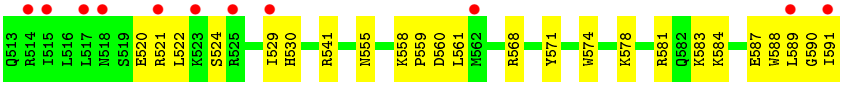
Chain C:



- Molecule 2: Phosphatidylinositol 3-kinase regulatory subunit beta

Chain D:




Q513
R514
I515
L516
L517
M518
S519
E520
R521
L522
K523
S524
R525
I529
H530
R541
N555
K558
P559
D560
L561
M562
R568
Y571
W574
K578
R581
Q582
K583
K584
E587
W588
L589
G590
I591

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	57.95Å 98.67Å 149.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.97 – 2.30 49.98 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.3 (49.97-2.30) 95.2 (49.98-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.66 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.5.0070	Depositor
R, R_{free}	0.232 , 0.292 0.236 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å^2)	35.5	Xtriage
Anisotropy	0.364	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 58.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Outliers	2 of 38826 reflections (0.005%)	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	4923	wwPDB-VP
Average B, all atoms (Å^2)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.41% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: GOL

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	1.08	0/948	0.94	1/1285 (0.1%)
1	B	1.06	0/942	0.94	1/1277 (0.1%)
2	C	0.96	0/1401	0.85	0/1868
2	D	0.85	0/1401	0.82	3/1868 (0.2%)
All	All	0.98	0/4692	0.88	5/6298 (0.1%)

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
2	C	0	1
All	All	0	3

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	561	LEU	CA-CB-CG	7.64	132.88	115.30
1	A	90	LEU	CA-CB-CG	-5.96	101.58	115.30
1	B	98	MET	CG-SD-CE	-5.49	91.42	100.20
2	D	560	ASP	CB-CG-OD1	5.28	123.05	118.30
2	D	500	LEU	CA-CB-CG	5.02	126.84	115.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	165	SER	Peptide
1	A	86	ALA	Peptide
2	C	568	ARG	Sidechain

5.2 Too-close contacts (i)

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	933	0	955	29	0
1	B	927	0	950	46	0
2	C	1385	0	1385	31	0
2	D	1385	0	1385	53	0
3	C	6	0	8	0	0
3	D	6	0	8	3	0
4	A	72	0	0	5	0
4	B	68	0	0	8	0
4	C	76	0	0	3	0
4	D	65	0	0	15	0
All	All	4923	0	4691	149	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 16.

All (149) 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:165:SER:HB3	1:A:166:LEU:CD2	1.68	1.22
2:C:506:GLU:CB	2:C:507:GLY:HA2	1.65	1.20
1:A:165:SER:CB	1:A:166:LEU:HD22	1.74	1.18
1:A:165:SER:HB3	1:A:166:LEU:HD22	1.20	1.15
1:B:84:VAL:HB	1:B:85:PRO:HD3	1.14	1.11
2:C:506:GLU:HB3	2:C:507:GLY:HA2	1.31	1.08
2:D:449:ASP:OD1	2:D:452:ARG:NH1	1.97	0.97
2:C:506:GLU:HB2	2:C:507:GLY:HA2	1.44	0.97
1:B:134:PHE:CZ	1:B:197:THR:CG2	2.52	0.92
1:B:84:VAL:CB	1:B:85:PRO:HD3	2.00	0.90
1:B:134:PHE:CZ	1:B:197:THR:HG22	2.08	0.88

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:506:GLU:HB3	2:C:507:GLY:CA	2.03	0.88
2:C:506:GLU:CB	2:C:507:GLY:CA	2.51	0.88
1:B:84:VAL:HB	1:B:85:PRO:CD	2.00	0.88
2:C:585:ILE:O	2:C:589:LEU:HD13	1.78	0.83
1:B:134:PHE:CD1	1:B:141:LEU:HD13	2.14	0.83
2:D:590:GLY:O	2:D:591:ILE:HG22	1.79	0.81
1:B:134:PHE:HZ	1:B:197:THR:CG2	1.94	0.78
1:B:163:LEU:HD12	1:B:166:LEU:CD1	2.13	0.78
2:C:489:GLY:HA2	2:C:522:LEU:HD21	1.65	0.78
1:A:165:SER:OG	1:A:166:LEU:HD22	1.85	0.77
1:A:165:SER:HB3	1:A:166:LEU:HD23	1.63	0.77
1:B:134:PHE:CE2	1:B:197:THR:HG22	2.20	0.76
2:C:571:TYR:CE2	1:B:167:PRO:HB2	2.20	0.76
1:B:114:PRO:HA	1:B:166:LEU:HD13	1.68	0.75
2:C:489:GLY:CA	2:C:522:LEU:HD21	2.16	0.75
2:D:469:GLN:OE1	4:D:233:HOH:O	2.05	0.73
1:B:134:PHE:CD1	1:B:141:LEU:CD1	2.72	0.73
2:D:590:GLY:O	2:D:591:ILE:CG2	2.39	0.70
2:C:505:ARG:O	4:C:45:HOH:O	2.10	0.69
2:D:590:GLY:O	2:D:591:ILE:CB	2.40	0.69
2:D:524:SER:HB2	4:D:67:HOH:O	1.91	0.69
1:A:189:ASP:OD2	4:A:265:HOH:O	2.09	0.69
1:B:163:LEU:HD12	1:B:166:LEU:HD12	1.73	0.69
1:B:125:ASP:HB3	4:B:251:HOH:O	1.94	0.68
2:D:441:LYS:HG3	2:D:588:TRP:O	1.92	0.68
2:D:503:PHE:CZ	2:D:512:MET:SD	2.87	0.68
1:B:163:LEU:HB2	1:B:166:LEU:HD12	1.75	0.67
2:C:475:ILE:HG13	2:C:536:LEU:HD23	1.76	0.66
1:B:134:PHE:CE2	1:B:197:THR:CG2	2.79	0.66
1:A:165:SER:CB	1:A:166:LEU:CD2	2.49	0.65
1:B:163:LEU:CD1	1:B:166:LEU:HD12	2.27	0.65
2:D:524:SER:CB	4:D:67:HOH:O	2.45	0.64
1:B:134:PHE:HZ	1:B:197:THR:HG22	1.57	0.63
2:D:590:GLY:O	2:D:591:ILE:HB	1.99	0.62
1:A:138:PHE:CE2	2:D:559:PRO:HB3	2.36	0.61
1:B:163:LEU:CD1	1:B:166:LEU:CD1	2.79	0.60
2:D:439:GLN:NE2	4:D:188:HOH:O	2.34	0.59
1:A:166:LEU:HD12	2:D:436:VAL:CG2	2.32	0.59
2:C:508:ASN:O	2:C:512:MET:HB3	2.02	0.59
1:B:165:SER:O	1:B:165:SER:OG	2.20	0.59
1:B:134:PHE:HZ	1:B:197:THR:HG23	1.67	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:95:LEU:HG	3:D:1:GOL:H2	1.86	0.58
2:D:496:SER:HA	2:D:499:TYR:HD2	1.67	0.58
1:B:134:PHE:CZ	1:B:197:THR:HG23	2.38	0.57
2:D:530:HIS:CE1	4:D:129:HOH:O	2.58	0.57
2:D:442:VAL:HB	4:D:188:HOH:O	2.04	0.57
2:D:444:HIS:HD2	2:D:589:LEU:O	1.88	0.56
1:A:124:MET:HE3	4:A:265:HOH:O	2.05	0.56
2:C:583:LYS:NZ	4:C:78:HOH:O	2.25	0.56
1:B:188:ASN:O	1:B:189:ASP:HB2	2.06	0.56
1:A:166:LEU:CD1	2:D:436:VAL:CG2	2.83	0.55
2:D:444:HIS:CD2	2:D:589:LEU:O	2.59	0.55
1:B:125:ASP:CB	4:B:251:HOH:O	2.52	0.55
2:D:472:ARG:O	2:D:476:GLU:HG2	2.06	0.55
1:B:85:PRO:O	1:B:86:ALA:C	2.44	0.55
2:C:440:LEU:HD21	2:C:589:LEU:CD1	2.36	0.54
2:C:458:TYR:O	2:C:462:THR:HG23	2.07	0.54
2:D:503:PHE:CE1	2:D:512:MET:SD	3.01	0.54
1:A:147:LEU:C	1:A:147:LEU:HD23	2.29	0.53
2:D:541:ARG:CD	4:D:160:HOH:O	2.56	0.53
2:C:489:GLY:HA3	2:C:522:LEU:HD21	1.89	0.53
2:D:530:HIS:HE1	4:D:129:HOH:O	1.89	0.53
1:A:166:LEU:CD1	2:D:436:VAL:HG21	2.39	0.53
1:A:86:ALA:HA	4:A:240:HOH:O	2.08	0.52
1:A:88:ARG:HA	2:C:562:MET:CE	2.39	0.52
2:C:537:GLU:OE2	2:C:540:LEU:HD23	2.10	0.52
2:D:590:GLY:C	2:D:591:ILE:HG22	2.31	0.52
1:B:84:VAL:CB	1:B:85:PRO:CD	2.71	0.51
2:C:496:SER:O	2:C:500:LEU:HG	2.11	0.51
2:D:499:TYR:O	2:D:503:PHE:HB2	2.11	0.50
2:D:520:GLU:OE1	2:D:521:ARG:HG3	2.12	0.50
2:D:449:ASP:HA	2:D:452:ARG:NH1	2.27	0.49
1:B:134:PHE:HD1	1:B:141:LEU:CD1	2.23	0.49
4:B:270:HOH:O	3:D:1:GOL:H31	2.12	0.49
2:D:496:SER:HA	2:D:499:TYR:CD2	2.47	0.49
1:B:166:LEU:C	1:B:167:PRO:O	2.46	0.49
1:B:139:ASP:HA	4:B:250:HOH:O	2.13	0.49
1:A:166:LEU:HD12	2:D:436:VAL:HG22	1.95	0.48
2:C:436:VAL:HG13	2:C:571:TYR:CD1	2.48	0.48
1:A:137:ILE:HG12	1:A:142:GLU:HB2	1.96	0.48
1:A:164:PRO:O	1:A:165:SER:C	2.50	0.48
2:C:440:LEU:HD21	2:C:589:LEU:HD12	1.94	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:505:ARG:HA	4:C:30:HOH:O	2.14	0.48
1:B:137:ILE:O	1:B:138:PHE:HB2	2.14	0.48
2:D:470:MET:O	2:D:473:THR:HG22	2.13	0.47
1:A:138:PHE:O	4:A:240:HOH:O	2.20	0.47
2:D:541:ARG:HD3	4:D:160:HOH:O	2.13	0.47
1:A:188:ASN:O	1:A:189:ASP:HB2	2.14	0.47
1:B:114:PRO:CA	1:B:166:LEU:HD13	2.42	0.47
1:A:108:LYS:HD2	1:A:121:GLN:CD	2.35	0.47
2:D:473:THR:HA	2:D:476:GLU:CG	2.45	0.47
1:B:108:LYS:HD3	1:B:121:GLN:CD	2.35	0.47
2:D:505:ARG:HG3	2:D:506:GLU:HG2	1.97	0.47
2:D:473:THR:HA	2:D:476:GLU:HG3	1.96	0.47
1:A:90:LEU:HD12	1:A:136:VAL:HG13	1.97	0.46
2:C:464:THR:OG1	2:C:547:ASN:OD1	2.32	0.46
1:B:85:PRO:HG2	1:B:88:ARG:HD3	1.98	0.46
2:D:466:GLN:HB2	4:D:261:HOH:O	2.16	0.46
2:D:504:ARG:HG3	4:D:81:HOH:O	2.15	0.46
2:D:568:ARG:HH22	3:D:1:GOL:H11	1.81	0.46
2:D:555:ASN:HA	2:D:558:LYS:HD2	1.98	0.46
2:D:486:GLU:O	2:D:490:GLN:HG2	2.16	0.46
2:C:490:GLN:O	2:C:494:LYS:HB2	2.15	0.45
2:D:574:TRP:CH2	2:D:578:LYS:HG3	2.51	0.45
2:C:506:GLU:HB3	2:C:508:ASN:H	1.81	0.45
2:C:571:TYR:CD2	1:B:167:PRO:HB2	2.51	0.45
1:A:88:ARG:HA	2:C:562:MET:SD	2.56	0.45
1:A:165:SER:HA	4:A:2:HOH:O	2.16	0.45
1:B:168:GLY:HA2	4:B:236:HOH:O	2.17	0.45
2:D:583:LYS:O	2:D:587:GLU:HG3	2.17	0.44
1:A:166:LEU:HD12	2:D:436:VAL:HG21	1.99	0.44
2:C:475:ILE:HG13	2:C:536:LEU:CD2	2.45	0.44
2:D:442:VAL:CB	4:D:188:HOH:O	2.65	0.44
2:D:439:GLN:HG2	2:D:571:TYR:CE1	2.53	0.44
1:B:95:LEU:HD23	1:B:98:MET:HE3	1.99	0.44
2:D:581:ARG:NH2	4:D:52:HOH:O	2.50	0.44
2:D:507:GLY:O	2:D:511:GLU:HB2	2.18	0.43
2:D:503:PHE:HZ	2:D:512:MET:SD	2.39	0.43
1:A:182:ILE:O	1:A:186:GLU:HG3	2.19	0.43
2:D:574:TRP:CZ3	2:D:578:LYS:HG3	2.54	0.43
1:B:193:ARG:HG2	4:B:249:HOH:O	2.19	0.43
2:C:447:TYR:CD1	2:C:568:ARG:NH1	2.87	0.43
2:D:584:LYS:HD2	2:D:584:LYS:HA	1.84	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:165:SER:HB3	4:B:33:HOH:O	2.19	0.42
2:D:478:PHE:CD1	2:D:529:ILE:HD11	2.54	0.42
1:B:147:LEU:HD23	1:B:147:LEU:C	2.40	0.42
2:C:489:GLY:HA2	2:C:522:LEU:CD2	2.43	0.42
1:B:137:ILE:HA	1:B:137:ILE:HD12	1.94	0.42
1:B:127:ASN:ND2	1:B:152:GLU:OE2	2.51	0.42
2:D:541:ARG:HD2	4:D:160:HOH:O	2.17	0.41
1:B:106:ILE:HD12	1:B:122:ALA:HB2	2.02	0.41
1:B:140:ARG:HB3	4:B:275:HOH:O	2.19	0.41
2:D:503:PHE:HB3	4:D:81:HOH:O	2.21	0.41
1:A:145:ILE:HD11	2:C:566:LYS:HD2	2.02	0.41
1:B:102:TRP:CZ3	1:B:104:MET:HG3	2.56	0.41
1:B:134:PHE:HB2	1:B:141:LEU:HD11	2.03	0.40
1:A:108:LYS:HD2	1:A:121:GLN:NE2	2.37	0.40
1:A:123:ILE:HG13	1:A:157:VAL:CG1	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	118/164 (72%)	116 (98%)	2 (2%)	0	100	100
1	B	117/164 (71%)	114 (97%)	3 (3%)	0	100	100
2	C	161/170 (95%)	158 (98%)	3 (2%)	0	100	100
2	D	161/170 (95%)	155 (96%)	6 (4%)	0	100	100
All	All	557/668 (83%)	543 (98%)	14 (2%)	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	104/143 (73%)	103 (99%)	1 (1%)	82 91
1	B	103/143 (72%)	102 (99%)	1 (1%)	82 91
2	C	150/157 (96%)	149 (99%)	1 (1%)	88 95
2	D	150/157 (96%)	148 (99%)	2 (1%)	76 87
All	All	507/600 (84%)	502 (99%)	5 (1%)	82 91

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	139	ASP
2	C	568	ARG
1	B	165	SER
2	D	450	LYS
2	D	522	LEU

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

Mol	Chain	Res	Type
2	C	513	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 (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	GOL	C	1	-	5,5,5	0.45	0	5,5,5	0.76	0
3	GOL	D	1	-	5,5,5	0.35	0	5,5,5	0.23	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	C	1	-	-	0/4/4/4	0/0/0/0
3	GOL	D	1	-	-	0/4/4/4	0/0/0/0

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.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	1	GOL	3	0

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	120/164 (73%)	0.44	3 (2%) 61 70	17, 30, 57, 75	0
1	B	119/164 (72%)	0.41	4 (3%) 49 58	13, 28, 57, 68	0
2	C	163/170 (95%)	1.14	32 (19%) 1 2	19, 48, 137, 142	0
2	D	163/170 (95%)	1.39	35 (21%) 1 2	17, 53, 137, 141	0
All	All	565/668 (84%)	0.91	74 (13%) 5 7	13, 41, 131, 142	0

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	507	GLY	12.0
2	C	505	ARG	9.6
2	D	500	LEU	8.7
2	C	503	PHE	8.3
2	D	518	ASN	8.0
2	D	506	GLU	7.8
2	C	507	GLY	7.4
2	C	501	GLU	7.1
2	D	509	GLU	6.9
2	D	517	LEU	6.7
2	C	510	LYS	6.6
2	D	505	ARG	6.4
2	C	513	GLN	6.4
2	D	521	ARG	6.2
2	D	503	PHE	6.1
2	D	508	ASN	5.7
2	C	514	ARG	5.6
2	C	516	LEU	5.5
1	A	83	SER	5.4
2	D	512	MET	5.4
2	D	504	ARG	5.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	D	514	ARG	5.2
2	D	499	TYR	5.0
2	C	506	GLU	4.9
2	C	515	ILE	4.8
2	C	497	LYS	4.8
2	C	504	ARG	4.7
2	C	470	MET	4.6
2	C	511	GLU	4.4
2	D	495	SER	4.4
2	D	502	ARG	4.3
2	C	499	TYR	4.3
2	C	495	SER	4.2
2	D	510	LYS	4.1
1	A	84	VAL	4.0
2	D	430	GLU	3.9
2	D	496	SER	3.8
2	D	591	ILE	3.7
2	D	494	LYS	3.7
2	D	523	LYS	3.7
2	C	512	MET	3.6
2	C	498	GLU	3.6
1	B	138	PHE	3.6
2	C	430	GLU	3.6
2	D	525	ARG	3.5
2	D	490	GLN	3.5
2	C	508	ASN	3.2
2	D	429	LYS	3.1
2	C	522	LEU	3.1
2	D	466	GLN	3.0
2	C	502	ARG	2.9
2	D	529	ILE	2.8
2	D	562	MET	2.8
1	B	202	ALA	2.8
2	C	518	ASN	2.7
2	D	497	LYS	2.7
1	A	165	SER	2.6
2	D	589	LEU	2.6
2	C	509	GLU	2.6
2	D	501	GLU	2.5
2	D	470	MET	2.4
2	C	492	GLN	2.4
2	D	511	GLU	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	C	525	ARG	2.3
2	D	515	ILE	2.3
1	B	200	ARG	2.3
2	C	521	ARG	2.3
2	C	459	GLU	2.2
2	D	493	GLU	2.2
2	C	589	LEU	2.1
1	B	167	PRO	2.1
2	C	536	LEU	2.1
2	C	500	LEU	2.0
2	C	490	GLN	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, 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	LLDF	B-factors(Å^2)	Q<0.9
3	GOL	C	1	6/6	0.55	0.30	6.81	20,20,20,20	0
3	GOL	D	1	6/6	0.90	0.18	1.84	20,20,20,20	0

6.5 Other polymers (i)

There are no such residues in this entry.