



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 10:01 AM UTC

PDB ID : 6BR8 / pdb_00006br8
Title : Structure of A6 reveals a novel lipid transporter
Authors : Deng, J.; Peng, S.; Pathak, P.
Deposited on : 2017-11-30
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

<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
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

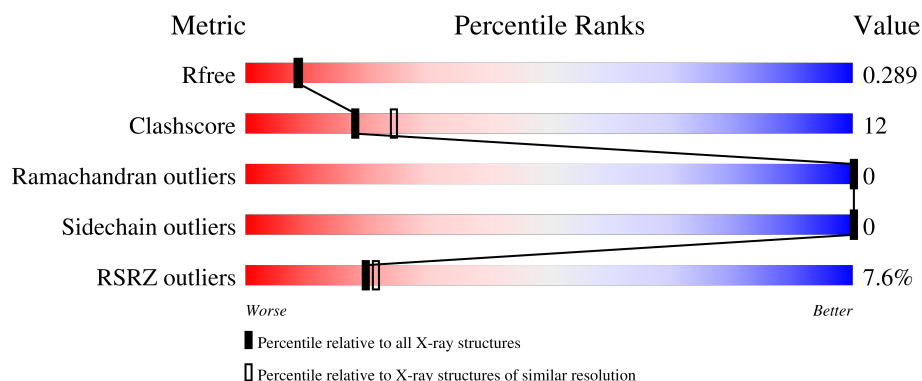
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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))
R_{free}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (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 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	252	8% 75% 23%
1	B	252	7% 77% 22%

2 Entry composition ⓘ

There are 4 unique types of molecules in this entry. The entry contains 4618 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.

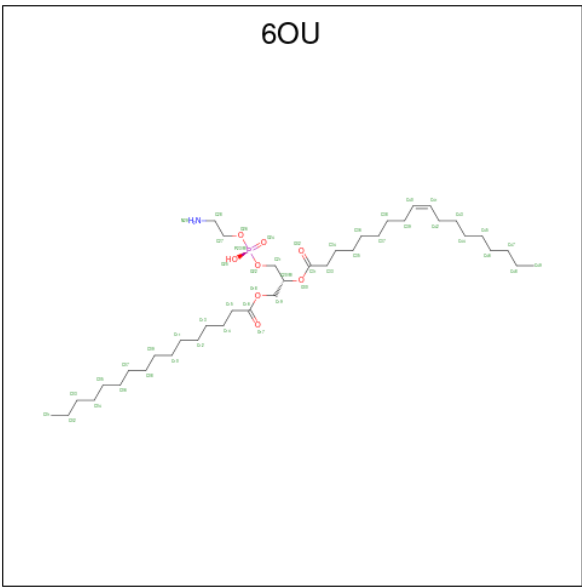
- Molecule 1 is a protein called Protein A6 homolog.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	249	2043	1323	328	384	4	4	137	0	0
1	B	249	2043	1323	328	384	4	4	138	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	123	MSE	-	expression tag	UNP Q9J563
B	123	MSE	-	expression tag	UNP Q9J563

- Molecule 2 is [(2 {R})-1-[2-azanylethoxy(oxidanyl)phosphoryl]oxy-3-hexadecanoyloxy-prop an-2-yl] ({Z})-octadec-9-enoate (CCD ID: 6OU) (formula: C₃₉H₇₆NO₈P).



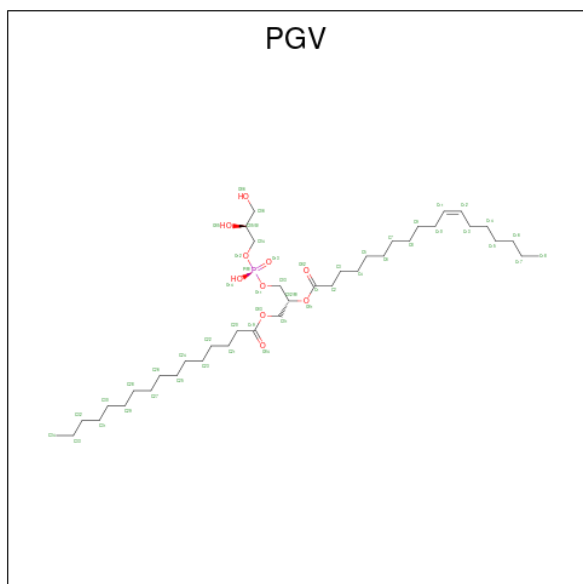
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	49	39	1	8	1	2	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	15	0
			49	39	1	8	1		
2	A	1	Total	C	N	O	P	11	0
			49	39	1	8	1		
2	A	1	Total	C	N	O	P	8	0
			49	39	1	8	1		
2	B	1	Total	C	N	O	P	1	0
			49	39	1	8	1		
2	B	1	Total	C	N	O	P	13	0
			49	39	1	8	1		
2	B	1	Total	C	N	O	P	10	0
			49	39	1	8	1		
2	B	1	Total	C	N	O	P	8	0
			49	39	1	8	1		

- Molecule 3 is (1R)-2-{{[(2S)-2,3-DIHYDROXYPROPYL]OXY}(HYDROXY)PHOSPHORYL]OXY}-1-[(PALMITOYLOXY)METHYL]ETHYL (11E)-OCTADEC-11-ENOATE (CCD ID: PGV) (formula: C₄₀H₇₇O₁₀P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	P	9	0
			51	40	10	1		
3	B	1	Total	C	O	P	6	0
			51	40	10	1		

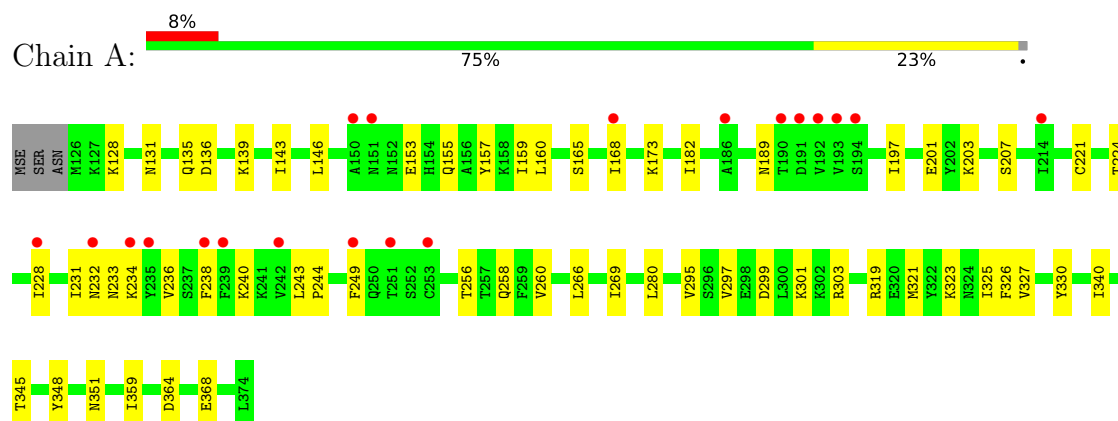
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	16	Total 16	O 16	0	0
4	B	22	Total 22	O 22	0	0

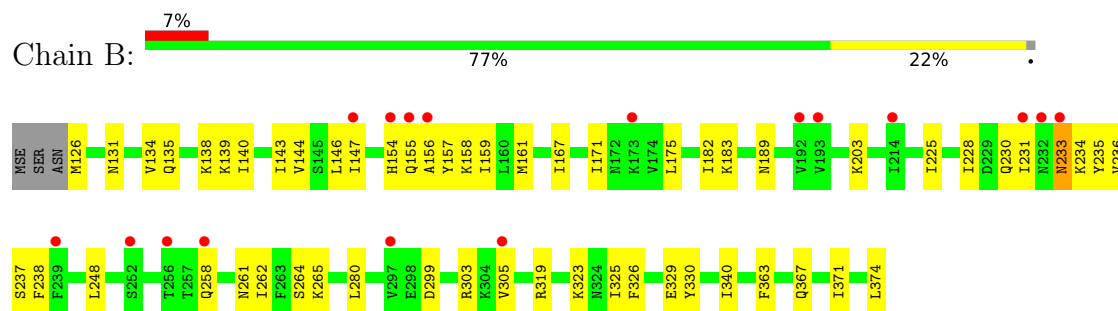
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Protein A6 homolog



• Molecule 1: Protein A6 homolog



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	54.91Å 75.16Å 148.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.34 – 2.30 44.34 – 2.30	Depositor EDS
% Data completeness (in resolution range)	96.5 (44.34-2.30) 87.1 (44.34-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.63 (at 2.29Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.228 , 0.289 0.236 , 0.289	Depositor DCC
R_{free} test set	1959 reflections (7.10%)	wwPDB-VP
Wilson B-factor (Å ²)	47.9	Xtriage
Anisotropy	0.152	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 72.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4618	wwPDB-VP
Average B, all atoms (Å ²)	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 50.53 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.3884e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PGV, 6OU

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	0.41	0/2071	0.67	0/2782
1	B	0.42	0/2071	0.71	1/2782 (0.0%)
All	All	0.41	0/4142	0.69	1/5564 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	233	ASN	N-CA-C	-5.15	101.53	109.52

There are no chirality outliers.

There are no planarity outliers.

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	2043	0	2102	48	0
1	B	2043	0	2102	52	0
2	A	196	0	0	0	0
2	B	196	0	0	2	0
3	A	51	0	76	4	0
3	B	51	0	76	9	0
4	A	16	0	0	0	0
4	B	22	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	4618	0	4356	99	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 12.

All (99) 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:233:ASN:OD1	1:B:236:VAL:HG23	1.37	1.21
1:A:182:ILE:HD11	1:A:203:LYS:HA	1.38	1.05
1:B:126:MSE:HE1	1:B:183:LYS:HG2	1.40	1.00
1:A:182:ILE:CD1	1:A:203:LYS:HA	2.01	0.88
1:B:233:ASN:OD1	1:B:236:VAL:CG2	2.20	0.87
1:B:161:MSE:HE2	1:B:238:PHE:HD1	1.40	0.86
1:B:228:ILE:HG23	1:B:265:LYS:HD2	1.68	0.74
1:A:197:ILE:O	1:A:201:GLU:HG2	1.88	0.74
1:B:154:HIS:O	1:B:157:TYR:HB3	1.90	0.72
1:B:147:ILE:HD13	2:B:405:6OU:C07	2.19	0.72
1:B:189:ASN:HA	1:B:319:ARG:HD3	1.73	0.70
1:B:155:GLN:O	1:B:158:LYS:N	2.26	0.68
1:B:134:VAL:O	1:B:138:LYS:HE2	1.99	0.62
1:B:126:MSE:CE	1:B:183:LYS:HG2	2.25	0.61
1:A:203:LYS:HG3	1:A:207:SER:HB3	1.83	0.61
1:A:160:LEU:HB3	1:A:238:PHE:CZ	2.35	0.61
1:A:146:LEU:HB3	1:A:159:ILE:HD13	1.83	0.59
1:A:345:THR:HG21	1:A:359:ILE:HD11	1.85	0.59
1:A:153:GLU:OE1	1:A:234:LYS:N	2.20	0.58
1:A:280:LEU:HD13	1:A:340:ILE:HG21	1.85	0.57
1:B:161:MSE:HE2	1:B:238:PHE:CD1	2.30	0.57
1:B:261:ASN:O	1:B:265:LYS:HG3	2.06	0.56
1:A:231:ILE:O	1:A:232:ASN:OD1	2.23	0.56
1:B:139:LYS:O	1:B:143:ILE:HG12	2.07	0.55
1:B:326:PHE:HE1	3:B:404:PGV:H232	1.72	0.54
1:A:232:ASN:HD21	1:B:230:GLN:NE2	2.06	0.54
1:A:236:VAL:O	1:A:240:LYS:HG3	2.09	0.53
1:A:131:ASN:O	1:A:135:GLN:HG2	2.08	0.53
1:A:160:LEU:HB3	1:A:238:PHE:CE1	2.44	0.53
1:A:128:LYS:HD3	1:A:131:ASN:HD22	1.74	0.53
1:A:249:PHE:HE2	1:A:256:THR:HG22	1.74	0.52
1:A:232:ASN:HD21	1:B:230:GLN:HE21	1.57	0.52
1:B:225:ILE:HG22	1:B:228:ILE:HG22	1.89	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:261:ASN:ND2	1:B:265:LYS:HE2	2.25	0.52
1:B:147:ILE:CD1	2:B:405:6OU:C07	2.86	0.52
1:B:234:LYS:O	1:B:237:SER:N	2.43	0.52
1:B:261:ASN:HD21	1:B:265:LYS:HE2	1.76	0.51
1:A:182:ILE:CD1	1:A:203:LYS:CA	2.83	0.51
1:A:326:PHE:CD1	3:A:404:PGV:H61	2.45	0.50
1:B:140:ILE:O	1:B:144:VAL:HG23	2.11	0.50
1:B:155:GLN:O	1:B:156:ALA:C	2.54	0.50
1:B:371:ILE:HG21	3:B:404:PGV:H231	1.93	0.50
1:B:175:LEU:HB3	1:B:248:LEU:HD12	1.93	0.50
1:B:233:ASN:O	1:B:236:VAL:HB	2.12	0.50
1:A:139:LYS:O	1:A:143:ILE:HG12	2.11	0.49
1:A:136:ASP:OD2	1:A:173:LYS:NZ	2.39	0.49
1:B:126:MSE:HE1	1:B:183:LYS:CG	2.27	0.49
1:A:221:CYS:O	1:A:258:GLN:NE2	2.46	0.49
1:A:153:GLU:OE1	1:A:233:ASN:HB2	2.13	0.49
1:A:128:LYS:HA	1:A:131:ASN:HB2	1.96	0.48
1:B:157:TYR:OH	1:B:161:MSE:HE3	2.13	0.48
1:B:367:GLN:HG3	3:B:404:PGV:H201	1.96	0.48
1:B:131:ASN:O	1:B:134:VAL:HG22	2.13	0.48
1:A:321:MSE:HE3	1:A:325:ILE:CD1	2.43	0.48
1:B:167:ILE:O	1:B:171:ILE:HG12	2.14	0.47
1:B:155:GLN:C	1:B:157:TYR:N	2.71	0.46
1:B:363:PHE:CE1	3:B:404:PGV:H301	2.51	0.46
1:B:135:GLN:HA	1:B:138:LYS:HE2	1.98	0.46
1:B:323:LYS:HG3	3:B:404:PGV:H22	1.97	0.46
1:A:321:MSE:HE3	1:A:325:ILE:HD12	1.98	0.46
1:B:234:LYS:O	1:B:235:TYR:C	2.56	0.46
1:B:135:GLN:HA	1:B:138:LYS:CE	2.46	0.45
1:A:295:VAL:HG22	1:A:321:MSE:HE1	1.98	0.45
1:A:155:GLN:O	1:A:159:ILE:HG13	2.17	0.45
1:A:327:VAL:HG21	3:A:404:PGV:H032	1.99	0.45
1:B:330:TYR:CD2	3:B:404:PGV:H221	2.52	0.45
1:A:323:LYS:HB3	3:A:404:PGV:H41	1.99	0.44
1:B:258:GLN:O	1:B:262:ILE:HG13	2.17	0.44
1:A:269:ILE:HG12	1:A:348:TYR:CE2	2.53	0.44
1:B:299:ASP:O	1:B:303:ARG:HG3	2.17	0.44
1:A:228:ILE:HG12	1:A:348:TYR:HD1	1.83	0.43
1:A:243:LEU:N	1:A:244:PRO:HD2	2.33	0.43
1:B:330:TYR:CZ	3:B:404:PGV:H242	2.53	0.43
1:A:299:ASP:O	1:A:303:ARG:HG3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:330:TYR:CZ	3:A:404:PGV:H241	2.53	0.43
1:A:224:THR:OG1	1:A:351:ASN:HB2	2.18	0.42
3:B:404:PGV:H302	3:B:404:PGV:H271	1.58	0.42
1:A:228:ILE:HG13	1:A:348:TYR:CE1	2.55	0.42
1:A:240:LYS:HG2	1:A:260:VAL:HG21	2.01	0.42
1:B:280:LEU:HD13	1:B:340:ILE:HG21	2.00	0.42
1:B:325:ILE:O	1:B:329:GLU:HG2	2.19	0.42
1:B:182:ILE:HD13	1:B:203:LYS:HG2	2.01	0.42
1:A:297:VAL:O	1:A:301:LYS:HG3	2.20	0.42
1:A:189:ASN:HA	1:A:319:ARG:NH1	2.34	0.41
1:A:228:ILE:CG1	1:A:348:TYR:CD1	3.03	0.41
1:A:249:PHE:CE2	1:A:256:THR:HG22	2.55	0.41
1:B:305:VAL:HG12	1:B:305:VAL:O	2.20	0.41
1:A:173:LYS:HE2	1:A:173:LYS:HB3	1.72	0.41
1:A:165:SER:HA	1:A:168:ILE:HG22	2.00	0.41
1:B:231:ILE:CD1	1:B:264:SER:C	2.94	0.41
1:A:228:ILE:HG12	1:A:348:TYR:CD1	2.55	0.41
1:A:157:TYR:CD1	1:A:234:LYS:HB3	2.56	0.41
1:A:266:LEU:HD23	1:A:266:LEU:HA	1.86	0.41
1:A:364:ASP:O	1:A:368:GLU:HG2	2.21	0.41
1:B:231:ILE:HD12	1:B:264:SER:CB	2.51	0.41
1:B:189:ASN:HA	1:B:319:ARG:NH1	2.36	0.41
1:B:146:LEU:HB3	1:B:159:ILE:CD1	2.51	0.41
1:B:155:GLN:O	1:B:157:TYR:N	2.55	0.40
1:B:374:LEU:HD12	3:B:404:PGV:H31	2.03	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	247/252 (98%)	237 (96%)	10 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	247/252 (98%)	234 (95%)	13 (5%)	0	100	100
All	All	494/504 (98%)	471 (95%)	23 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	239/237 (101%)	239 (100%)	0	100	100
1	B	239/237 (101%)	239 (100%)	0	100	100
All	All	478/474 (101%)	478 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	131	ASN
1	A	318	ASN
1	A	351	ASN
1	A	355	ASN
1	B	230	GLN
1	B	250	GLN
1	B	333	HIS
1	B	369	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

10 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	PGV	B	404	-	50,50,50	1.26	5 (10%)	53,56,56	1.13	4 (7%)
3	PGV	A	404	-	50,50,50	1.15	4 (8%)	53,56,56	1.08	4 (7%)
2	6OU	B	401	-	48,48,48	0.91	4 (8%)	51,53,53	0.92	3 (5%)
2	6OU	B	403	2	48,48,48	0.85	3 (6%)	51,53,53	0.97	3 (5%)
2	6OU	B	402	2	48,48,48	0.90	4 (8%)	51,53,53	0.99	1 (1%)
2	6OU	A	403	-	48,48,48	0.90	4 (8%)	51,53,53	0.92	2 (3%)
2	6OU	A	401	-	48,48,48	0.89	4 (8%)	51,53,53	1.09	2 (3%)
2	6OU	A	402	-	48,48,48	0.89	3 (6%)	51,53,53	1.18	4 (7%)
2	6OU	B	405	-	48,48,48	0.92	3 (6%)	51,53,53	0.98	3 (5%)
2	6OU	A	405	-	48,48,48	0.90	4 (8%)	51,53,53	1.00	2 (3%)

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	PGV	B	404	-	-	32/55/55/55	-
3	PGV	A	404	-	-	29/55/55/55	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	6OU	B	401	-	-	31/52/52/52	-
2	6OU	B	403	2	-	27/52/52/52	-
2	6OU	B	402	2	-	31/52/52/52	-
2	6OU	A	403	-	-	31/52/52/52	-
2	6OU	A	401	-	-	28/52/52/52	-
2	6OU	A	402	-	-	28/52/52/52	-
2	6OU	B	405	-	-	22/52/52/52	-
2	6OU	A	405	-	-	26/52/52/52	-

All (38) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	404	PGV	C01-C02	4.02	1.63	1.50
3	A	404	PGV	C01-C02	3.83	1.62	1.50
3	B	404	PGV	P-O12	3.34	1.72	1.59
3	A	404	PGV	P-O11	3.19	1.71	1.59
3	B	404	PGV	P-O11	2.80	1.70	1.59
3	A	404	PGV	P-O12	2.79	1.70	1.59
2	B	405	6OU	O18-C16	2.74	1.41	1.33
2	B	401	6OU	O30-C20	-2.72	1.40	1.46
2	B	405	6OU	O30-C20	-2.71	1.40	1.46
2	A	402	6OU	O30-C31	2.66	1.41	1.34
2	A	403	6OU	O30-C20	-2.59	1.40	1.46
2	B	401	6OU	O18-C19	-2.54	1.39	1.45
2	B	402	6OU	O30-C31	2.49	1.41	1.34
2	B	402	6OU	O18-C19	-2.46	1.39	1.45
2	A	401	6OU	O30-C31	2.43	1.41	1.34
2	A	405	6OU	O30-C31	2.39	1.41	1.34
3	B	404	PGV	C04-C05	2.38	1.59	1.51
2	A	405	6OU	O18-C16	2.33	1.40	1.33
2	A	403	6OU	O18-C16	2.32	1.40	1.33
2	A	403	6OU	O18-C19	-2.32	1.40	1.45
2	B	403	6OU	O18-C16	2.32	1.40	1.33
2	A	401	6OU	O18-C16	2.29	1.40	1.33
2	A	405	6OU	O18-C19	-2.28	1.40	1.45
2	A	402	6OU	O18-C19	-2.28	1.40	1.45
2	A	402	6OU	O18-C16	2.28	1.40	1.33
2	B	401	6OU	O30-C31	2.20	1.40	1.34
2	B	405	6OU	O30-C31	2.19	1.40	1.34
2	A	401	6OU	O18-C19	-2.16	1.40	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	405	6OU	O30-C20	-2.15	1.41	1.46
2	B	401	6OU	O18-C16	2.15	1.39	1.33
2	A	401	6OU	O30-C20	-2.14	1.41	1.46
2	A	403	6OU	O30-C31	2.12	1.40	1.34
2	B	402	6OU	O30-C20	-2.11	1.41	1.46
2	B	403	6OU	O18-C19	-2.11	1.40	1.45
3	A	404	PGV	O01-C02	-2.10	1.41	1.46
2	B	403	6OU	O30-C31	2.06	1.40	1.34
3	B	404	PGV	O03-C19	2.05	1.39	1.33
2	B	402	6OU	O18-C16	2.04	1.39	1.33

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	402	6OU	O30-C31-C33	5.33	123.02	111.48
3	B	404	PGV	O01-C1-C2	5.07	122.44	111.48
3	A	404	PGV	O01-C1-C2	4.58	121.39	111.48
2	A	401	6OU	O30-C31-C33	4.51	121.25	111.48
2	A	405	6OU	O30-C31-C33	4.43	121.07	111.48
2	B	402	6OU	O30-C31-C33	4.29	120.77	111.48
2	A	403	6OU	O30-C31-C33	4.01	120.16	111.48
2	B	405	6OU	O30-C31-C33	3.99	120.11	111.48
2	B	403	6OU	O30-C31-C33	3.87	119.85	111.48
3	B	404	PGV	O03-C19-C20	3.85	123.59	111.83
3	A	404	PGV	O03-C19-C20	3.71	123.16	111.83
2	A	401	6OU	O18-C16-C15	3.31	121.92	111.83
2	B	405	6OU	O18-C16-C15	2.88	120.60	111.83
2	B	401	6OU	O30-C31-C33	2.82	117.58	111.48
3	B	404	PGV	O01-C1-O02	-2.73	117.32	123.70
3	B	404	PGV	O03-C19-O04	-2.67	116.96	123.63
3	A	404	PGV	O01-C1-O02	-2.64	117.54	123.70
2	A	402	6OU	C20-O30-C31	2.59	124.00	117.80
2	A	402	6OU	O18-C16-C15	2.54	119.58	111.83
2	B	401	6OU	O18-C16-C15	2.52	119.53	111.83
2	A	405	6OU	O18-C16-C15	2.51	119.47	111.83
3	A	404	PGV	O03-C19-O04	-2.43	117.55	123.63
2	B	401	6OU	C20-O30-C31	2.32	123.35	117.80
2	B	403	6OU	O30-C20-C21	2.16	116.10	108.34
2	B	403	6OU	O18-C16-C15	2.15	118.40	111.83
2	A	403	6OU	O18-C16-C15	2.14	118.37	111.83
2	A	402	6OU	O30-C31-O32	-2.10	118.80	123.70
2	B	405	6OU	C20-O30-C31	-2.08	112.81	117.80

There are no chirality outliers.

All (285) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	6OU	C33-C31-O30-C20
2	A	402	6OU	C27-O26-P23-O25
2	A	402	6OU	O26-C27-C28-N29
2	A	402	6OU	O32-C31-O30-C20
2	A	402	6OU	C33-C31-O30-C20
2	A	403	6OU	O26-C27-C28-N29
2	A	405	6OU	C33-C31-O30-C20
2	B	401	6OU	C21-O22-P23-O24
2	B	401	6OU	C21-O22-P23-O25
2	B	401	6OU	C21-O22-P23-O26
2	B	401	6OU	C27-O26-P23-O22
2	B	401	6OU	C27-O26-P23-O24
2	B	401	6OU	C28-C27-O26-P23
2	B	402	6OU	C15-C16-O18-C19
2	B	402	6OU	O17-C16-O18-C19
2	B	402	6OU	C21-O22-P23-O24
2	B	402	6OU	C21-O22-P23-O25
2	B	402	6OU	C28-C27-O26-P23
2	B	402	6OU	O26-C27-C28-N29
2	B	402	6OU	C33-C31-O30-C20
2	B	403	6OU	C21-O22-P23-O25
2	B	403	6OU	C21-O22-P23-O26
2	B	403	6OU	O32-C31-O30-C20
2	B	405	6OU	C21-O22-P23-O24
2	B	405	6OU	C21-O22-P23-O25
2	B	405	6OU	C21-O22-P23-O26
2	B	405	6OU	O26-C27-C28-N29
3	A	404	PGV	C04-O12-P-O13
3	A	404	PGV	C02-C03-O11-P
3	A	404	PGV	O04-C19-O03-C01
3	A	404	PGV	C20-C19-O03-C01
3	B	404	PGV	C03-O11-P-O12
3	B	404	PGV	C03-O11-P-O13
3	B	404	PGV	C03-O11-P-O14
3	B	404	PGV	C04-O12-P-O13
3	B	404	PGV	O04-C19-O03-C01
3	B	404	PGV	C20-C19-O03-C01
2	A	402	6OU	O17-C16-O18-C19
2	B	402	6OU	O32-C31-O30-C20
2	A	402	6OU	C15-C16-O18-C19

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Mol	Chain	Res	Type	Atoms
2	B	403	6OU	C33-C31-O30-C20
2	B	405	6OU	C39-C40-C41-C42
2	B	405	6OU	O17-C16-O18-C19
2	A	401	6OU	O32-C31-O30-C20
2	A	405	6OU	O32-C31-O30-C20
3	A	404	PGV	O12-C04-C05-O05
2	A	403	6OU	C33-C31-O30-C20
3	A	404	PGV	C2-C1-O01-C02
3	B	404	PGV	C2-C1-O01-C02
2	B	405	6OU	C15-C16-O18-C19
3	A	404	PGV	C7-C8-C9-C10
2	A	403	6OU	C39-C40-C41-C42
2	A	403	6OU	O32-C31-O30-C20
3	A	404	PGV	O02-C1-O01-C02
3	B	404	PGV	O02-C1-O01-C02
2	B	401	6OU	C15-C16-O18-C19
2	A	405	6OU	C09-C10-C11-C12
2	A	405	6OU	C11-C12-C13-C14
2	B	402	6OU	C04-C05-C06-C07
2	A	401	6OU	C13-C14-C15-C16
2	B	401	6OU	O17-C16-O18-C19
3	B	404	PGV	C27-C28-C29-C30
2	A	403	6OU	C31-C33-C34-C35
2	A	402	6OU	C31-C33-C34-C35
2	B	402	6OU	C20-C21-O22-P23
2	B	402	6OU	C31-C33-C34-C35
3	A	404	PGV	C19-C20-C21-C22
2	B	401	6OU	C13-C14-C15-C16
2	B	402	6OU	C39-C40-C41-C42
2	A	401	6OU	C15-C16-O18-C19
3	B	404	PGV	C19-C20-C21-C22
3	A	404	PGV	O12-C04-C05-C06
2	A	401	6OU	C19-C20-O30-C31
2	B	403	6OU	C21-C20-O30-C31
3	B	404	PGV	C03-C02-O01-C1
3	A	404	PGV	C5-C6-C7-C8
2	B	403	6OU	O18-C19-C20-O30
2	B	402	6OU	C35-C36-C37-C38
3	B	404	PGV	C14-C15-C16-C17
2	A	401	6OU	C07-C08-C09-C10
2	A	403	6OU	C08-C09-C10-C11
2	A	405	6OU	C02-C03-C04-C05

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Mol	Chain	Res	Type	Atoms
2	B	402	6OU	C09-C10-C11-C12
2	B	403	6OU	C39-C40-C41-C42
2	A	405	6OU	C35-C36-C37-C38
2	B	402	6OU	C08-C09-C10-C11
2	B	402	6OU	C43-C44-C45-C46
2	B	403	6OU	C34-C35-C36-C37
2	A	402	6OU	C10-C11-C12-C13
2	A	402	6OU	C44-C45-C46-C47
2	B	401	6OU	C10-C11-C12-C13
3	A	404	PGV	C30-C31-C32-C33
3	B	404	PGV	C25-C26-C27-C28
2	B	405	6OU	C44-C45-C46-C47
3	A	404	PGV	C14-C15-C16-C17
2	A	402	6OU	C43-C44-C45-C46
3	B	404	PGV	C7-C8-C9-C10
2	B	405	6OU	C35-C36-C37-C38
2	A	402	6OU	C02-C03-C04-C05
2	B	401	6OU	C03-C04-C05-C06
3	B	404	PGV	C20-C21-C22-C23
2	A	401	6OU	O17-C16-O18-C19
2	A	401	6OU	C33-C34-C35-C36
2	B	403	6OU	C44-C45-C46-C47
3	A	404	PGV	C3-C4-C5-C6
3	B	404	PGV	C22-C23-C24-C25
2	B	403	6OU	C33-C34-C35-C36
3	B	404	PGV	C13-C14-C15-C16
2	A	401	6OU	C09-C10-C11-C12
2	A	405	6OU	C41-C42-C43-C44
2	B	403	6OU	C31-C33-C34-C35
2	A	401	6OU	C34-C35-C36-C37
2	A	405	6OU	C04-C05-C06-C07
3	B	404	PGV	C3-C4-C5-C6
2	B	401	6OU	C42-C43-C44-C45
2	B	402	6OU	C10-C11-C12-C13
2	B	403	6OU	C03-C04-C05-C06
2	B	405	6OU	C03-C04-C05-C06
3	A	404	PGV	C20-C21-C22-C23
2	B	401	6OU	C38-C39-C40-C41
2	A	405	6OU	C43-C44-C45-C46
2	B	402	6OU	C33-C34-C35-C36
2	B	402	6OU	C03-C04-C05-C06
2	B	401	6OU	C41-C42-C43-C44

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Mol	Chain	Res	Type	Atoms
2	A	402	6OU	C03-C04-C05-C06
2	B	401	6OU	C43-C44-C45-C46
2	A	401	6OU	C36-C37-C38-C39
2	B	403	6OU	C35-C36-C37-C38
2	A	402	6OU	C41-C42-C43-C44
2	A	403	6OU	C37-C38-C39-C40
3	B	404	PGV	C24-C25-C26-C27
2	A	405	6OU	C15-C16-O18-C19
2	A	403	6OU	C10-C11-C12-C13
3	B	404	PGV	C30-C31-C32-C33
2	B	405	6OU	C33-C34-C35-C36
2	A	401	6OU	C40-C41-C42-C43
2	A	401	6OU	C11-C12-C13-C14
2	B	403	6OU	C20-C21-O22-P23
3	B	404	PGV	C6-C7-C8-C9
2	B	401	6OU	C40-C41-C42-C43
2	A	405	6OU	C42-C43-C44-C45
2	B	402	6OU	C37-C38-C39-C40
2	A	405	6OU	C12-C13-C14-C15
3	A	404	PGV	C13-C14-C15-C16
2	B	402	6OU	C05-C06-C07-C08
3	A	404	PGV	C29-C30-C31-C32
2	B	405	6OU	C13-C14-C15-C16
2	B	403	6OU	O18-C19-C20-C21
2	A	403	6OU	C15-C16-O18-C19
2	A	405	6OU	C45-C46-C47-C48
2	A	405	6OU	O17-C16-O18-C19
2	B	405	6OU	C08-C09-C10-C11
2	B	402	6OU	C21-C20-O30-C31
3	A	404	PGV	C03-C02-O01-C1
2	A	403	6OU	C06-C07-C08-C09
2	B	403	6OU	C43-C44-C45-C46
2	A	401	6OU	C41-C42-C43-C44
3	B	404	PGV	C12-C13-C14-C15
2	B	401	6OU	C34-C35-C36-C37
2	B	403	6OU	C02-C03-C04-C05
2	A	402	6OU	C42-C43-C44-C45
2	B	402	6OU	C36-C37-C38-C39
2	B	402	6OU	C42-C43-C44-C45
2	A	402	6OU	C39-C40-C41-C42
3	B	404	PGV	C5-C6-C7-C8
2	B	401	6OU	C04-C05-C06-C07

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Mol	Chain	Res	Type	Atoms
2	A	403	6OU	C33-C34-C35-C36
2	A	405	6OU	C07-C08-C09-C10
2	B	402	6OU	C06-C07-C08-C09
2	B	402	6OU	C11-C12-C13-C14
2	A	402	6OU	O18-C19-C20-O30
2	A	402	6OU	C33-C34-C35-C36
2	B	401	6OU	C45-C46-C47-C48
2	B	403	6OU	C04-C05-C06-C07
2	A	403	6OU	C12-C13-C14-C15
2	A	401	6OU	C42-C43-C44-C45
2	B	405	6OU	C07-C08-C09-C10
2	A	403	6OU	C11-C12-C13-C14
2	B	401	6OU	C01-C02-C03-C04
2	A	401	6OU	C19-C20-C21-O22
2	B	405	6OU	C02-C03-C04-C05
2	A	402	6OU	C34-C35-C36-C37
2	B	405	6OU	C42-C43-C44-C45
2	B	401	6OU	C12-C13-C14-C15
2	B	403	6OU	C06-C07-C08-C09
2	A	403	6OU	O17-C16-O18-C19
2	A	405	6OU	C33-C34-C35-C36
2	B	405	6OU	C04-C05-C06-C07
2	A	405	6OU	O18-C19-C20-C21
2	B	401	6OU	C35-C36-C37-C38
2	B	403	6OU	C14-C15-C16-O18
2	B	405	6OU	C20-C21-O22-P23
2	B	401	6OU	C44-C45-C46-C47
2	A	402	6OU	C06-C07-C08-C09
2	B	402	6OU	C44-C45-C46-C47
2	A	402	6OU	C07-C08-C09-C10
2	A	403	6OU	C01-C02-C03-C04
2	B	401	6OU	C07-C08-C09-C10
2	A	402	6OU	C05-C06-C07-C08
2	A	405	6OU	C19-C20-O30-C31
3	A	404	PGV	C12-C13-C14-C15
2	B	403	6OU	C08-C09-C10-C11
2	B	401	6OU	O18-C19-C20-C21
2	A	403	6OU	C02-C03-C04-C05
2	A	405	6OU	C08-C09-C10-C11
3	A	404	PGV	O03-C01-C02-O01
3	B	404	PGV	C26-C27-C28-C29
2	A	401	6OU	C04-C05-C06-C07

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Mol	Chain	Res	Type	Atoms
3	A	404	PGV	C25-C26-C27-C28
2	A	401	6OU	C10-C11-C12-C13
2	A	403	6OU	C09-C10-C11-C12
2	B	405	6OU	C12-C13-C14-C15
3	B	404	PGV	C15-C16-C17-C18
2	B	403	6OU	C15-C16-O18-C19
2	B	401	6OU	C11-C12-C13-C14
3	A	404	PGV	C28-C29-C30-C31
2	A	403	6OU	C05-C06-C07-C08
2	A	403	6OU	C14-C15-C16-O18
2	A	403	6OU	C07-C08-C09-C10
2	B	403	6OU	O17-C16-O18-C19
2	B	401	6OU	O18-C19-C20-O30
2	B	401	6OU	C09-C10-C11-C12
2	A	402	6OU	O18-C19-C20-C21
3	A	404	PGV	O03-C01-C02-C03
2	A	403	6OU	C04-C05-C06-C07
2	A	401	6OU	C21-O22-P23-O24
2	A	401	6OU	C27-O26-P23-O22
2	A	402	6OU	C27-O26-P23-O22
2	A	402	6OU	C27-O26-P23-O24
2	A	403	6OU	C21-O22-P23-O24
2	A	403	6OU	C21-O22-P23-O25
2	A	403	6OU	C21-O22-P23-O26
2	A	403	6OU	C27-O26-P23-O24
2	A	405	6OU	C27-O26-P23-O22
2	A	405	6OU	C27-O26-P23-O24
2	A	405	6OU	C27-O26-P23-O25
2	B	402	6OU	C21-O22-P23-O26
3	B	404	PGV	C04-O12-P-O11
2	A	403	6OU	C21-C20-O30-C31
2	B	401	6OU	C21-C20-O30-C31
2	A	401	6OU	O30-C20-C21-O22
2	A	401	6OU	C03-C04-C05-C06
2	A	405	6OU	O18-C19-C20-O30
2	A	403	6OU	C38-C39-C40-C41
3	A	404	PGV	C15-C16-C17-C18
2	A	401	6OU	C37-C38-C39-C40
3	A	404	PGV	C11-C12-C13-C14
2	A	405	6OU	C46-C47-C48-C49
3	B	404	PGV	C29-C30-C31-C32
2	A	405	6OU	C37-C38-C39-C40

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Mol	Chain	Res	Type	Atoms
2	B	402	6OU	C38-C39-C40-C41
2	A	402	6OU	C36-C37-C38-C39
2	A	402	6OU	C21-C20-O30-C31
3	A	404	PGV	C27-C28-C29-C30
3	B	404	PGV	C05-C04-O12-P
2	A	403	6OU	C43-C44-C45-C46
3	B	404	PGV	C11-C12-C13-C14
3	B	404	PGV	C2-C3-C4-C5
2	B	402	6OU	C02-C03-C04-C05
2	A	401	6OU	C39-C40-C41-C42
2	A	401	6OU	C05-C06-C07-C08
3	A	404	PGV	C31-C32-C33-C34
2	B	403	6OU	C14-C15-C16-O17
3	B	404	PGV	C9-C10-C11-C12
2	B	402	6OU	O30-C31-C33-C34
3	A	404	PGV	C23-C24-C25-C26
2	B	403	6OU	C45-C46-C47-C48
2	B	405	6OU	C45-C46-C47-C48
2	B	405	6OU	C11-C12-C13-C14
2	A	401	6OU	C01-C02-C03-C04
2	A	403	6OU	O18-C19-C20-O30
2	A	402	6OU	C08-C09-C10-C11
2	B	401	6OU	C36-C37-C38-C39
2	A	402	6OU	C37-C38-C39-C40
3	B	404	PGV	C28-C29-C30-C31
2	A	405	6OU	O30-C31-C33-C34
2	B	403	6OU	O30-C31-C33-C34
2	A	403	6OU	O30-C31-C33-C34
2	B	401	6OU	C05-C06-C07-C08
2	A	401	6OU	C38-C39-C40-C41
3	A	404	PGV	C05-C04-O12-P
2	A	403	6OU	O32-C31-C33-C34
2	B	403	6OU	O32-C31-C33-C34
2	A	401	6OU	O30-C31-C33-C34
2	B	405	6OU	C38-C39-C40-C41

There are no ring outliers.

3 monomers are involved in 15 short contacts:

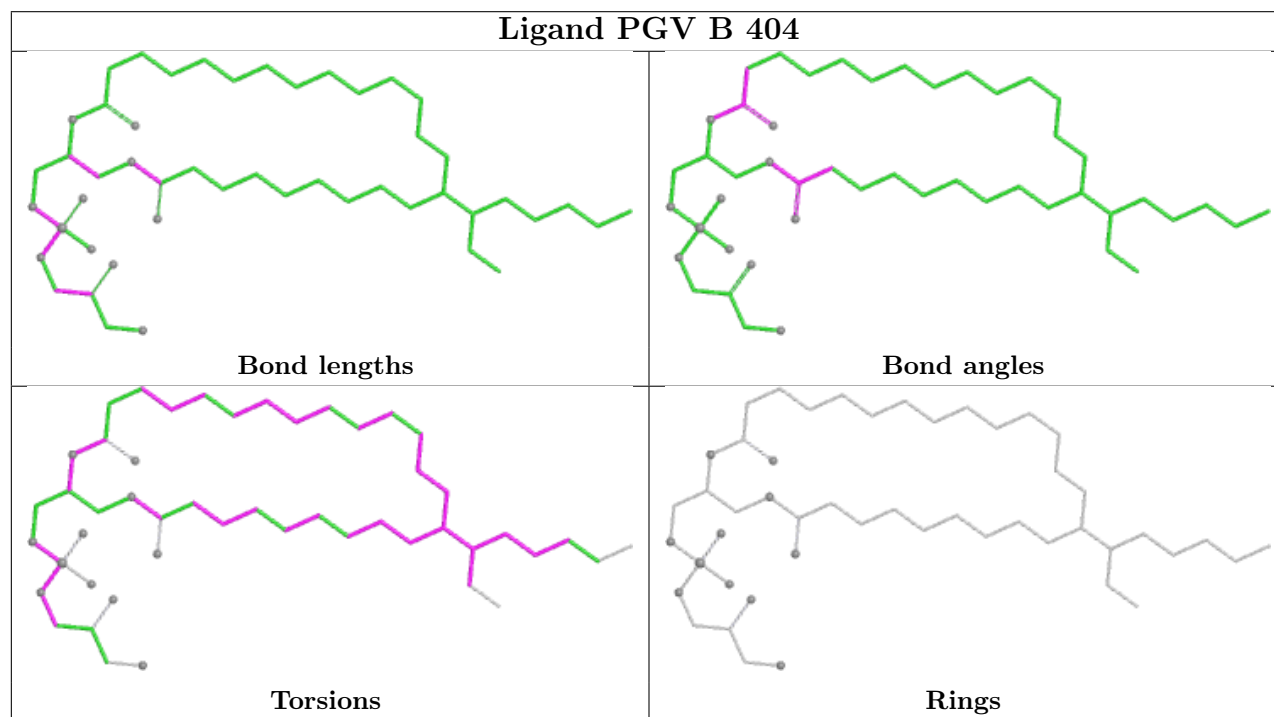
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	404	PGV	9	0
3	A	404	PGV	4	0

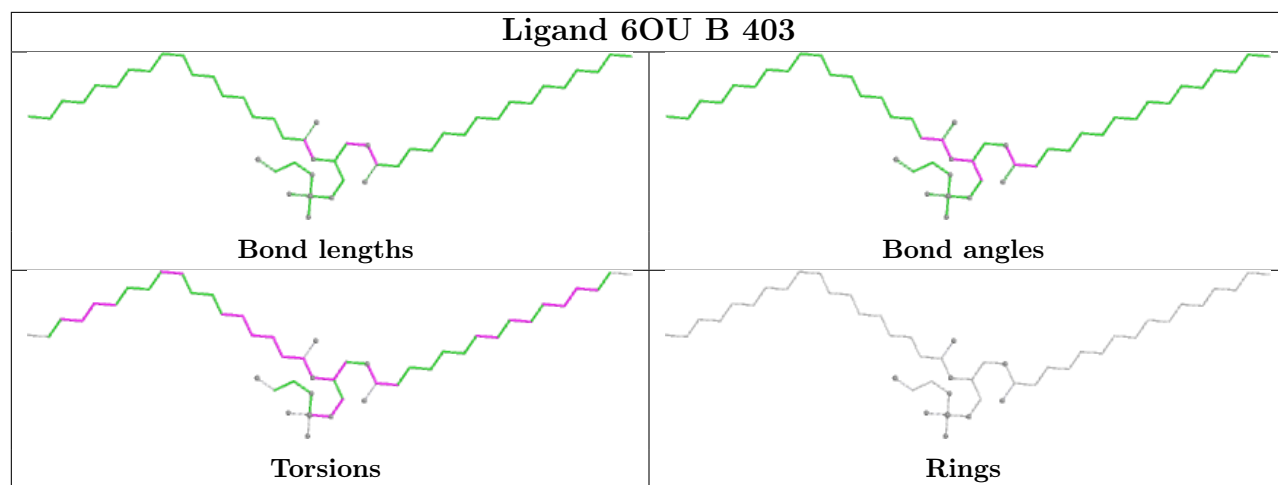
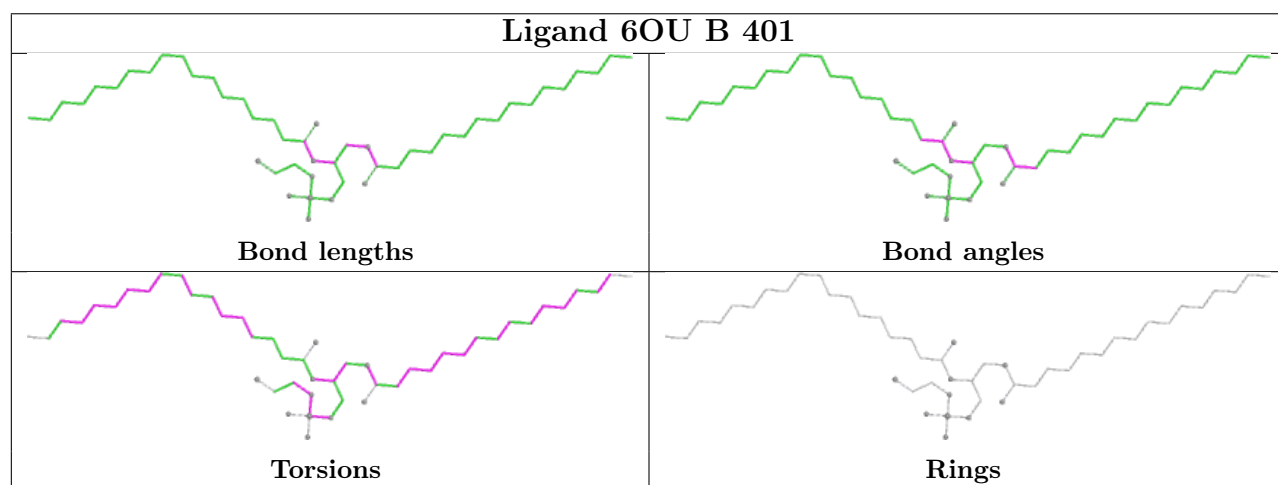
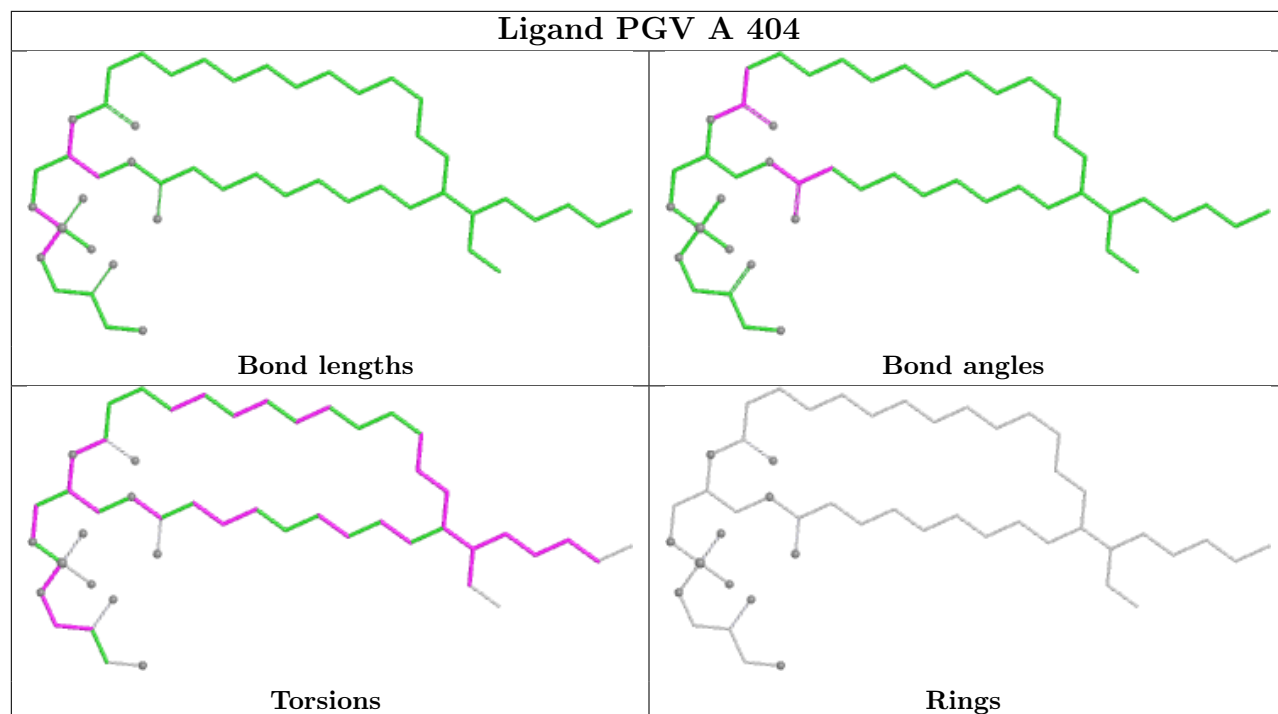
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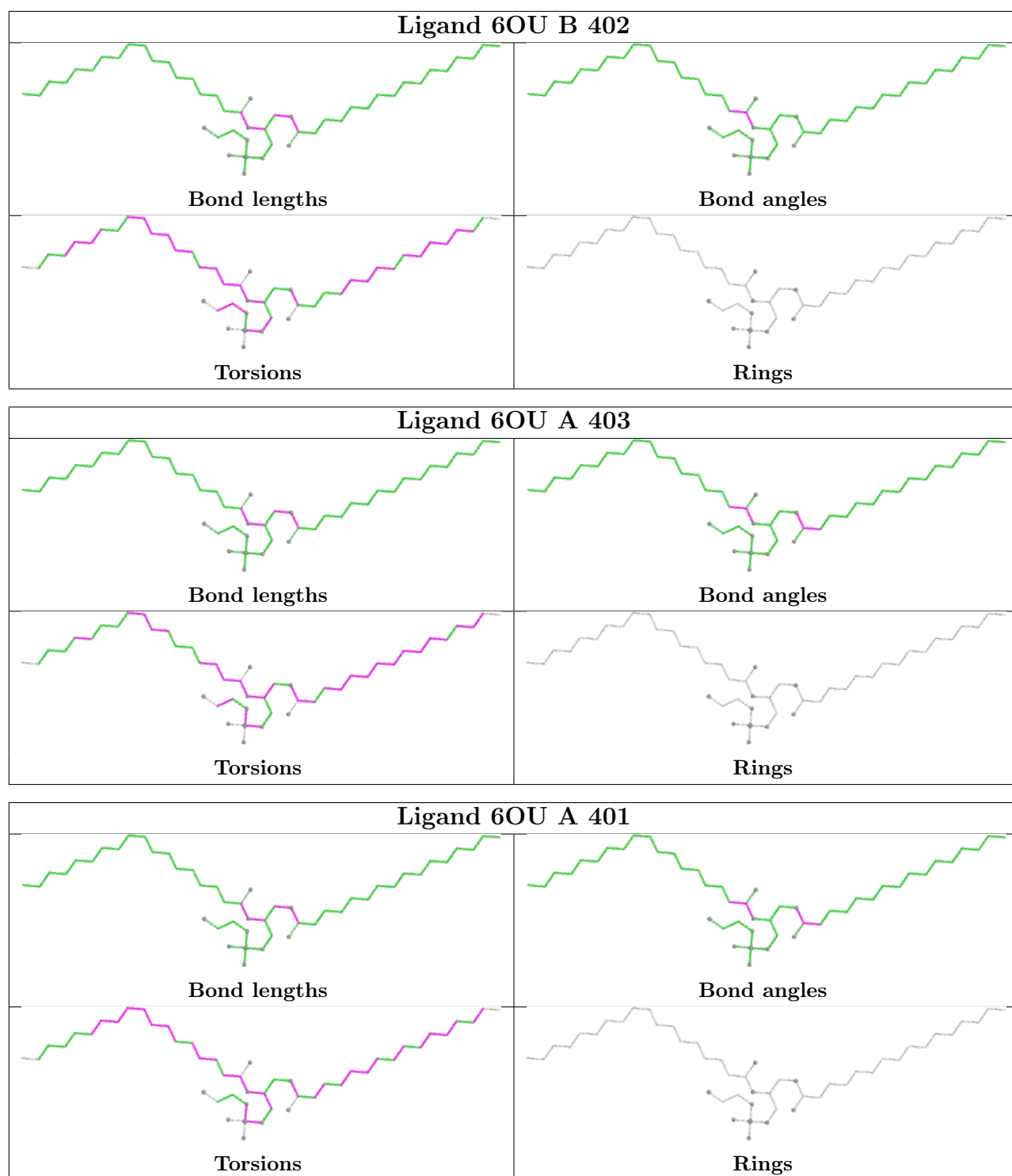
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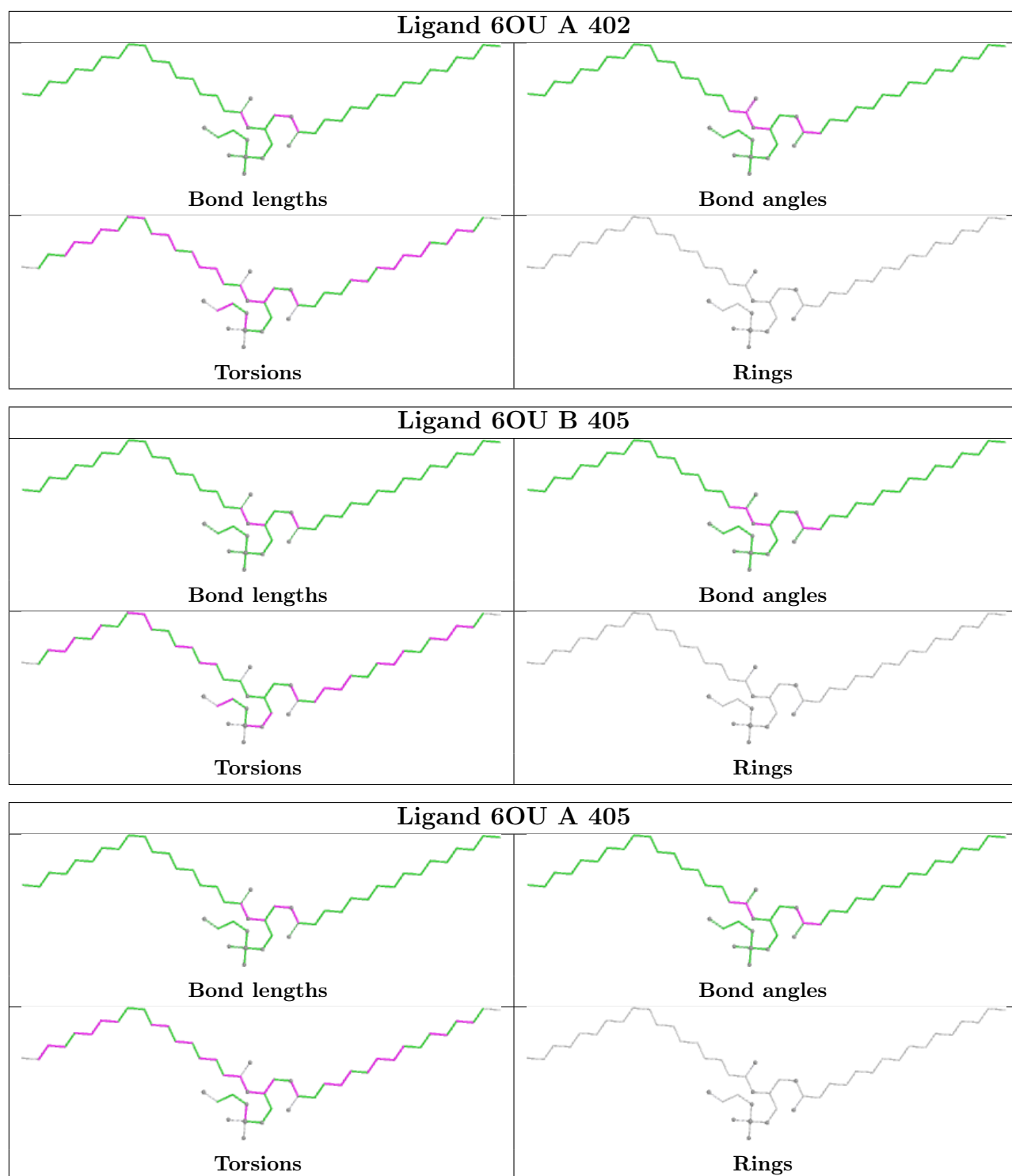
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	405	6OU	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.









5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	245/252 (97%)	0.70	20 (8%) 17 19	19, 69, 95, 143	47 (19%)
1	B	245/252 (97%)	0.62	17 (6%) 23 25	29, 65, 95, 116	52 (21%)
All	All	490/504 (97%)	0.66	37 (7%) 20 21	19, 67, 96, 143	99 (20%)

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	193	VAL	6.2
1	A	191	ASP	5.0
1	A	192	VAL	4.8
1	A	186	ALA	4.4
1	B	233	ASN	3.8
1	A	151	ASN	3.4
1	B	193	VAL	3.3
1	B	231	ILE	3.2
1	A	190	THR	3.1
1	A	194	SER	3.0
1	B	156	ALA	2.9
1	A	235	TYR	2.8
1	B	305	VAL	2.7
1	B	214	ILE	2.7
1	A	228	ILE	2.5
1	A	251	THR	2.4
1	B	297	VAL	2.4
1	A	232	ASN	2.3
1	A	239	PHE	2.3
1	A	168	ILE	2.3
1	A	150	ALA	2.2
1	B	239	PHE	2.2
1	A	242	VAL	2.2
1	B	232	ASN	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	147	ILE	2.2
1	A	234	LYS	2.2
1	B	192	VAL	2.1
1	B	155	GLN	2.1
1	B	258	GLN	2.1
1	B	256	THR	2.1
1	A	214	ILE	2.1
1	A	249	PHE	2.1
1	B	252	SER	2.1
1	A	238	PHE	2.1
1	B	154	HIS	2.0
1	A	253	CYS	2.0
1	B	173	LYS	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](#)

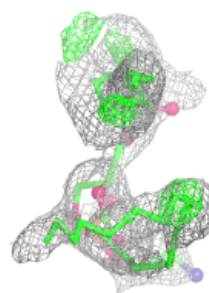
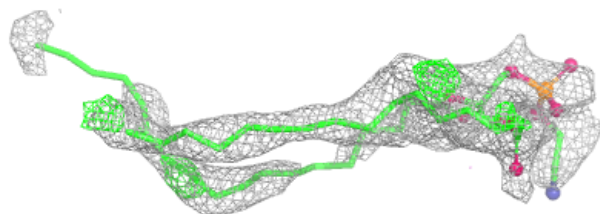
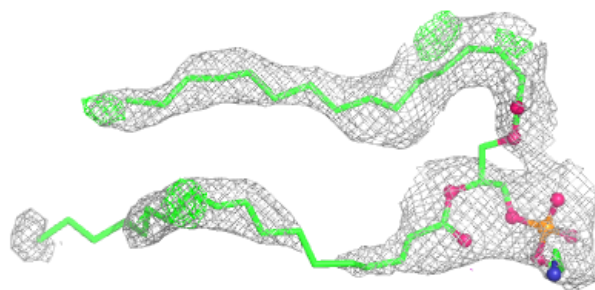
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	6OU	B	405	49/49	0.73	0.20	90,108,135,157	8
2	6OU	A	405	49/49	0.76	0.20	96,108,141,144	8
2	6OU	B	402	49/49	0.79	0.17	92,104,118,121	13
2	6OU	A	403	49/49	0.82	0.17	79,98,123,146	11
2	6OU	A	402	49/49	0.82	0.17	91,105,119,132	15
2	6OU	B	403	49/49	0.84	0.15	76,85,111,131	10
3	PGV	A	404	51/51	0.86	0.16	75,90,107,111	9
3	PGV	B	404	51/51	0.86	0.17	80,97,132,143	6
2	6OU	B	401	49/49	0.87	0.16	72,86,97,99	1
2	6OU	A	401	49/49	0.89	0.16	78,86,95,97	2

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

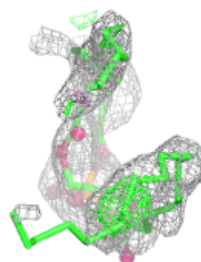
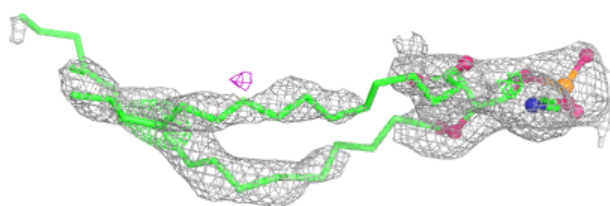
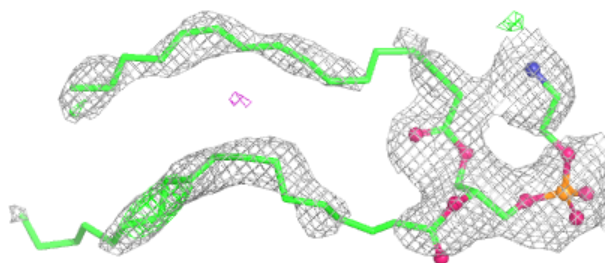
Electron density around 6OU B 405:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

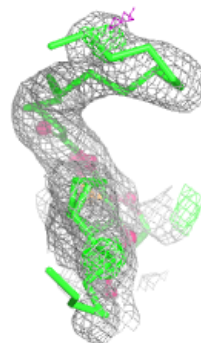
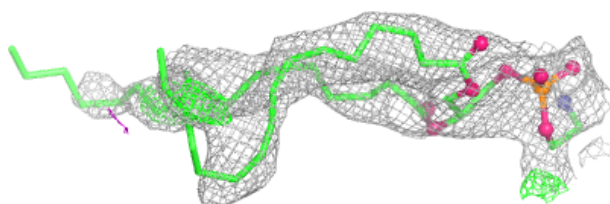
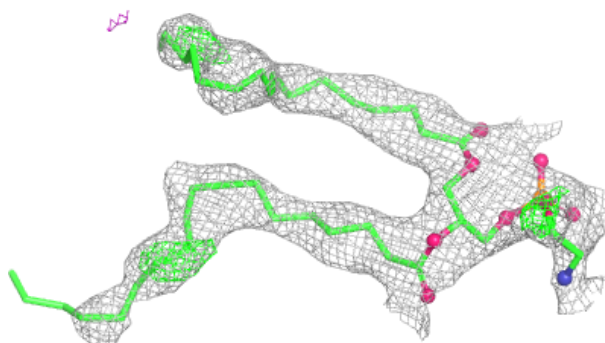


Electron density around 6OU A 405:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

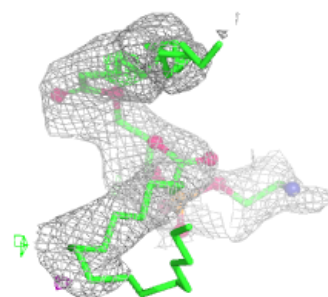
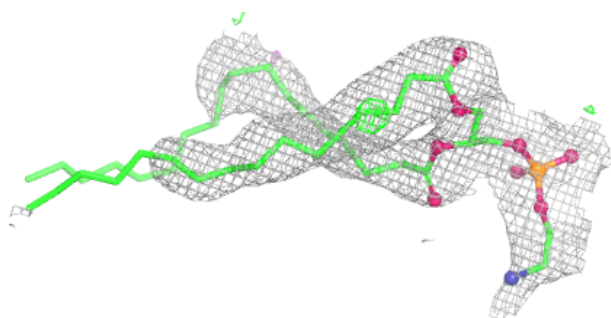
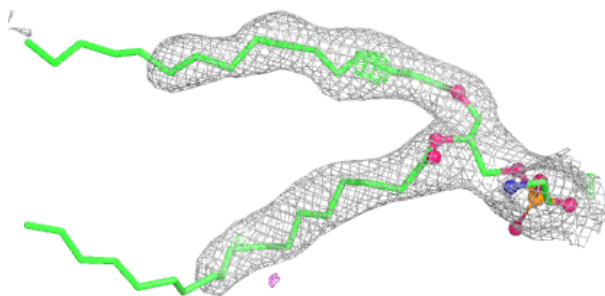
**Electron density around 6OU B 402:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

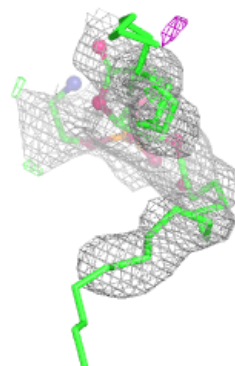
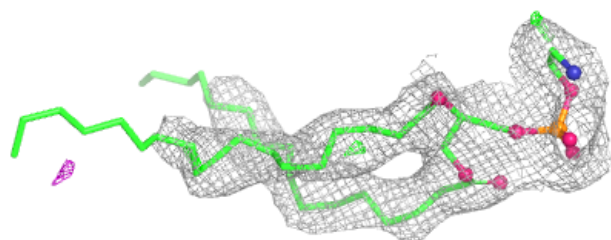
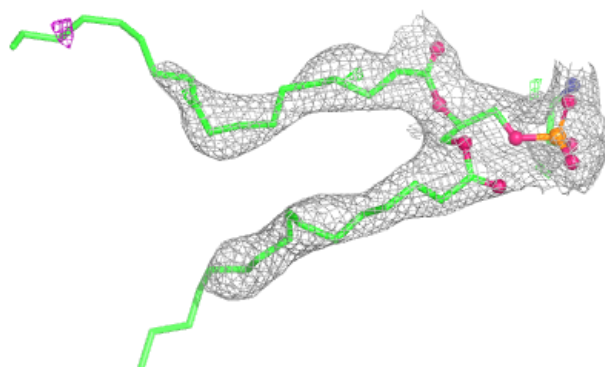


Electron density around 6OU A 403:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

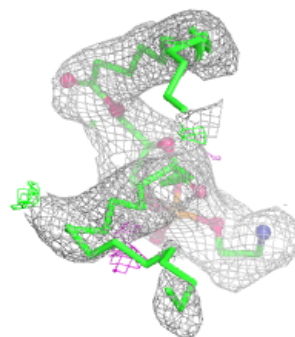
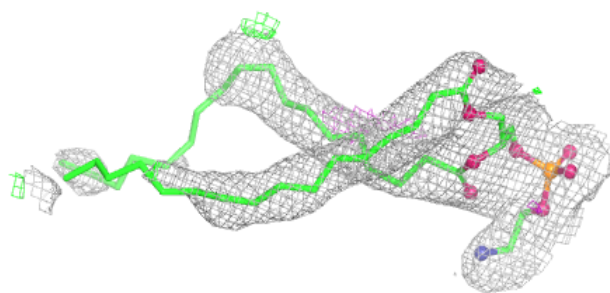
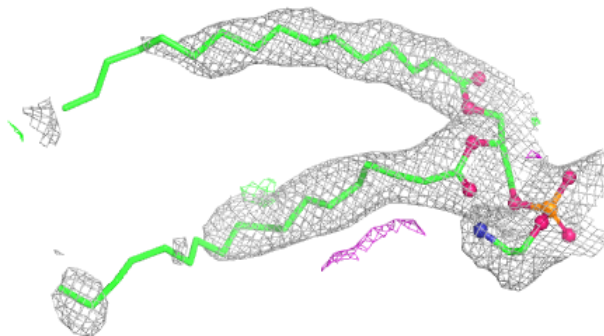
**Electron density around 6OU A 402:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

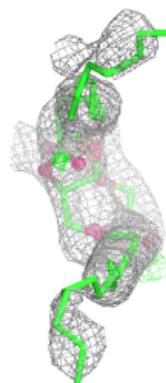
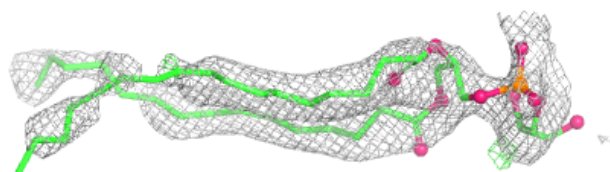
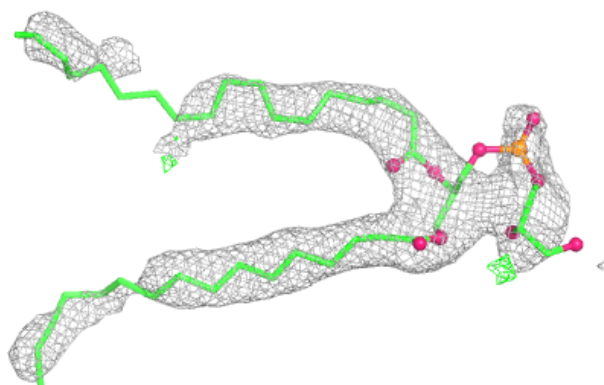


Electron density around 6OU B 403:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

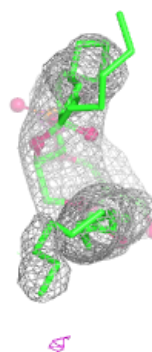
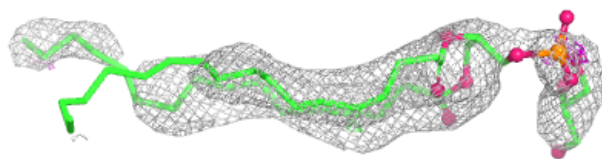
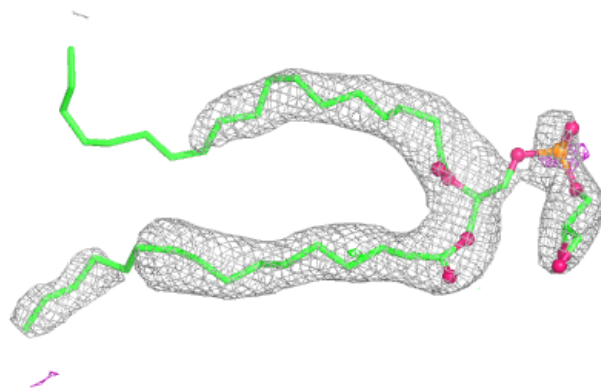
**Electron density around PGV A 404:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

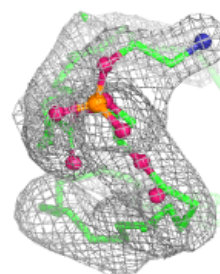
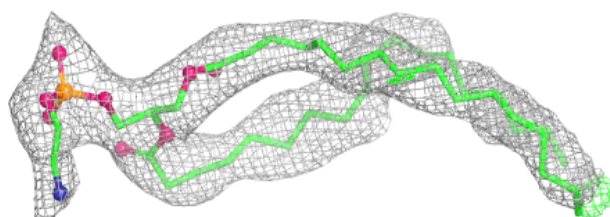
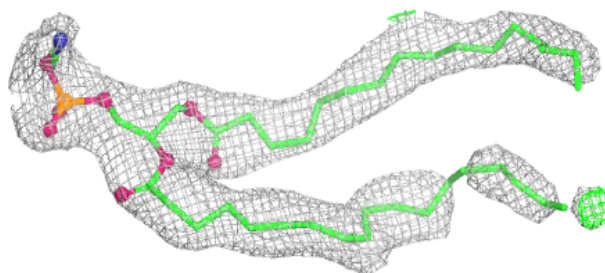


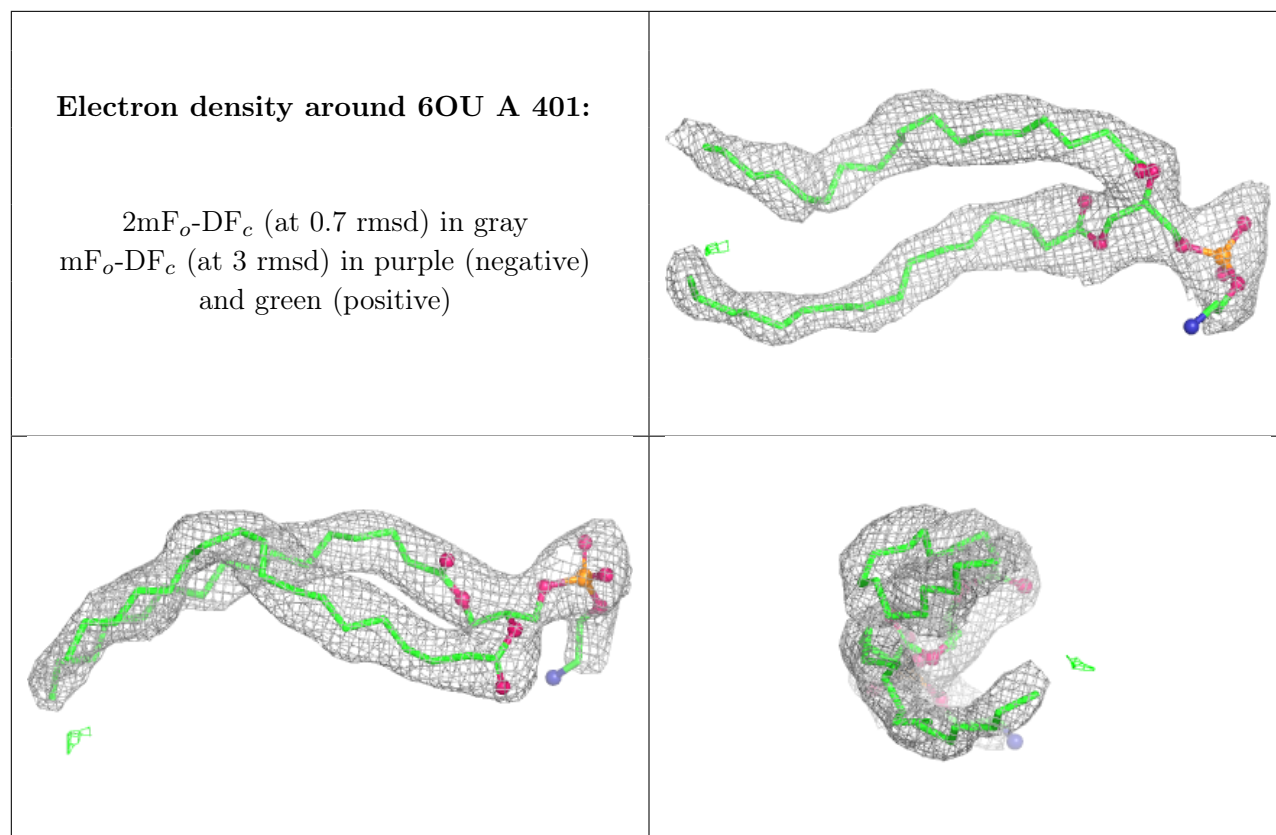
Electron density around PGV B 404:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around 6OU B 401:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.5 Other polymers [i](#)

There are no such residues in this entry.