



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:39 AM UTC

PDB ID : 4XAQ / pdb_00004xaq
Title : mGluR2 ECD and mGluR3 ECD with ligands
Authors : Clawson, D.K.
Deposited on : 2014-12-15
Resolution : 2.21 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

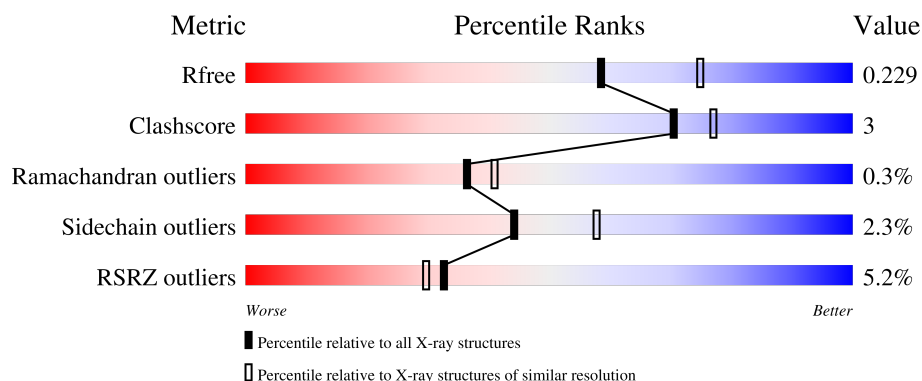
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.21 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}	180053	7682 (2.24-2.20)
Clashscore	190562	8402 (2.24-2.20)
Ramachandran outliers	187476	8303 (2.24-2.20)
Sidechain outliers	187428	8304 (2.24-2.20)
RSRZ outliers	180081	7683 (2.24-2.20)

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 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	503	6% 79% 9% 12%
1	B	503	3% 77% 11% 12%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7532 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 Metabotropic glutamate receptor 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	443	Total	C	N	O	S	0	0	0
			3475	2206	623	633	13			
1	B	442	Total	C	N	O	S	0	4	0
			3491	2215	624	639	13			

There are 26 discrepancies between the modelled and reference sequences:

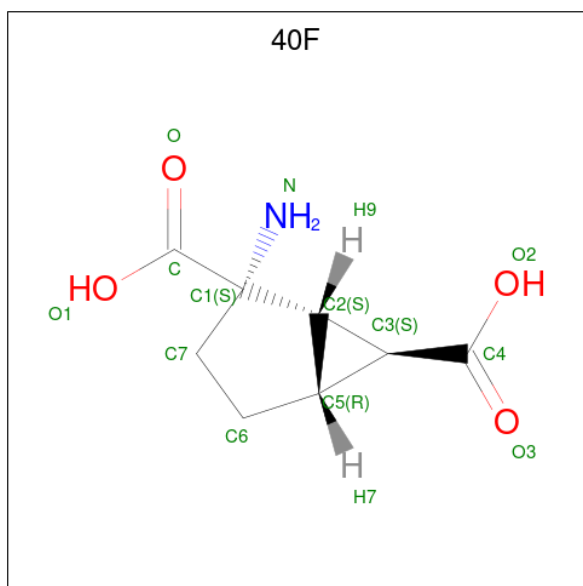
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	initiating methionine	UNP Q14416
A	0	ALA	-	expression tag	UNP Q14416
A	1	LEU	-	expression tag	UNP Q14416
A	234	SER	CYS	conflict	UNP Q14416
A	302	GLU	SER	conflict	UNP Q14416
A	494	GLU	-	expression tag	UNP Q14416
A	495	GLY	-	expression tag	UNP Q14416
A	496	HIS	-	expression tag	UNP Q14416
A	497	HIS	-	expression tag	UNP Q14416
A	498	HIS	-	expression tag	UNP Q14416
A	499	HIS	-	expression tag	UNP Q14416
A	500	HIS	-	expression tag	UNP Q14416
A	501	HIS	-	expression tag	UNP Q14416
B	-1	MET	-	initiating methionine	UNP Q14416
B	0	ALA	-	expression tag	UNP Q14416
B	1	LEU	-	expression tag	UNP Q14416
B	234	SER	CYS	conflict	UNP Q14416
B	302	GLU	SER	conflict	UNP Q14416
B	494	GLU	-	expression tag	UNP Q14416
B	495	GLY	-	expression tag	UNP Q14416
B	496	HIS	-	expression tag	UNP Q14416
B	497	HIS	-	expression tag	UNP Q14416
B	498	HIS	-	expression tag	UNP Q14416
B	499	HIS	-	expression tag	UNP Q14416
B	500	HIS	-	expression tag	UNP Q14416

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Chain	Residue	Modelled	Actual	Comment	Reference
B	501	HIS	-	expression tag	UNP Q14416

- Molecule 2 is (1S,2S,5R,6S)-2-aminobicyclo[3.1.0]hexane-2,6-dicarboxylic acid (CCD ID: 40F) (formula: C₈H₁₁NO₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			13	8	1	4		
2	B	1	Total	C	N	O	0	0
			13	8	1	4		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Cl	0	0
			2	2		
4	B	1	Total	Cl	0	0
			1	1		

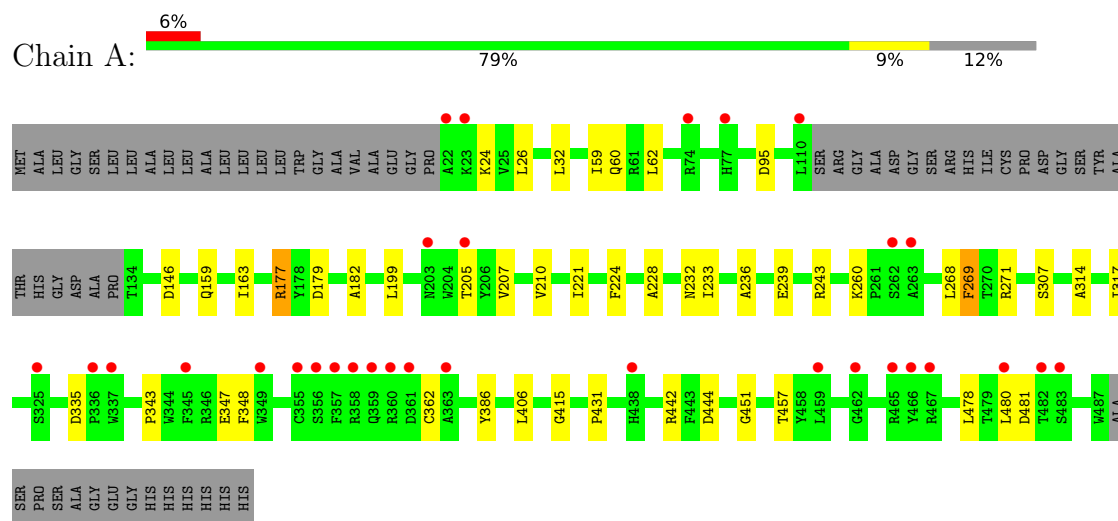
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	226	Total	O	0	0
			226	226		
5	B	301	Total	O	0	0
			301	301		

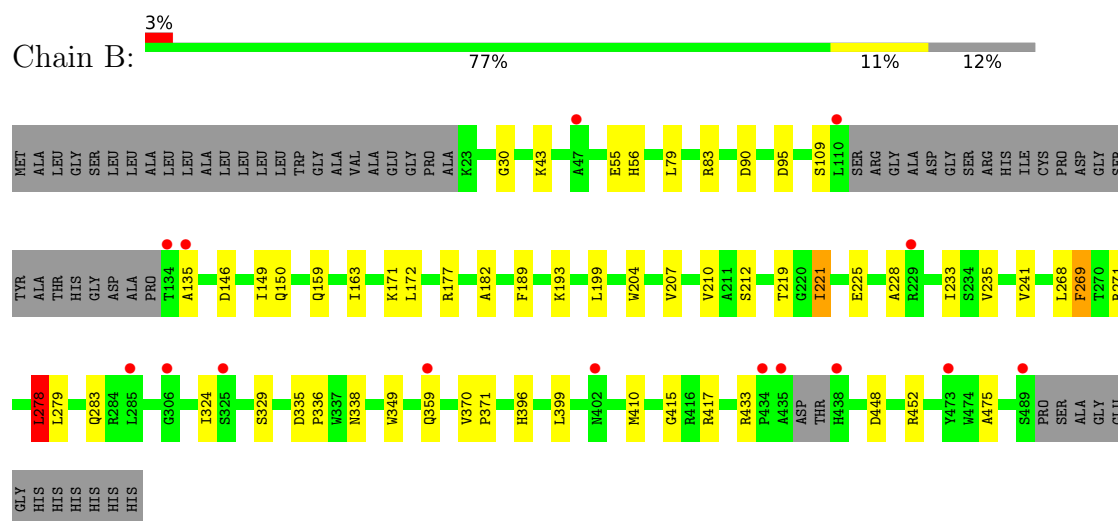
3 Residue-property plots [i](#)

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: Metabotropic glutamate receptor 2



• Molecule 1: Metabotropic glutamate receptor 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	81.64Å 159.65Å 93.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.52 – 2.21 25.52 – 2.21	Depositor EDS
% Data completeness (in resolution range)	99.6 (25.52-2.21) 99.5 (25.52-2.21)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.33 (at 2.22Å)	Xtriage
Refinement program	BUSTER-TNT BUSTER 2.11.5	Depositor
R, R_{free}	0.186 , 0.225 0.193 , 0.229	Depositor DCC
R_{free} test set	1898 reflections (3.06%)	wwPDB-VP
Wilson B-factor (Å ²)	36.1	Xtriage
Anisotropy	0.612	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 58.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7532	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.93% 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: 40F, SO4, 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	0.85	0/3559	1.25	12/4824 (0.2%)
1	B	0.89	1/3573 (0.0%)	1.24	9/4842 (0.2%)
All	All	0.87	1/7132 (0.0%)	1.25	21/9666 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	79	LEU	CA-C	7.93	1.58	1.53

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	224	PHE	CA-C-N	6.28	128.70	120.28
1	A	224	PHE	C-N-CA	6.28	128.70	120.28
1	B	55	GLU	CB-CG-CD	6.08	122.94	112.60
1	A	362	CYS	CA-C-N	6.03	128.68	120.54
1	A	362	CYS	C-N-CA	6.03	128.68	120.54
1	B	90	ASP	CA-CB-CG	5.90	118.50	112.60
1	A	362	CYS	N-CA-C	-5.62	105.24	111.36
1	B	146	ASP	CA-CB-CG	5.53	118.13	112.60
1	B	283	GLN	CA-C-N	5.43	127.55	120.28
1	B	283	GLN	C-N-CA	5.43	127.55	120.28
1	B	448	ASP	CA-CB-CG	5.41	118.01	112.60
1	A	146	ASP	CA-CB-CG	5.24	117.84	112.60
1	A	481	ASP	CA-C-N	5.21	127.99	120.38
1	A	481	ASP	C-N-CA	5.21	127.99	120.38
1	B	278	LEU	CA-C-N	5.20	127.20	120.44
1	B	278	LEU	C-N-CA	5.20	127.20	120.44
1	A	444	ASP	CA-CB-CG	5.20	117.80	112.60
1	B	271	ARG	N-CA-C	-5.17	103.21	110.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	307	SER	CA-C-N	5.16	127.50	120.54
1	A	307	SER	C-N-CA	5.16	127.50	120.54
1	A	179	ASP	CA-CB-CG	5.14	117.74	112.60

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	3475	0	3362	20	0
1	B	3491	0	3368	28	0
2	A	13	0	8	0	0
2	B	13	0	8	0	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	2	0	0	1	0
4	B	1	0	0	0	0
5	A	226	0	0	1	0
5	B	301	0	0	2	0
All	All	7532	0	6746	47	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 (47) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:399:LEU:HD21	1:B:417:ARG:HH22	1.49	0.75
1:B:95:ASP:HB2	1:B:150:GLN:HG3	1.79	0.65
1:A:221:ILE:HG12	1:A:269:PHE:HB2	1.79	0.64
1:A:210:VAL:HB	1:A:268:LEU:HD22	1.83	0.59
1:B:199:LEU:HD13	1:B:207:VAL:HG11	1.85	0.58
1:A:236:ALA:HB1	1:A:260:LYS:HG2	1.85	0.58
1:B:56:HIS:HD2	5:B:828:HOH:O	1.87	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:24:LYS:HD3	1:A:343:PRO:HB2	1.87	0.57
1:B:210:VAL:HG11	1:B:278:LEU:HD11	1.89	0.55
1:A:199:LEU:HD13	1:A:207:VAL:HG11	1.89	0.54
1:B:370:VAL:HB	1:B:371:PRO:CD	2.36	0.54
1:A:478:LEU:HD11	1:A:480:LEU:HD23	1.91	0.53
1:B:210:VAL:HB	1:B:268:LEU:HD22	1.92	0.51
1:A:26:LEU:HD13	1:A:62:LEU:HD11	1.92	0.51
1:B:336:PRO:HG3	1:B:349:TRP:CD2	2.47	0.49
1:A:32:LEU:HG	1:A:406:LEU:HD11	1.94	0.49
1:B:56:HIS:CD2	5:B:828:HOH:O	2.64	0.48
1:A:271:ARG:HB3	4:A:604:CL:CL	2.50	0.48
1:B:225:GLU:HG2	1:B:235:VAL:HG21	1.95	0.47
1:A:386:TYR:CG	1:A:431:PRO:HG3	2.50	0.47
5:A:818:HOH:O	1:B:177:ARG:HD2	2.14	0.46
1:B:171:LYS:HE3	1:B:219:THR:HG21	1.98	0.46
1:B:199:LEU:HD22	1:B:204:TRP:HE3	1.81	0.45
1:A:95:ASP:CG	1:A:243:ARG:HH22	2.24	0.45
1:A:177:ARG:HH11	1:A:177:ARG:HB3	1.80	0.45
1:B:370:VAL:HB	1:B:371:PRO:HD2	1.98	0.45
1:B:149:ILE:HG13	1:B:172:LEU:HD21	1.98	0.45
1:B:452:ARG:HH11	1:B:475:ALA:HB1	1.82	0.45
1:B:396:HIS:HD2	1:B:410:MET:HE2	1.82	0.44
1:B:212:SER:HA	1:B:241:VAL:HG23	1.99	0.44
1:B:163:ILE:HA	1:B:182:ALA:O	2.18	0.43
1:A:243:ARG:CZ	1:B:177:ARG:HD3	2.48	0.43
1:B:335:ASP:HB3	1:B:338[A]:ASN:CG	2.43	0.42
1:A:210:VAL:HG22	1:A:239:GLU:HB2	2.02	0.42
1:B:228:ALA:HB1	1:B:233:ILE:HB	2.02	0.42
1:A:205:THR:HG23	1:A:232:ASN:O	2.20	0.41
1:B:30:GLY:HA2	1:B:83:ARG:HG2	2.01	0.41
1:B:396:HIS:HB2	1:B:410:MET:HE1	2.03	0.41
1:B:189:PHE:CE2	1:B:193:LYS:HE2	2.56	0.41
1:A:59:ILE:HG13	1:A:348:PHE:HB2	2.02	0.41
1:A:163:ILE:HA	1:A:182:ALA:O	2.20	0.41
1:A:228:ALA:HB1	1:A:233:ILE:HB	2.03	0.41
1:A:159:GLN:O	1:A:415:GLY:HA3	2.21	0.41
1:A:314:ALA:O	1:A:457:THR:HA	2.21	0.41
1:B:221:ILE:HD13	1:B:269:PHE:HB2	2.03	0.41
1:B:159:GLN:O	1:B:415:GLY:HA3	2.21	0.40
1:B:396:HIS:CD2	1:B:410:MET:HE2	2.56	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	439/503 (87%)	420 (96%)	18 (4%)	1 (0%)	43	50
1	B	440/503 (88%)	424 (96%)	14 (3%)	2 (0%)	24	26
All	All	879/1006 (87%)	844 (96%)	32 (4%)	3 (0%)	36	41

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	135	ALA
1	B	109	SER
1	A	451	GLY

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	353/402 (88%)	346 (98%)	7 (2%)	48	63
1	B	355/402 (88%)	346 (98%)	9 (2%)	42	55
All	All	708/804 (88%)	692 (98%)	16 (2%)	44	58

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	60	GLN
1	A	177	ARG
1	A	269	PHE

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Mol	Chain	Res	Type
1	A	317	ILE
1	A	335	ASP
1	A	347	GLU
1	A	442	ARG
1	B	43	LYS
1	B	221	ILE
1	B	269	PHE
1	B	278	LEU
1	B	279	LEU
1	B	324	ILE
1	B	329	SER
1	B	359	GLN
1	B	433	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	150	GLN
1	A	283	GLN
1	A	351	GLN
1	A	359	GLN
1	A	439	ASN
1	B	283	GLN
1	B	351	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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 7 ligands modelled in this entry, 3 are monoatomic - leaving 4 for Mogul analysis.

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
2	40F	A	601	-	11,14,14	1.82	2 (18%)	10,23,23	1.96	3 (30%)
3	SO4	A	602	-	4,4,4	0.25	0	6,6,6	0.26	0
2	40F	B	601	-	11,14,14	2.09	4 (36%)	10,23,23	2.30	5 (50%)
3	SO4	B	602	-	4,4,4	0.29	0	6,6,6	0.16	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
2	40F	A	601	-	-	2/8/31/31	0/2/2/2
2	40F	B	601	-	-	4/8/31/31	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	40F	O3-C4	4.56	1.35	1.22
2	A	601	40F	O-C	4.24	1.35	1.22
2	B	601	40F	C7-C1	3.40	1.58	1.54
2	B	601	40F	O2-C4	-2.65	1.22	1.30
2	B	601	40F	C3-C4	-2.23	1.46	1.51
2	A	601	40F	O1-C	-2.14	1.22	1.30

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	40F	O1-C-C1	4.59	125.47	113.53
2	B	601	40F	O2-C4-C3	4.13	125.78	113.91
2	B	601	40F	C6-C7-C1	3.11	107.58	103.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	40F	O2-C4-O3	-2.78	117.77	124.08
2	B	601	40F	O1-C-O	-2.55	115.69	123.86
2	B	601	40F	O3-C4-C3	-2.51	116.42	122.84
2	A	601	40F	C6-C7-C1	2.36	106.53	103.27
2	A	601	40F	O1-C-O	-2.35	116.34	123.86

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	601	40F	O1-C-C1-C7
2	B	601	40F	O-C-C1-C7
2	B	601	40F	O1-C-C1-C2
2	B	601	40F	O-C-C1-C2
2	A	601	40F	C2-C3-C4-O2
2	A	601	40F	O-C-C1-C2

There are no ring outliers.

No monomer is involved in short contacts.

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	443/503 (88%)	0.44	31 (6%)	22 19	23, 45, 76, 118	0
1	B	442/503 (87%)	0.06	15 (3%)	48 45	17, 38, 65, 102	4 (0%)
All	All	885/1006 (87%)	0.25	46 (5%)	33 30	17, 42, 73, 118	4 (0%)

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	22	ALA	4.8
1	B	438	HIS	4.4
1	B	110	LEU	4.2
1	B	435	ALA	4.2
1	A	482	THR	3.9
1	A	110	LEU	3.8
1	A	359	GLN	3.6
1	A	337	TRP	3.5
1	A	465	ARG	3.3
1	A	459	LEU	3.2
1	B	434	PRO	3.2
1	A	363	ALA	3.1
1	A	358	ARG	3.0
1	A	355	CYS	3.0
1	A	480	LEU	2.9
1	A	361	ASP	2.9
1	B	134	THR	2.8
1	A	325	SER	2.7
1	B	489	SER	2.6
1	A	262	SER	2.6
1	A	74	ARG	2.5
1	A	438	HIS	2.4
1	B	47	ALA	2.4
1	B	229	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	467	ARG	2.4
1	A	263	ALA	2.4
1	B	306	GLY	2.4
1	A	357	PHE	2.4
1	B	285	LEU	2.3
1	A	203	ASN	2.3
1	A	23	LYS	2.3
1	B	359	GLN	2.3
1	A	483	SER	2.3
1	A	345	PHE	2.2
1	A	205	THR	2.2
1	B	325	SER	2.2
1	A	77	HIS	2.2
1	A	349	TRP	2.2
1	B	402	ASN	2.2
1	A	466	TYR	2.1
1	A	462	GLY	2.1
1	B	135	ALA	2.1
1	A	356	SER	2.1
1	A	336	PRO	2.1
1	B	473	TYR	2.1
1	A	360	ARG	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 oligosaccharides 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(Å ²)	Q<0.9
3	SO4	B	602	5/5	0.91	0.09	60,61,65,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	SO4	A	602	5/5	0.92	0.10	67,69,71,73	0
4	CL	A	604	1/1	0.94	0.11	68,68,68,68	0
2	40F	B	601	13/13	0.97	0.06	20,23,26,27	0
2	40F	A	601	13/13	0.97	0.06	25,29,33,34	0
4	CL	A	603	1/1	0.98	0.05	35,35,35,35	0
4	CL	B	603	1/1	0.99	0.05	28,28,28,28	0

6.5 Other polymers [i](#)

There are no such residues in this entry.