



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 04:19 am BST

PDB ID : 1ECC
Title : ESCHERICHIA COLI GLUTAMINE PHOSPHORIBOSYLPYROPHOSPHATE (PRPP) AMIDOTRANSFERASE COMPLEXED WITH MN-CPRPP AND 5-OXO-NORLEUCINE
Authors : Krahn, J.M.; Smith, J.L.
Deposited on : 1997-07-09
Resolution : 2.40 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

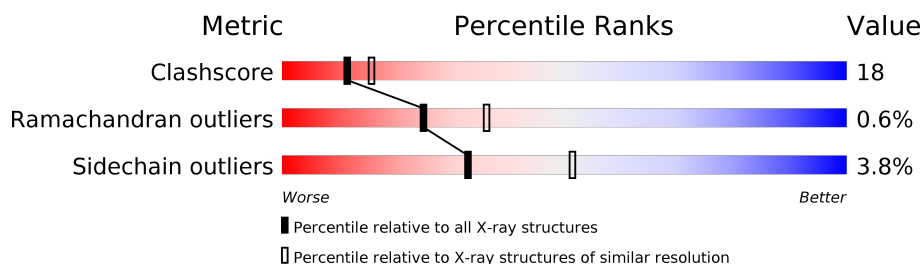
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	504	
1	B	504	

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	ONL	A	2377	-	-	X	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 8092 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.

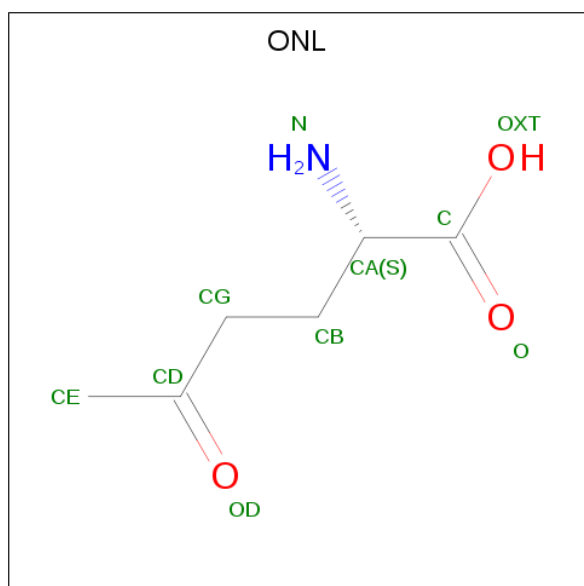
- Molecule 1 is a protein called GLUTAMINE PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	492	Total	C	N	O	S	0	0	0
			3866	2426	692	731	17			
1	B	492	Total	C	N	O	S	0	0	0
			3866	2426	692	731	17			

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

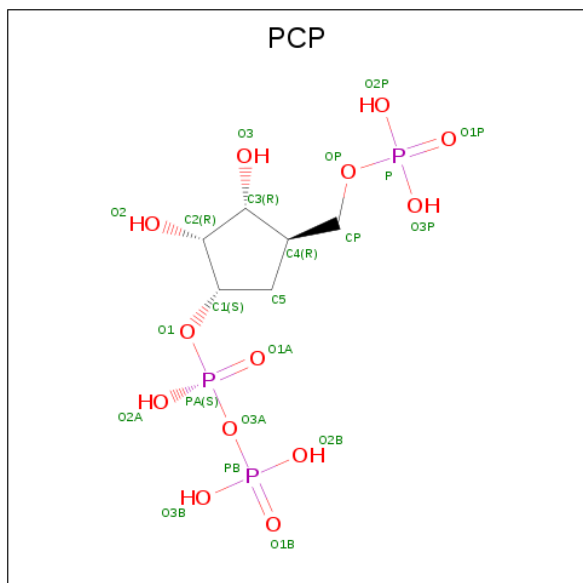
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	3	Total	Mn	0	0
			3	3		
2	A	2	Total	Mn	0	0
			2	2		

- Molecule 3 is 5-OXO-L-NORLEUCINE (three-letter code: ONL) (formula: C₆H₁₁NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			10	6	1	3		
3	B	1	Total	C	N	O	0	0
			10	6	1	3		

- Molecule 4 is 1-ALPHA-PYROPHOSPHORYL-2-ALPHA,3-ALPHA-DIHYDROXY-4-BETA-CYCLOPENTANE-METHANOL-5-PHOSPHATE (three-letter code: PCP) (formula: $C_6H_{15}O_{13}P_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	O	P	0	0
			22	6	13	3		
4	B	1	Total	C	O	P	0	0
			22	6	13	3		

- Molecule 5 is water.

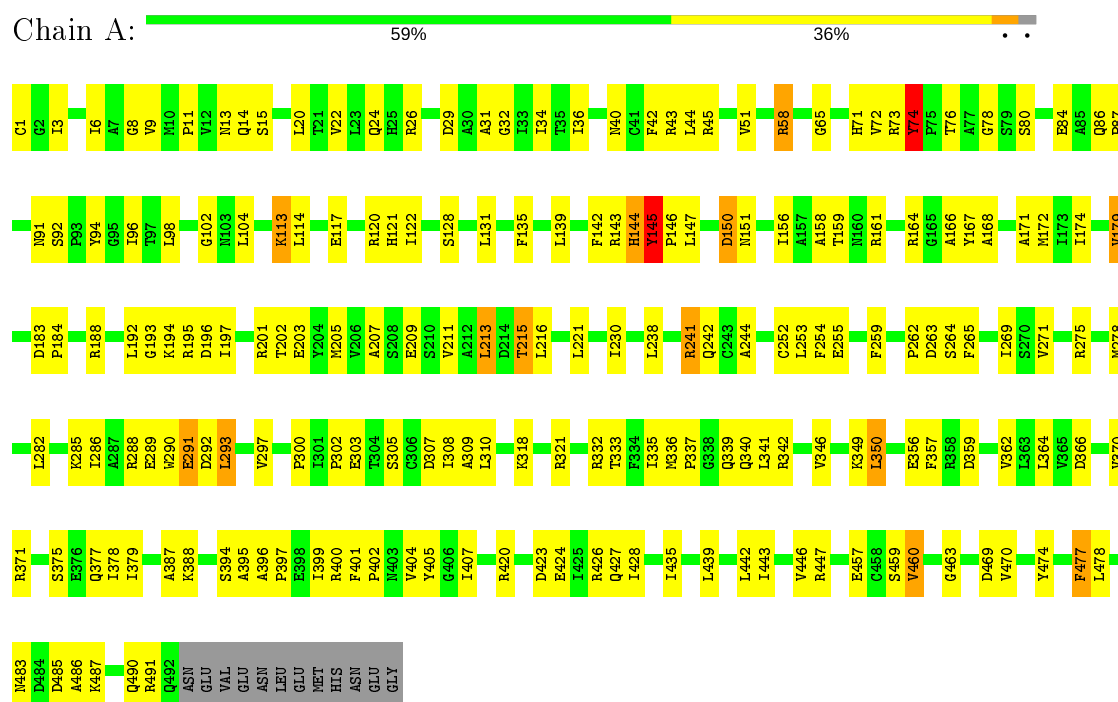
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	141	Total	O	0	0
			141	141		
5	B	150	Total	O	0	0
			150	150		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

Note EDS was not executed.

- Molecule 1: GLUTAMINE PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE



- Molecule 1: GLUTAMINE PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE



Q339	D438	L439	N440	D441	V446	R447	A448	E449	N450	P451	F456	N462	G463	V464	D469	L475	D476	F477	T480	L481	R482	N483	D484	D485	A486	V489	Q492	ASN	GLU	VAL	GLU	GLU	ASN	LEU	GLU	MET	HIS	ASN	GLU	GLY															
R342	R343	R344	S345		K349	L350	N353	R354		F357		V365	D366	D367		V370		Q377	I378	I379	E380	M381		A387		V390	Y391	L392	A393	S394	A395		L399	R400	F401	P402	N403		M409	P410		E414	L415	I416	A417		D423	E424	I425	R426	Q427	I428	I429		L434

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	78.20 Å 78.20 Å 308.80 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 2.40	Depositor
% Data completeness (in resolution range)	88.3 (25.00-2.40)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.04	Depositor
Refinement program	X-PLOR 3.8	Depositor
R, R_{free}	0.176 , 0.265	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	8092	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PCP, MN, ONL

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	0.60	0/3934	0.81	4/5324 (0.1%)
1	B	0.62	0/3934	0.80	3/5324 (0.1%)
All	All	0.61	0/7868	0.80	7/10648 (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	1

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	263	ASP	CB-CG-OD1	5.87	123.58	118.30
1	B	353	ASN	N-CA-C	-5.84	95.24	111.00
1	B	73	ARG	NE-CZ-NH2	-5.41	117.59	120.30
1	A	168	ALA	N-CA-C	-5.32	96.64	111.00
1	A	241	ARG	NE-CZ-NH2	-5.27	117.66	120.30
1	B	168	ALA	N-CA-C	-5.17	97.05	111.00
1	A	74	TYR	N-CA-C	-5.09	97.27	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	145	TYR	Sidechain

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	3866	0	3831	150	0
1	B	3866	0	3831	125	0
2	A	2	0	0	0	0
2	B	3	0	0	0	0
3	A	10	0	9	6	0
3	B	10	0	9	3	0
4	A	22	0	8	1	0
4	B	22	0	8	2	0
5	A	141	0	0	14	0
5	B	150	0	0	7	0
All	All	8092	0	7696	273	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 18.

All (273) 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:333:THR:HA	1:A:336:MET:SD	2.22	0.79
1:A:275:ARG:HA	1:A:278:MET:HE3	1.66	0.78
1:A:285:LYS:HD3	1:A:435:ILE:HD11	1.64	0.78
1:A:404:VAL:HG12	1:A:478:LEU:HD11	1.68	0.74
1:A:1:CYS:H1	3:A:2377:ONL:HE1	1.50	0.74
1:A:253:LEU:HD21	1:A:442:LEU:HD23	1.68	0.74
1:A:282:LEU:HD22	1:A:395:ALA:HA	1.72	0.72
1:B:336:MET:HB2	1:B:342:ARG:HG2	1.70	0.72
1:A:9:VAL:HG11	1:A:201:ARG:HD2	1.74	0.69
1:B:9:VAL:CG2	1:B:197:ILE:HG13	2.22	0.69
1:B:334:PHE:HE1	1:B:370:VAL:HG11	1.57	0.69
5:A:2383:HOH:O	1:B:326:LYS:HD3	1.93	0.69
1:B:113:LYS:HB3	1:B:113:LYS:NZ	2.08	0.68
1:B:350:LEU:CD1	1:B:378:ILE:HD11	2.23	0.68
1:A:487:LYS:O	1:A:491:ARG:HG3	1.94	0.68
1:B:139:LEU:HD21	1:B:173:ILE:HD13	1.76	0.67
1:B:379:ILE:HG23	1:B:390:VAL:HG21	1.74	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:9:VAL:HG21	1:B:197:ILE:HG13	1.75	0.67
1:A:333:THR:HG23	1:A:349:LYS:HD2	1.77	0.67
1:B:476:ASP:O	1:B:480:THR:HG23	1.94	0.67
1:A:36:ILE:O	1:A:65:GLY:HA3	1.96	0.66
1:A:282:LEU:O	1:A:286:ILE:HG13	1.97	0.65
1:B:447:ARG:HG2	1:B:456:PHE:HE2	1.61	0.65
1:B:199:GLU:O	1:B:200:ASN:HB2	1.97	0.65
1:A:135:PHE:O	1:A:139:LEU:HB2	1.98	0.64
1:B:30:ALA:HB2	1:B:48:ASN:HD22	1.63	0.64
1:A:58:ARG:HG2	5:A:2389:HOH:O	1.97	0.62
1:B:211:VAL:HG13	1:B:264:SER:OG	1.98	0.62
1:B:333:THR:HG22	1:B:345:SER:HB3	1.81	0.62
1:A:423:ASP:O	1:A:427:GLN:HG3	1.99	0.62
1:B:1:CYS:N	3:B:2450:ONL:HE1	2.14	0.62
1:B:334:PHE:CE1	1:B:370:VAL:HG11	2.35	0.62
1:B:334:PHE:HB2	4:B:505:PCP:H52	1.81	0.62
1:A:98:LEU:HD12	1:A:171:ALA:HB2	1.80	0.62
1:A:269:ILE:HD13	1:A:446:VAL:HG12	1.82	0.61
1:A:192:LEU:HG	1:A:221:LEU:HD12	1.83	0.61
1:A:285:LYS:O	1:A:289:GLU:HG2	2.00	0.61
1:A:1:CYS:N	3:A:2377:ONL:HE1	2.16	0.60
1:A:265:PHE:CZ	1:B:354:ARG:HD2	2.36	0.60
1:B:410:PRO:CB	1:B:482:ARG:HB2	2.31	0.60
1:B:350:LEU:HD12	1:B:378:ILE:HD11	1.83	0.60
1:A:114:LEU:HD22	1:A:120:ARG:HG3	1.83	0.60
1:A:86:GLN:HB3	1:A:87:PRO:HA	1.82	0.60
1:B:114:LEU:HD13	1:B:122:ILE:HD11	1.83	0.59
1:B:1:CYS:H3	3:B:2450:ONL:HE1	1.65	0.59
1:A:150:ASP:CG	1:A:241:ARG:HH22	2.04	0.59
1:A:443:ILE:O	1:A:447:ARG:HG3	2.03	0.59
1:A:24:GLN:OE1	1:A:51:VAL:HG23	2.03	0.59
1:B:36:ILE:HD13	1:B:174:ILE:HD13	1.83	0.59
1:A:253:LEU:CD2	1:A:442:LEU:HD23	2.33	0.59
1:A:339:GLN:OE1	1:A:371:ARG:HD2	2.03	0.59
1:B:462:ASN:CG	1:B:464:VAL:HG13	2.22	0.59
1:B:28:GLN:HE22	1:B:332:ARG:H	1.50	0.58
1:B:282:LEU:HD22	1:B:395:ALA:HA	1.84	0.58
1:A:474:TYR:O	1:A:477:PHE:HB3	2.04	0.57
1:B:410:PRO:HB2	1:B:482:ARG:HB2	1.86	0.57
1:B:36:ILE:O	1:B:65:GLY:HA3	2.04	0.57
1:A:76:THR:OG1	3:A:2377:ONL:HG2	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:285:LYS:CD	1:A:435:ILE:HD11	2.33	0.57
1:A:401:PHE:HB2	1:A:459:SER:O	2.04	0.56
1:B:3:ILE:HG22	1:B:71:HIS:HD2	1.70	0.56
1:A:346:VAL:HB	1:A:377:GLN:NE2	2.20	0.56
1:A:193:GLY:HA2	1:A:221:LEU:HG	1.86	0.56
1:B:423:ASP:O	1:B:427:GLN:HG3	2.05	0.56
1:A:164:ARG:HG3	5:A:2444:HOH:O	2.05	0.56
1:B:262:PRO:O	1:B:272:TYR:HB2	2.05	0.55
1:B:340:GLN:HG3	1:B:344:LYS:HE3	1.87	0.55
1:B:128:SER:OG	3:B:2450:ONL:HA	2.07	0.55
1:B:287:ALA:O	1:B:291:GLU:HB3	2.07	0.55
1:B:269:ILE:HG23	1:B:449:GLU:HB2	1.88	0.55
1:A:357:PHE:HB3	1:A:387:ALA:HB2	1.88	0.55
1:B:275:ARG:O	1:B:308:ILE:HG12	2.07	0.55
1:A:336:MET:HB3	1:A:341:LEU:HD23	1.89	0.54
1:B:10:MET:HB3	1:B:11:PRO:HD2	1.88	0.54
1:B:350:LEU:HD13	1:B:378:ILE:HD11	1.88	0.54
1:B:485:ASP:O	1:B:489:VAL:HG23	2.08	0.54
1:B:269:ILE:HG23	1:B:449:GLU:CB	2.38	0.54
1:B:67:MET:HG2	1:B:172:MET:SD	2.48	0.54
1:B:36:ILE:HG12	1:B:42:PHE:CE1	2.42	0.54
1:A:370:VAL:HG22	1:A:399:ILE:HD12	1.89	0.53
1:B:139:LEU:HD21	1:B:173:ILE:CD1	2.38	0.53
1:B:308:ILE:HG21	1:B:395:ALA:HB2	1.91	0.53
1:A:26:ARG:HD2	1:A:209:GLU:OE2	2.09	0.53
1:B:379:ILE:HD11	1:B:429:ILE:HD12	1.90	0.53
1:A:271:VAL:O	1:A:275:ARG:HG3	2.08	0.53
1:A:74:TYR:O	3:A:2377:ONL:HE3	2.09	0.53
1:B:333:THR:HG22	1:B:345:SER:CB	2.39	0.53
1:A:332:ARG:HB2	1:A:335:ILE:HG12	1.91	0.53
1:A:167:TYR:CE1	1:A:183:ASP:HA	2.44	0.52
1:A:275:ARG:CA	1:A:278:MET:HE3	2.36	0.52
1:A:34:ILE:HB	1:A:44:LEU:HD12	1.91	0.52
1:A:308:ILE:HD13	1:A:395:ALA:CB	2.40	0.52
1:A:241:ARG:HG2	1:A:242:GLN:N	2.24	0.52
1:A:254:PHE:HD2	1:A:407:ILE:HD13	1.75	0.52
1:A:15:SER:HB3	1:A:216:LEU:HD13	1.92	0.51
1:A:184:PRO:HB3	1:A:244:ALA:HB1	1.92	0.51
1:A:102:GLY:HA2	1:A:188:ARG:CD	2.41	0.51
1:A:8:GLY:HA2	1:A:203:GLU:HG2	1.92	0.51
1:A:194:LYS:HA	1:A:203:GLU:O	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:164:ARG:HB3	1:A:469:ASP:OD2	2.10	0.50
1:B:189:PRO:HB2	1:B:208:SER:O	2.11	0.50
1:A:3:ILE:O	1:A:207:ALA:HA	2.10	0.50
1:A:29:ASP:HB2	1:A:73:ARG:O	2.12	0.50
1:A:364:LEU:HD13	1:A:378:ILE:HG22	1.93	0.50
1:A:156:ILE:O	1:A:159:THR:HB	2.11	0.50
1:B:225:ALA:O	1:B:228:GLU:HB3	2.12	0.50
1:B:31:ALA:HA	1:B:71:HIS:O	2.12	0.50
1:A:262:PRO:HA	1:A:271:VAL:HB	1.93	0.50
1:A:404:VAL:HG21	1:A:470:VAL:HG21	1.93	0.50
1:B:113:LYS:HB3	1:B:113:LYS:HZ2	1.76	0.50
1:A:31:ALA:HA	1:A:71:HIS:O	2.12	0.49
1:A:300:PRO:HB3	1:A:309:ALA:HB3	1.93	0.49
1:A:290:TRP:O	1:A:293:LEU:HB2	2.11	0.49
1:A:375:SER:O	1:A:379:ILE:HG13	2.12	0.49
1:A:6:ILE:HG12	1:A:205:MET:HB2	1.95	0.49
1:B:145:TYR:CD1	1:B:146:PRO:HA	2.48	0.49
1:B:377:GLN:O	1:B:381:MET:HG3	2.12	0.49
1:A:194:LYS:HB2	1:A:202:THR:CG2	2.42	0.49
1:A:424:GLU:O	1:A:428:ILE:HG13	2.13	0.49
1:A:121:HIS:CE1	5:A:2515:HOH:O	2.66	0.49
1:A:102:GLY:HA2	1:A:188:ARG:HD2	1.94	0.48
1:B:282:LEU:HD23	1:B:312:ILE:HD11	1.94	0.48
1:A:307:ASP:HB2	5:A:2506:HOH:O	2.13	0.48
1:A:337:PRO:HB2	1:A:491:ARG:NH1	2.29	0.48
1:A:401:PHE:O	1:A:460:VAL:HG12	2.13	0.48
1:B:338:GLY:O	1:B:342:ARG:HG3	2.12	0.48
1:A:11:PRO:HA	1:A:65:GLY:O	2.14	0.48
1:A:166:ALA:HB1	1:A:188:ARG:HG2	1.96	0.48
1:A:359:ASP:O	1:A:388:LYS:HD3	2.14	0.48
1:B:330:VAL:HG11	1:B:349:LYS:HB2	1.95	0.48
1:A:357:PHE:CD1	1:A:362:VAL:HG11	2.49	0.48
1:B:447:ARG:NH1	1:B:451:PRO:O	2.47	0.48
1:A:188:ARG:HD2	1:A:405:TYR:O	2.13	0.48
1:A:404:VAL:HG22	5:A:2398:HOH:O	2.13	0.48
1:B:86:GLN:HB3	1:B:87:PRO:HA	1.96	0.48
1:A:44:LEU:HG	1:A:45:ARG:N	2.29	0.47
1:B:293:LEU:HD11	1:B:391:TYR:CE1	2.49	0.47
1:A:102:GLY:O	3:A:2377:ONL:HB1	2.14	0.47
1:B:34:ILE:HA	1:B:43:ARG:O	2.14	0.47
1:A:486:ALA:O	1:A:490:GLN:HG3	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:32:GLY:HA3	1:A:86:GLN:O	2.15	0.47
1:B:425:ILE:O	1:B:429:ILE:HG12	2.14	0.47
1:A:14:GLN:HB3	5:A:2395:HOH:O	2.15	0.47
1:A:483:ASN:O	1:A:486:ALA:N	2.47	0.47
1:A:128:SER:OG	3:A:2377:ONL:HA	2.14	0.47
1:A:195:ARG:HB3	1:A:203:GLU:HB2	1.97	0.47
1:A:22:VAL:HG11	1:A:215:THR:HG21	1.97	0.47
1:B:318:LYS:HA	1:B:318:LYS:HD3	1.69	0.47
1:A:195:ARG:HA	5:A:2453:HOH:O	2.14	0.47
1:A:446:VAL:HG23	5:A:2514:HOH:O	2.14	0.46
1:A:491:ARG:HD2	5:A:2491:HOH:O	2.14	0.46
1:B:321:ARG:HA	1:B:321:ARG:HD3	1.71	0.46
1:B:403:ASN:H	1:B:409:MET:HB2	1.79	0.46
1:A:131:LEU:HD23	1:A:131:LEU:O	2.15	0.46
1:B:75:PRO:HD2	5:B:2561:HOH:O	2.15	0.46
1:A:34:ILE:HD11	1:A:42:PHE:HB3	1.97	0.46
1:B:26:ARG:HD2	1:B:209:GLU:OE2	2.16	0.46
1:B:440:ASN:H	1:B:440:ASN:ND2	2.13	0.46
1:A:145:TYR:CD1	1:A:146:PRO:HA	2.51	0.46
1:A:401:PHE:CD2	1:A:463:GLY:N	2.84	0.46
1:B:261:ARG:HB3	1:B:263:ASP:OD1	2.16	0.46
1:A:252:CYS:HA	1:A:457:GLU:HB3	1.97	0.46
1:A:34:ILE:HA	1:A:43:ARG:O	2.16	0.46
1:A:442:LEU:HG	5:A:2514:HOH:O	2.14	0.46
1:B:302:PRO:HG3	5:B:2576:HOH:O	2.15	0.46
1:A:13:ASN:OD1	1:A:14:GLN:N	2.48	0.46
1:A:333:THR:O	1:A:342:ARG:HG2	2.16	0.46
1:B:99:ALA:HB3	1:B:170:VAL:HG12	1.98	0.46
1:B:212:ALA:O	1:B:215:THR:HG22	2.15	0.46
1:A:302:PRO:HA	1:A:303:GLU:HA	1.58	0.45
1:B:477:PHE:O	1:B:481:LEU:HD13	2.16	0.45
1:A:113:LYS:O	1:A:117:GLU:HB2	2.16	0.45
1:A:265:PHE:HA	1:A:269:ILE:O	2.17	0.45
1:B:301:ILE:HD12	1:B:366:ASP:HB2	1.98	0.45
1:B:392:LEU:HD12	1:B:393:ALA:N	2.32	0.45
5:A:2497:HOH:O	1:B:22:VAL:HG13	2.16	0.45
1:A:400:ARG:HD3	5:A:2394:HOH:O	2.16	0.45
1:B:9:VAL:HG22	1:B:197:ILE:HG13	1.95	0.45
1:B:150:ASP:HB2	5:B:2572:HOH:O	2.16	0.45
1:B:475:LEU:HD23	1:B:475:LEU:HA	1.82	0.45
1:A:288:ARG:HB2	1:A:288:ARG:HE	1.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:198:ASP:O	1:B:200:ASN:N	2.50	0.45
1:A:350:LEU:HD13	1:A:378:ILE:HD11	1.98	0.44
1:A:426:ARG:HG2	1:A:426:ARG:HH11	1.82	0.44
1:B:42:PHE:HD2	1:B:89:TYR:CE2	2.35	0.44
1:A:211:VAL:HG13	1:A:264:SER:OG	2.18	0.44
4:A:505:PCP:O3B	1:B:328:ARG:NH1	2.51	0.44
1:B:447:ARG:HG2	1:B:456:PHE:CE2	2.45	0.44
1:A:401:PHE:HA	1:A:402:PRO:HD3	1.77	0.44
1:A:310:LEU:HD21	1:B:320:TYR:O	2.17	0.44
1:B:357:PHE:O	1:B:387:ALA:HA	2.17	0.44
1:B:392:LEU:O	1:B:434:LEU:HA	2.18	0.44
1:B:486:ALA:HB1	5:B:2579:HOH:O	2.18	0.44
1:A:94:TYR:CE2	1:A:147:LEU:HG	2.52	0.44
1:A:321:ARG:HG3	1:A:356:GLU:OE1	2.18	0.44
1:A:96:ILE:HA	1:A:172:MET:O	2.17	0.44
1:A:357:PHE:HD1	1:A:362:VAL:HG11	1.83	0.43
1:B:282:LEU:O	1:B:286:ILE:HG13	2.18	0.43
1:B:462:ASN:OD1	1:B:464:VAL:HG13	2.17	0.43
1:A:94:TYR:O	1:A:174:ILE:HB	2.18	0.43
1:B:240:THR:O	1:B:241:ARG:HB2	2.18	0.43
1:B:25:HIS:CE1	1:B:261:ARG:HG3	2.54	0.43
1:B:304:THR:HB	1:B:367:ASP:OD1	2.18	0.43
1:B:2:GLY:O	1:B:71:HIS:HA	2.18	0.43
1:A:196:ASP:HA	1:A:202:THR:HA	2.00	0.43
1:A:255:GLU:HA	1:A:259:PHE:HB3	1.98	0.43
1:B:462:ASN:ND2	1:B:464:VAL:HG13	2.33	0.43
1:A:378:ILE:HA	1:A:378:ILE:HD13	1.76	0.43
1:A:213:LEU:N	1:A:213:LEU:HD23	2.32	0.43
1:B:88:PHE:O	1:B:97:THR:HA	2.19	0.43
1:A:34:ILE:HG22	1:A:87:PRO:HG3	2.00	0.43
1:B:244:ALA:HB1	5:B:2473:HOH:O	2.19	0.43
1:B:438:ASP:O	1:B:441:ASP:HB2	2.18	0.43
1:B:269:ILE:HD13	1:B:446:VAL:HG12	2.00	0.43
1:A:349:LYS:NZ	5:A:2512:HOH:O	2.52	0.43
1:B:103:ASN:HA	1:B:127:ASP:OD2	2.19	0.43
1:B:401:PHE:HA	1:B:402:PRO:HD3	1.84	0.43
1:A:104:LEU:HD21	1:A:131:LEU:HD12	2.01	0.43
1:B:8:GLY:HA2	1:B:203:GLU:HG2	2.00	0.43
1:A:139:LEU:HD23	1:A:139:LEU:HA	1.59	0.42
1:A:144:HIS:CE1	1:A:151:ASN:OD1	2.72	0.42
1:B:308:ILE:HG13	5:B:2508:HOH:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:142:PHE:C	1:A:143:ARG:HG3	2.39	0.42
1:A:404:VAL:HG12	1:A:478:LEU:CD1	2.42	0.42
1:B:199:GLU:O	1:B:200:ASN:CB	2.65	0.42
1:B:102:GLY:HA2	1:B:188:ARG:HD2	2.01	0.42
1:B:354:ARG:HG2	5:B:2582:HOH:O	2.18	0.42
1:A:300:PRO:O	1:A:302:PRO:HD3	2.19	0.42
1:B:33:ILE:HG13	1:B:55:PHE:CZ	2.54	0.42
1:A:305:SER:HB3	1:A:366:ASP:HA	2.01	0.42
1:B:312:ILE:HD12	1:B:365:VAL:HG11	2.00	0.42
1:A:179:VAL:HA	1:A:230:ILE:O	2.20	0.42
1:B:265:PHE:CE2	1:B:270:SER:HB2	2.54	0.42
1:B:367:ASP:OD1	4:B:505:PCP:O2	2.37	0.42
1:B:343:ARG:O	1:B:377:GLN:NE2	2.52	0.42
1:A:366:ASP:O	1:A:394:SER:HA	2.19	0.42
1:A:114:LEU:HD13	1:A:122:ILE:HD11	2.01	0.42
1:A:340:GLN:HA	1:A:340:GLN:NE2	2.34	0.42
1:B:230:ILE:HG23	1:B:238:LEU:HD11	2.02	0.42
1:B:333:THR:HA	1:B:336:MET:SD	2.60	0.42
1:A:333:THR:CG2	1:A:349:LYS:HD2	2.49	0.41
1:A:364:LEU:HD13	1:A:378:ILE:CG2	2.50	0.41
1:A:3:ILE:HG22	1:A:71:HIS:HD2	1.84	0.41
1:A:297:VAL:HG12	1:A:362:VAL:HG12	2.02	0.41
1:B:314:ARG:NH2	1:B:315:ILE:HD11	2.35	0.41
1:A:230:ILE:HG23	1:A:238:LEU:HD11	2.03	0.41
1:A:318:LYS:HD3	1:A:318:LYS:HA	1.88	0.41
1:A:20:LEU:HD22	1:A:72:VAL:HG13	2.02	0.41
1:B:280:THR:O	1:B:284:GLU:HG3	2.21	0.41
1:B:28:GLN:HB3	1:B:50:LEU:HD21	2.03	0.41
1:B:34:ILE:HD11	1:B:42:PHE:HB3	2.02	0.41
1:B:379:ILE:CD1	1:B:429:ILE:HD12	2.49	0.41
1:A:143:ARG:C	1:A:145:TYR:H	2.24	0.41
1:A:300:PRO:HB3	1:A:309:ALA:CB	2.51	0.41
1:A:158:ALA:O	1:A:161:ARG:HB2	2.21	0.41
1:B:312:ILE:O	1:B:316:LEU:HG	2.21	0.41
1:B:42:PHE:CD2	1:B:89:TYR:CE2	3.09	0.41
1:A:396:ALA:HA	1:A:397:PRO:HD3	1.85	0.41
1:A:420:ARG:NE	1:A:428:ILE:HD11	2.36	0.41
1:A:439:LEU:O	1:A:443:ILE:HD12	2.21	0.41
1:B:194:LYS:HB3	1:B:204:TYR:CD1	2.56	0.41
1:B:410:PRO:HG3	1:B:482:ARG:HB3	2.03	0.41
1:B:221:LEU:HD23	1:B:221:LEU:HA	1.83	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:142:PHE:CD2	1:A:151:ASN:HB3	2.56	0.40
1:B:159:THR:O	1:B:163:ILE:HG12	2.21	0.40
1:B:399:ILE:HG22	1:B:415:LEU:HD13	2.02	0.40
1:B:35:THR:OG1	1:B:43:ARG:HB2	2.22	0.40
1:A:166:ALA:CB	1:A:405:TYR:HB3	2.51	0.40
1:A:197:ILE:HB	1:A:201:ARG:O	2.21	0.40
1:A:9:VAL:CG2	1:A:197:ILE:HG13	2.51	0.40
1:A:78:GLY:HA3	1:A:84:GLU:OE1	2.20	0.40
1:A:370:VAL:HG22	1:A:399:ILE:CD1	2.52	0.40
1:B:417:ALA:HA	1:B:425:ILE:HD11	2.03	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	490/504 (97%)	460 (94%)	27 (6%)	3 (1%)	25	36
1	B	490/504 (97%)	457 (93%)	30 (6%)	3 (1%)	25	36
All	All	980/1008 (97%)	917 (94%)	57 (6%)	6 (1%)	25	36

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	145	TYR
1	B	199	GLU
1	B	200	ASN
1	B	469	ASP
1	A	144	HIS
1	A	291	GLU

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	411/422 (97%)	393 (96%)	18 (4%)	28	45
1	B	411/422 (97%)	398 (97%)	13 (3%)	39	59
All	All	822/844 (97%)	791 (96%)	31 (4%)	33	51

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	ASN
1	A	58	ARG
1	A	74	TYR
1	A	80	SER
1	A	91	ASN
1	A	92	SER
1	A	113	LYS
1	A	150	ASP
1	A	179	VAL
1	A	213	LEU
1	A	215	THR
1	A	291	GLU
1	A	292	ASP
1	A	293	LEU
1	A	350	LEU
1	A	460	VAL
1	A	477	PHE
1	A	485	ASP
1	B	10	MET
1	B	11	PRO
1	B	22	VAL
1	B	91	ASN
1	B	92	SER
1	B	111	ARG
1	B	150	ASP
1	B	292	ASP
1	B	410	PRO

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Mol	Chain	Res	Type
1	B	414	GLU
1	B	440	ASN
1	B	464	VAL
1	B	483	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	48	ASN
1	A	141	ASN
1	A	144	HIS
1	B	28	GLN
1	B	48	ASN
1	B	144	HIS
1	B	185	ASN
1	B	427	GLN
1	B	440	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 5 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	$\# Z > 2$
3	ONL	B	2450	1	5,9,9	0.32	0	5,11,11	0.85	0
4	PCP	B	505	2	20,22,22	1.46	4 (20%)	29,35,35	1.78	7 (24%)
4	PCP	A	505	2	20,22,22	1.86	4 (20%)	29,35,35	1.65	1 (3%)
3	ONL	A	2377	1	5,9,9	0.45	0	5,11,11	1.22	1 (20%)

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	ONL	B	2450	1	-	2/5/9/9	-
4	PCP	B	505	2	-	5/17/33/33	0/1/1/1
4	PCP	A	505	2	-	5/17/33/33	0/1/1/1
3	ONL	A	2377	1	-	1/5/9/9	-

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	505	PCP	PA-O1	4.21	1.71	1.60
4	B	505	PCP	PA-O1	3.25	1.69	1.60
4	A	505	PCP	CP-C4	3.23	1.58	1.51
4	B	505	PCP	C4-C3	-2.88	1.46	1.54
4	B	505	PCP	P-O2P	-2.43	1.45	1.54
4	A	505	PCP	C5-C4	-2.41	1.47	1.53
4	B	505	PCP	P-O3P	-2.22	1.46	1.54
4	A	505	PCP	C3-C2	-2.09	1.47	1.53

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	505	PCP	P-OP-CP	7.20	138.14	118.30
4	B	505	PCP	P-OP-CP	4.68	131.19	118.30
4	B	505	PCP	O3A-PA-O1	3.69	109.93	102.48
4	B	505	PCP	O3-C3-C4	-3.20	104.46	112.75
4	B	505	PCP	O3P-P-OP	-2.80	99.27	106.73
4	B	505	PCP	O2B-PB-O3A	2.75	113.86	104.64
3	A	2377	ONL	CB-CG-CD	-2.72	111.78	114.57

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	505	PCP	OP-P-O1P	2.70	114.04	106.47
4	B	505	PCP	C5-C4-C3	2.11	107.85	102.66

There are no chirality outliers.

All (13) torsion outliers are listed below:

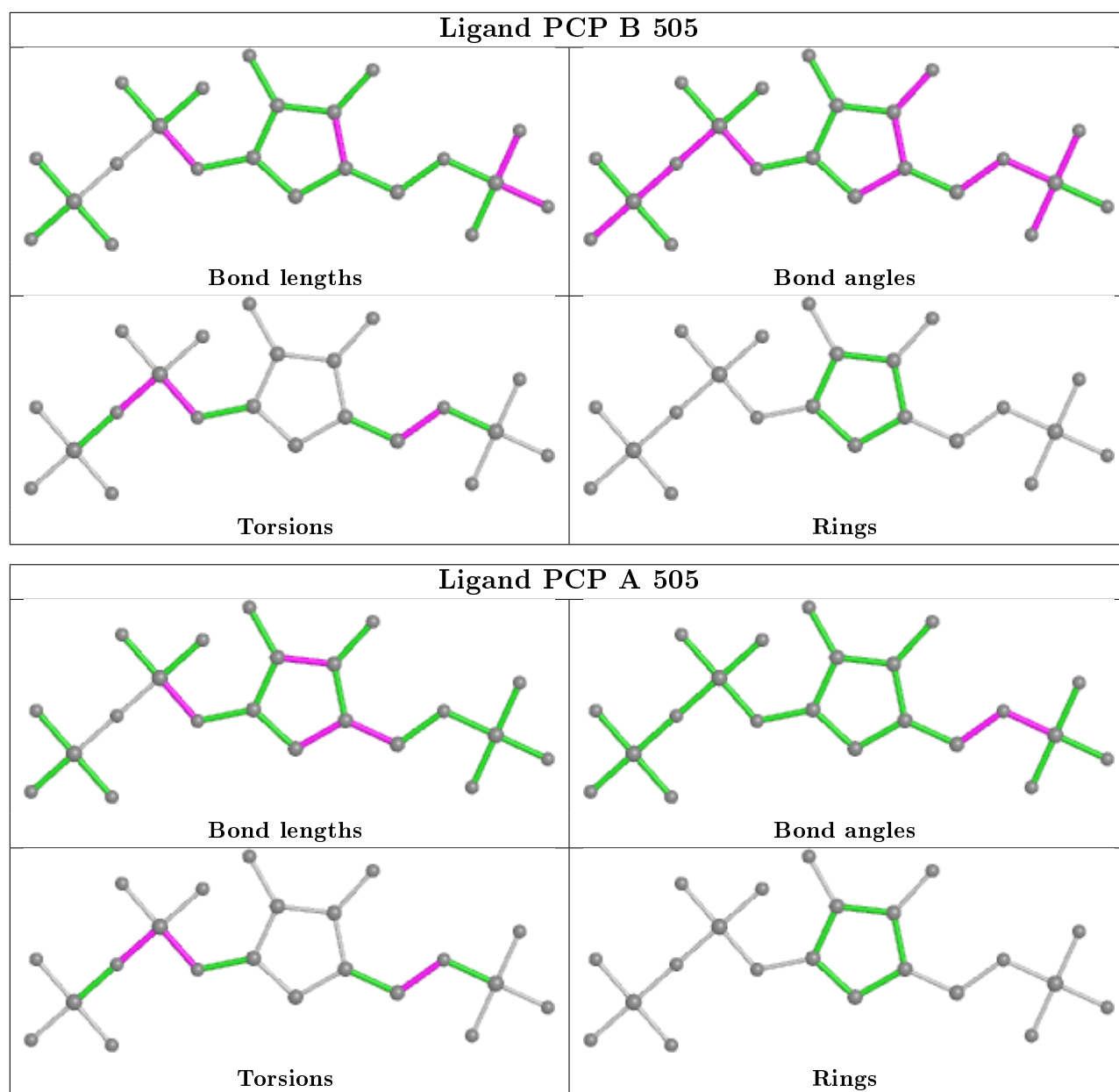
Mol	Chain	Res	Type	Atoms
4	A	505	PCP	C1-O1-PA-O1A
4	A	505	PCP	C1-O1-PA-O2A
4	A	505	PCP	PB-O3A-PA-O1
4	B	505	PCP	C1-O1-PA-O3A
4	A	505	PCP	C1-O1-PA-O3A
3	B	2450	ONL	OD-CD-CG-CB
3	B	2450	ONL	CE-CD-CG-CB
4	B	505	PCP	C1-O1-PA-O1A
4	B	505	PCP	C1-O1-PA-O2A
4	B	505	PCP	PB-O3A-PA-O1
3	A	2377	ONL	CE-CD-CG-CB
4	B	505	PCP	C4-CP-OP-P
4	A	505	PCP	C4-CP-OP-P

There are no ring outliers.

4 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	2450	ONL	3	0
4	B	505	PCP	2	0
4	A	505	PCP	1	0
3	A	2377	ONL	6	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 [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 ⓘ

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.