



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:33 AM GMT

PDB ID : 3IVI
Title : Design and Synthesis of Potent BACE-1 Inhibitors with Cellular Activity:
Structure-Activity Relationship of P1 Substituents
Authors : Pan, H.
Deposited on : 2009-09-01
Resolution : 2.20 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
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

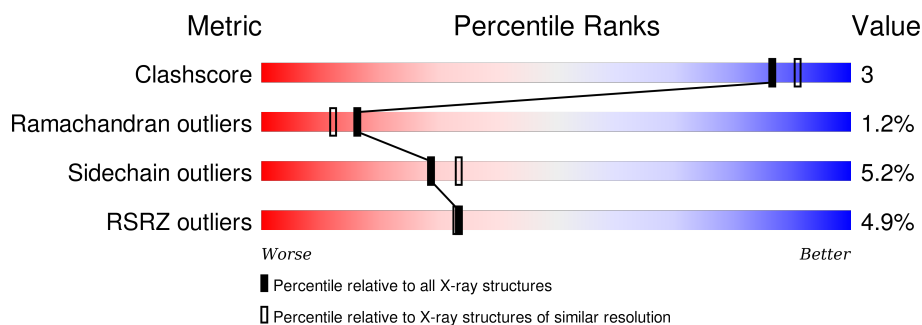
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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	406	<div> <div>3%</div> <div>82% 9% • 6%</div> </div>
1	B	406	<div> <div>4%</div> <div>84% 8% • 7%</div> </div>
1	C	406	<div> <div>6%</div> <div>83% 8% • 8%</div> </div>

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
2	SO4	A	899	-	-	-	X
2	SO4	B	899	-	-	-	X
2	SO4	C	899	-	-	-	X
3	GOL	A	901	-	-	-	X
3	GOL	B	901	-	-	-	X
3	GOL	C	901	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9299 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 Beta-secretase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	380	Total	C	N	O	S	0	0	0
			2991	1919	496	562	14			
1	B	378	Total	C	N	O	S	0	0	0
			2978	1910	494	560	14			
1	C	373	Total	C	N	O	S	0	0	0
			2936	1882	488	552	14			

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	56	MET	-	expression tag	UNP P56817
A	454	ARG	-	expression tag	UNP P56817
A	455	SER	-	expression tag	UNP P56817
A	456	HIS	-	expression tag	UNP P56817
A	457	HIS	-	expression tag	UNP P56817
A	458	HIS	-	expression tag	UNP P56817
A	459	HIS	-	expression tag	UNP P56817
A	460	HIS	-	expression tag	UNP P56817
A	461	HIS	-	expression tag	UNP P56817
B	56	MET	-	expression tag	UNP P56817
B	454	ARG	-	expression tag	UNP P56817
B	455	SER	-	expression tag	UNP P56817
B	456	HIS	-	expression tag	UNP P56817
B	457	HIS	-	expression tag	UNP P56817
B	458	HIS	-	expression tag	UNP P56817
B	459	HIS	-	expression tag	UNP P56817
B	460	HIS	-	expression tag	UNP P56817
B	461	HIS	-	expression tag	UNP P56817
C	56	MET	-	expression tag	UNP P56817
C	454	ARG	-	expression tag	UNP P56817
C	455	SER	-	expression tag	UNP P56817
C	456	HIS	-	expression tag	UNP P56817
C	457	HIS	-	expression tag	UNP P56817

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Chain	Residue	Modelled	Actual	Comment	Reference
C	458	HIS	-	expression tag	UNP P56817
C	459	HIS	-	expression tag	UNP P56817
C	460	HIS	-	expression tag	UNP P56817
C	461	HIS	-	expression tag	UNP P56817

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



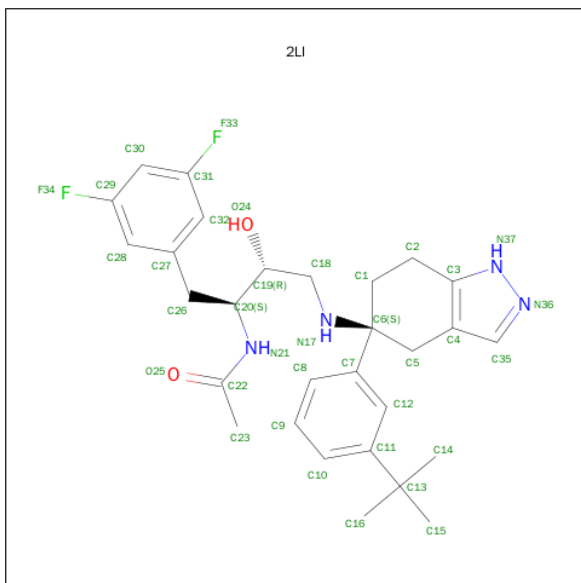
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

- Molecule 4 is N-[(1S,2R)-3-{[(5S)-5-(3-TERT-BUTYLPHENYL)-4,5,6,7-TETRAHYDRO-1H-INDAZOL-5-YL]AMINO}-1-(3,5-DIFLUOROBENZYL)-2-HYDROXYPROPYL]ACETAMIDE (three-letter code: 2LI) (formula: C₂₉H₃₆F₂N₄O₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	F	N	O	0	0
			37	29	2	4	2		
4	B	1	Total	C	F	N	O	0	0
			37	29	2	4	2		
4	C	1	Total	C	F	N	O	0	0
			37	29	2	4	2		

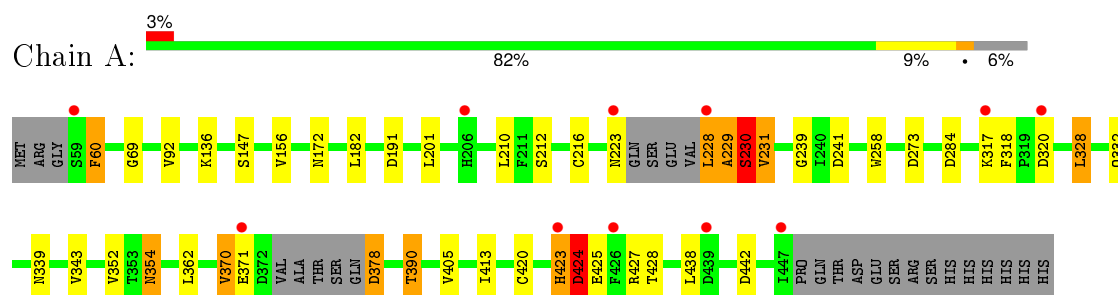
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	91	Total	O	0	0
			91	91		
5	B	82	Total	O	0	0
			82	82		
5	C	62	Total	O	0	0
			62	62		

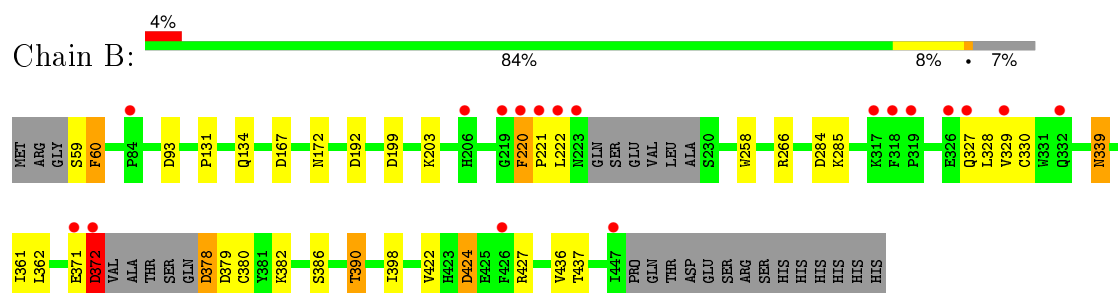
3 Residue-property plots [i](#)

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 ($\text{RSRZ} > 2$). 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.

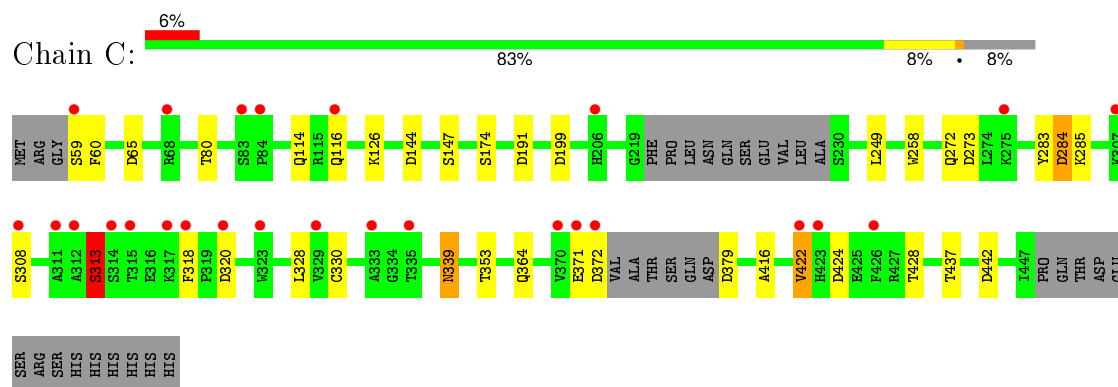
• Molecule 1: Beta-secretase 1



• Molecule 1: Beta-secretase 1



• Molecule 1: Beta-secretase 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	82.71Å 104.48Å 100.62Å 90.00° 104.83° 90.00°	Depositor
Resolution (Å)	95.35 – 2.20 55.22 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.2 (95.35-2.20) 99.3 (55.22-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.1.25	Depositor
R, R_{free}	0.195 , 0.229 0.203 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	44.0	Xtriage
Anisotropy	0.425	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 41.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 83371 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9299	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.65% 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, 0.375 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, 2LI, SO4

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	0.47	0/3067	0.81	8/4167 (0.2%)
1	B	0.47	0/3054	0.81	8/4149 (0.2%)
1	C	0.49	1/3010 (0.0%)	0.79	9/4088 (0.2%)
All	All	0.48	1/9131 (0.0%)	0.80	25/12404 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	313	SER	CB-OG	6.00	1.50	1.42

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	192	ASP	CB-CG-OD2	7.88	125.40	118.30
1	B	199	ASP	CB-CG-OD2	6.65	124.28	118.30
1	A	378	ASP	CB-CG-OD2	6.52	124.17	118.30
1	A	442	ASP	CB-CG-OD2	6.17	123.86	118.30
1	B	167	ASP	CB-CG-OD2	6.16	123.84	118.30
1	C	191	ASP	CB-CG-OD2	6.13	123.82	118.30
1	C	144	ASP	CB-CG-OD2	5.89	123.60	118.30
1	A	424	ASP	CB-CG-OD2	5.79	123.52	118.30
1	A	423	HIS	N-CA-C	5.67	126.31	111.00
1	C	65	ASP	CB-CG-OD2	5.66	123.39	118.30
1	B	424	ASP	CB-CG-OD2	5.53	123.27	118.30
1	B	372	ASP	CB-CG-OD2	5.49	123.24	118.30
1	C	320	ASP	CB-CG-OD2	5.37	123.14	118.30
1	C	379	ASP	CB-CG-OD2	5.35	123.11	118.30
1	B	93	ASP	CB-CG-OD2	5.32	123.09	118.30
1	C	442	ASP	CB-CG-OD2	5.28	123.05	118.30
1	C	372	ASP	CB-CG-OD2	5.26	123.04	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	320	ASP	CB-CG-OD2	5.25	123.03	118.30
1	C	273	ASP	CB-CG-OD2	5.15	122.94	118.30
1	C	199	ASP	CB-CG-OD2	5.15	122.93	118.30
1	A	273	ASP	CB-CG-OD2	5.14	122.93	118.30
1	B	379	ASP	CB-CG-OD2	5.10	122.89	118.30
1	A	241	ASP	CB-CG-OD2	5.07	122.86	118.30
1	A	191	ASP	CB-CG-OD2	5.04	122.83	118.30
1	B	378	ASP	CB-CG-OD2	5.01	122.81	118.30

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	2991	0	2909	18	0
1	B	2978	0	2891	16	0
1	C	2936	0	2854	10	0
2	A	10	0	0	0	0
2	B	10	0	0	0	0
2	C	10	0	0	0	0
3	A	6	0	8	0	0
3	B	6	0	8	0	0
3	C	6	0	8	0	0
4	A	37	0	36	1	0
4	B	37	0	36	2	0
4	C	37	0	36	1	0
5	A	91	0	0	0	0
5	B	82	0	0	0	0
5	C	62	0	0	0	0
All	All	9299	0	8786	44	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 3.

All (44) 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:69:GLY:O	1:A:230:SER:O	2.11	0.69
1:B:285:LYS:NZ	4:B:2:2LI:HN37	2.01	0.58
1:B:220:PHE:CB	1:B:221:PRO:CD	2.82	0.58
1:A:423:HIS:CG	1:A:424:ASP:H	2.27	0.52
1:C:364:GLN:NE2	1:C:424:ASP:OD2	2.42	0.52
1:A:423:HIS:CG	1:A:424:ASP:N	2.78	0.52
1:C:249:LEU:HD23	1:C:416:ALA:HB2	1.91	0.52
1:B:285:LYS:HZ1	4:B:2:2LI:HN37	1.57	0.52
1:A:390:THR:OG1	4:A:1:2LI:N36	2.39	0.51
1:A:216:CYS:HG	1:A:420:CYS:CB	2.22	0.51
1:B:220:PHE:CB	1:B:221:PRO:HD3	2.42	0.50
1:B:220:PHE:HB2	1:B:221:PRO:CD	2.43	0.49
1:A:328:LEU:CD2	1:A:370:VAL:HG21	2.43	0.49
1:B:266:ARG:NH2	1:B:437:THR:HG22	2.28	0.48
1:A:228:LEU:O	1:A:229:ALA:HB2	2.14	0.48
1:C:114:GLN:HE21	1:C:116:GLN:HE22	1.61	0.48
1:B:220:PHE:HB3	1:B:221:PRO:HD3	1.95	0.47
1:B:339:ASN:HD22	1:B:339:ASN:H	1.62	0.47
1:B:59:SER:OG	1:B:60:PHE:N	2.48	0.46
1:C:114:GLN:NE2	1:C:116:GLN:HE22	2.13	0.46
1:B:390:THR:O	1:B:390:THR:OG1	2.34	0.46
1:A:390:THR:O	1:A:390:THR:OG1	2.33	0.46
1:A:352:VAL:HG12	1:A:354:ASN:ND2	2.32	0.44
1:C:285:LYS:NZ	4:C:3:2LI:HN37	2.16	0.43
1:A:156:VAL:HG11	1:A:201:LEU:HA	1.99	0.43
1:C:339:ASN:HD22	1:C:339:ASN:N	2.16	0.43
1:C:80:THR:OG1	1:C:147:SER:HB2	2.17	0.43
1:C:313:SER:HG	1:C:318:PHE:HE1	1.65	0.43
1:A:60:PHE:CZ	1:A:239:GLY:HA3	2.54	0.42
1:B:371:GLU:O	1:B:372:ASP:C	2.57	0.42
1:C:364:GLN:HB3	1:C:422:VAL:HG11	2.01	0.42
1:B:362:LEU:HD12	1:B:422:VAL:HG23	2.02	0.41
1:B:330:CYS:SG	1:B:380:CYS:SG	3.01	0.41
1:A:405:VAL:O	1:A:413:ILE:HA	2.21	0.41
1:A:370:VAL:HG23	1:A:371:GLU:N	2.35	0.41
1:C:283:TYR:O	1:C:284:ASP:CB	2.67	0.41
1:A:92:VAL:HG13	1:A:182:LEU:HD11	2.01	0.41
1:A:230:SER:O	1:A:231:VAL:HG22	2.21	0.41
1:B:424:ASP:HB3	1:B:427:ARG:O	2.20	0.41
1:B:339:ASN:HD22	1:B:339:ASN:N	2.18	0.41
1:A:328:LEU:HD23	1:A:370:VAL:HG21	2.03	0.41
1:B:361:ILE:HD13	1:B:398:ILE:HD12	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:424:ASP:HB3	1:A:427:ARG:O	2.21	0.40
1:A:343:VAL:HG12	1:A:362:LEU:HD22	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	374/406 (92%)	353 (94%)	14 (4%)	7 (2%)	10	6
1	B	372/406 (92%)	357 (96%)	11 (3%)	4 (1%)	17	14
1	C	367/406 (90%)	352 (96%)	13 (4%)	2 (0%)	34	35
All	All	1113/1218 (91%)	1062 (95%)	38 (3%)	13 (1%)	16	12

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	230	SER
1	A	284	ASP
1	A	424	ASP
1	B	220	PHE
1	B	284	ASP
1	C	284	ASP
1	A	60	PHE
1	A	229	ALA
1	A	231	VAL
1	B	60	PHE
1	C	60	PHE
1	B	131	PRO
1	A	370	VAL

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	324/348 (93%)	304 (94%)	20 (6%)	23	25
1	B	323/348 (93%)	308 (95%)	15 (5%)	33	40
1	C	318/348 (91%)	303 (95%)	15 (5%)	32	39
All	All	965/1044 (92%)	915 (95%)	50 (5%)	29	33

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	136	LYS
1	A	147	SER
1	A	172	ASN
1	A	210	LEU
1	A	212	SER
1	A	223	ASN
1	A	228	LEU
1	A	230	SER
1	A	258	TRP
1	A	317	LYS
1	A	318	PHE
1	A	328	LEU
1	A	332	GLN
1	A	339	ASN
1	A	354	ASN
1	A	378	ASP
1	A	390	THR
1	A	425	GLU
1	A	428	THR
1	A	438	LEU
1	B	134	GLN
1	B	172	ASN
1	B	203	LYS
1	B	222	LEU
1	B	258	TRP
1	B	327	GLN

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Mol	Chain	Res	Type
1	B	328	LEU
1	B	329	VAL
1	B	339	ASN
1	B	372	ASP
1	B	378	ASP
1	B	382	LYS
1	B	386	SER
1	B	390	THR
1	B	436	VAL
1	C	59	SER
1	C	126	LYS
1	C	174	SER
1	C	258	TRP
1	C	272	GLN
1	C	308	SER
1	C	313	SER
1	C	328	LEU
1	C	330	CYS
1	C	339	ASN
1	C	353	THR
1	C	371	GLU
1	C	422	VAL
1	C	428	THR
1	C	437	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	172	ASN
1	A	339	ASN
1	A	354	ASN
1	A	446	ASN
1	B	159	ASN
1	B	172	ASN
1	B	339	ASN
1	B	354	ASN
1	C	110	HIS
1	C	114	GLN
1	C	159	ASN
1	C	339	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 ⓘ

12 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$
4	2LI	A	1	-	37,40,40	1.09	1 (2%)	43,59,59	1.46	9 (20%)
2	SO4	A	899	-	4,4,4	0.21	0	6,6,6	0.10	0
2	SO4	A	900	-	4,4,4	0.42	0	6,6,6	0.18	0
3	GOL	A	901	-	5,5,5	0.33	0	5,5,5	0.34	0
4	2LI	B	2	-	37,40,40	0.96	1 (2%)	43,59,59	1.34	6 (13%)
2	SO4	B	899	-	4,4,4	0.16	0	6,6,6	0.18	0
2	SO4	B	900	-	4,4,4	0.32	0	6,6,6	0.52	0
3	GOL	B	901	-	5,5,5	0.36	0	5,5,5	0.29	0
4	2LI	C	3	-	37,40,40	0.95	1 (2%)	43,59,59	1.29	7 (16%)
2	SO4	C	899	-	4,4,4	0.21	0	6,6,6	0.07	0
2	SO4	C	900	-	4,4,4	0.23	0	6,6,6	0.39	0
3	GOL	C	901	-	5,5,5	0.33	0	5,5,5	0.28	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
4	2LI	A	1	-	-	0/29/41/41	0/4/4/4
2	SO4	A	899	-	-	0/0/0/0	0/0/0/0
2	SO4	A	900	-	-	0/0/0/0	0/0/0/0
3	GOL	A	901	-	-	0/4/4/4	0/0/0/0
4	2LI	B	2	-	-	0/29/41/41	0/4/4/4
2	SO4	B	899	-	-	0/0/0/0	0/0/0/0
2	SO4	B	900	-	-	0/0/0/0	0/0/0/0
3	GOL	B	901	-	-	0/4/4/4	0/0/0/0
4	2LI	C	3	-	-	0/29/41/41	0/4/4/4
2	SO4	C	899	-	-	0/0/0/0	0/0/0/0
2	SO4	C	900	-	-	0/0/0/0	0/0/0/0
3	GOL	C	901	-	-	0/4/4/4	0/0/0/0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	3	2LI	C4-C3	4.32	1.47	1.41
4	B	2	2LI	C4-C3	4.50	1.47	1.41
4	A	1	2LI	C4-C3	4.55	1.47	1.41

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	2	2LI	C27-C26-C20	-3.58	107.79	113.48
4	C	3	2LI	C1-C2-C3	-3.22	106.66	112.30
4	A	1	2LI	C32-C31-C30	-2.64	120.03	123.52
4	B	2	2LI	C30-C29-C28	-2.36	120.41	123.52
4	C	3	2LI	C27-C26-C20	-2.34	109.75	113.48
4	B	2	2LI	C32-C31-C30	-2.30	120.48	123.52
4	B	2	2LI	C1-C2-C3	-2.29	108.29	112.30
4	A	1	2LI	C1-C2-C3	-2.18	108.48	112.30
4	C	3	2LI	C30-C29-C28	-2.15	120.69	123.52
4	A	1	2LI	C5-C4-C35	-2.12	127.74	131.84
4	C	3	2LI	C32-C31-C30	-2.07	120.79	123.52
4	A	1	2LI	C26-C20-N21	-2.00	107.95	110.14
4	C	3	2LI	F34-C29-C28	2.08	120.99	118.22
4	A	1	2LI	C19-C20-N21	2.11	113.13	109.73
4	A	1	2LI	C18-N17-C6	2.12	120.78	116.86
4	B	2	2LI	C31-C30-C29	2.21	119.45	116.07
4	A	1	2LI	F33-C31-C30	2.24	121.20	118.22
4	B	2	2LI	C18-N17-C6	2.29	121.11	116.86
4	C	3	2LI	C19-C18-N17	2.71	113.96	110.61
4	C	3	2LI	C18-N17-C6	3.03	122.48	116.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1	2LI	C19-C18-N17	3.33	114.72	110.61
4	A	1	2LI	C27-C32-C31	3.35	121.63	118.84

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1	2LI	1	0
4	B	2	2LI	2	0
4	C	3	2LI	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

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	380/406 (93%)	0.20	11 (2%) 55 54	27, 35, 49, 58	0
1	B	378/406 (93%)	0.44	18 (4%) 34 34	26, 35, 48, 70	0
1	C	373/406 (91%)	0.40	26 (6%) 19 19	27, 36, 47, 64	0
All	All	1131/1218 (92%)	0.34	55 (4%) 33 33	26, 35, 48, 70	0

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	447	ILE	8.9
1	A	447	ILE	7.1
1	B	221	PRO	6.6
1	B	220	PHE	5.3
1	C	423	HIS	5.2
1	C	371	GLU	5.0
1	C	320	ASP	4.9
1	C	315	THR	4.7
1	B	317	LYS	4.2
1	B	372	ASP	4.0
1	A	426	PHE	3.9
1	B	219	GLY	3.9
1	B	371	GLU	3.8
1	A	59	SER	3.8
1	C	370	VAL	3.5
1	C	311	ALA	3.4
1	A	423	HIS	3.2
1	A	228	LEU	3.1
1	B	222	LEU	3.1
1	C	59	SER	3.1
1	B	426	PHE	3.1
1	C	372	ASP	3.1
1	C	206	HIS	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	307	LYS	3.0
1	C	329	VAL	2.9
1	B	84	PRO	2.8
1	C	422	VAL	2.8
1	B	327	GLN	2.7
1	C	275	LYS	2.6
1	A	317	LYS	2.6
1	C	314	SER	2.5
1	B	318	PHE	2.5
1	B	223	ASN	2.4
1	C	426	PHE	2.4
1	C	84	PRO	2.4
1	A	371	GLU	2.4
1	C	323	TRP	2.4
1	B	332	GLN	2.4
1	B	326	GLU	2.3
1	C	83	SER	2.3
1	B	319	PRO	2.3
1	C	318	PHE	2.3
1	A	206	HIS	2.3
1	B	206	HIS	2.2
1	C	317	LYS	2.2
1	B	329	VAL	2.2
1	C	308	SER	2.1
1	C	68	ARG	2.1
1	C	116	GLN	2.1
1	A	439	ASP	2.1
1	A	223	ASN	2.1
1	C	335	THR	2.1
1	C	333	ALA	2.1
1	A	320	ASP	2.0
1	C	312	ALA	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
3	GOL	A	901	6/6	0.81	0.33	12.67	84,85,86,86	0
2	SO4	A	899	5/5	0.94	0.32	11.56	101,102,102,102	0
3	GOL	C	901	6/6	0.79	0.32	10.74	87,87,87,88	0
3	GOL	B	901	6/6	0.83	0.26	8.30	80,81,82,83	0
2	SO4	C	899	5/5	0.90	0.30	7.15	108,108,108,108	0
2	SO4	B	899	5/5	0.97	0.28	4.99	98,98,99,99	0
4	2LI	B	2	37/37	0.96	0.15	0.21	41,45,53,54	0
4	2LI	A	1	37/37	0.95	0.15	0.01	39,42,52,56	0
4	2LI	C	3	37/37	0.96	0.14	-0.08	40,44,55,57	0
2	SO4	A	900	5/5	0.97	0.12	-0.65	64,64,64,67	0
2	SO4	B	900	5/5	0.97	0.13	-1.37	67,67,68,69	0
2	SO4	C	900	5/5	0.95	0.11	-2.17	65,65,68,69	0

6.5 Other polymers [i](#)

There are no such residues in this entry.