

# Full wwPDB X-ray Structure Validation Report (i)

Sep 16, 2021 – 02:22 pm BST

PDB ID : 7OT3

Title : Human Prolyl-tRNA Synthetase in Complex with L-proline and Compound

3b

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Deposited on : 2021-06-09

Resolution : 2.53 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 (i) symbol.

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

MolProbity: 4.02b-467

Mogul: 1.8.5 (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)

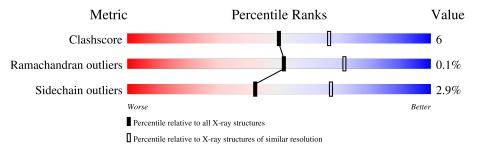
Validation Pipeline (wwPDB-VP) : 2.23.1

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X- $RAY\ DIFFRACTION$ 

The reported resolution of this entry is 2.53 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	Similar resolution		
Metric	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{resolution range}( ext{Å}))$		
Clashscore	141614	6463 (2.54-2.50)		
Ramachandran outliers	138981	6335 (2.54-2.50)		
Sidechain outliers	138945	6337 (2.54-2.50)		

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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain		
1	A	512	81%	15%	• •
1	В	512	78%	16%	• 6%



# 2 Entry composition (i)

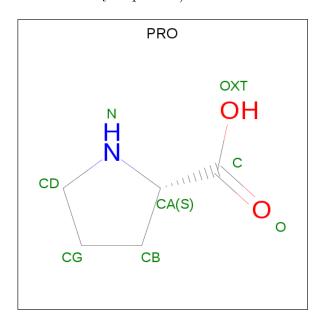
There are 6 unique types of molecules in this entry. The entry contains 7581 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Bifunctional glutamate/proline--tRNA ligase.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	496	Total	С	• '	0	S	0	0	0
			3802	2434	641	702	25	Ü	)	
1	B	483	Total	С	N	О	S	0	0	0
1	Б	400	3679	2358	621	678	22		U	

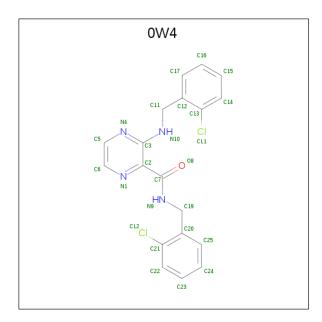
• Molecule 2 is PROLINE (three-letter code: PRO) (formula: C<sub>5</sub>H<sub>9</sub>NO<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total 8		N 1	0	0
2	В	1	Total 8		N 1	0	0

• Molecule 3 is {N}-[(2-chlorophenyl)methyl]-3-[(2-chlorophenyl)methylamino]pyrazine -2-carboxamide (three-letter code: 0W4) (formula: C<sub>19</sub>H<sub>16</sub>Cl<sub>2</sub>N<sub>4</sub>O) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf		
2	Λ.	1	Total	С	Cl	N	О	0	0	
3	3 A	1	26	19	2	4	1	U		
9	D	1	Total	С	Cl	N	О	0	0	
3	D	1	26	19	2	4	1	U		

• Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Zn 1 1	0	0
4	В	1	Total Zn 1 1	0	0

• Molecule 5 is STRONTIUM ION (three-letter code: SR) (formula: Sr).

Mol	Chain	Residues	${f Atoms}$	ZeroOcc	AltConf
5	A	3	Total Sr 3 3	0	0
5	В	1	Total Sr 1 1	0	0

 $\bullet\,$  Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	16	Total O 16 16	0	0



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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	В	10	Total O 10 10	0	0

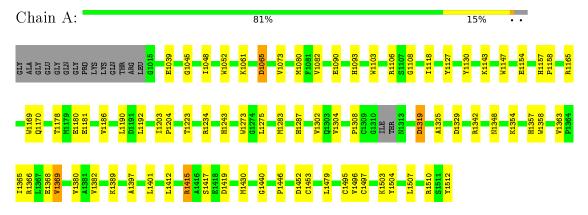


# 3 Residue-property plots (i)

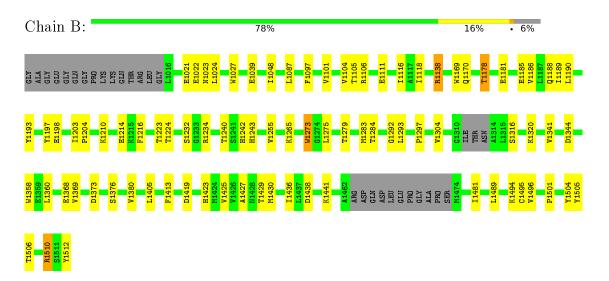
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: Bifunctional glutamate/proline--tRNA ligase



• Molecule 1: Bifunctional glutamate/proline--tRNA ligase





# 4 Data and refinement statistics (i)

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

Property	Value	Source	
Space group	P 1 21 1	Depositor	
Cell constants	71.87Å 92.42Å 87.26Å	Depositor	
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $108.88^{\circ}$ $90.00^{\circ}$	Depositor	
Resolution (Å)	54.77 - 2.53	Depositor	
% Data completeness	99.1 (54.77-2.53)	Depositor	
(in resolution range)	33.1 (04.11 2.00)	Depositor	
$R_{merge}$	0.05	Depositor	
$R_{sym}$	(Not available)	Depositor	
Refinement program	PHENIX 1.17.1_3660	Depositor	
$R, R_{free}$	0.218 , 0.276	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	7581	wwPDB-VP	
Average B, all atoms (Å <sup>2</sup> )	115.0	wwPDB-VP	



# 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: SR, 0W4, ZN

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		
MIOI	Chain	RMSZ	# Z >5	RMSZ	# Z  > 5	
1	A	0.24	0/3897	0.40	0/5309	
1	В	0.24	0/3770	0.41	0/5141	
All	All	0.24	0/7667	0.40	0/10450	

There are no bond length outliers.

There are no bond angle outliers.

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	3802	0	3588	44	0
1	В	3679	0	3448	42	0
2	A	8	0	7	0	0
2	В	8	0	7	0	0
3	A	26	0	0	0	0
3	В	26	0	0	0	0
4	A	1	0	0	0	0
4	В	1	0	0	0	0
5	A	3	0	0	0	0
5	В	1	0	0	0	0
6	A	16	0	0	0	0



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Mol	Chain	Non-H	$\mathbf{H}(\mathbf{model})$	$\mathbf{H}(\mathbf{added})$	Clashes	Symm-Clashes	
6	В	10	0	0	0	0	
All	All	7581	0	7050	84	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 6.

All (84) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1       Atom         1:B:1255:VAL:HG11       1:B:1265:L         1:A:1368:GLU:HB2       1:A:1380:V         1:B:1234:ARG:HH21       1:B:1512:T         1:B:1178:THR:HG23       1:B:1181:G         1:B:1427:ALA:HB2       1:B:1436:II         1:A:1382:VAL:HG22       1:A:1389:L         1:A:1302:VAL:HG11       1:A:1342:A         1:A:1103:TRP:HB2       1:B:1106:A	YS:HE3 VAL:HB CYR:HA LU:HB2 LE:HD11 YS:HG2 RG:HB2 RG:HG3	1.61 1.70 1.55 1.74 1.77 1.80 1.80 1.80	overlap (Å)       0.79       0.73       0.71       0.69       0.67       0.63
1:A:1368:GLU:HB2       1:A:1380:V         1:B:1234:ARG:HH21       1:B:1512:T         1:B:1178:THR:HG23       1:B:1181:G         1:B:1427:ALA:HB2       1:B:1436:II         1:A:1382:VAL:HG22       1:A:1389:L         1:A:1302:VAL:HG11       1:A:1342:A         1:A:1103:TRP:HB2       1:B:1106:A	VAL:HB TYR:HA LU:HB2 LE:HD11 YS:HG2 RG:HB2 RG:HG3	1.70 1.55 1.74 1.77 1.80 1.80	0.73 0.71 0.69 0.67 0.63
1:B:1234:ARG:HH21       1:B:1512:T         1:B:1178:THR:HG23       1:B:1181:G         1:B:1427:ALA:HB2       1:B:1436:H         1:A:1382:VAL:HG22       1:A:1389:L         1:A:1302:VAL:HG11       1:A:1342:A         1:A:1103:TRP:HB2       1:B:1106:A	CYR:HA ELU:HB2 E:HD11 YS:HG2 RG:HB2 RG:HG3	1.55 1.74 1.77 1.80 1.80	0.71 0.69 0.67 0.63
1:B:1178:THR:HG23       1:B:1181:G         1:B:1427:ALA:HB2       1:B:1436:II         1:A:1382:VAL:HG22       1:A:1389:L         1:A:1302:VAL:HG11       1:A:1342:A         1:A:1103:TRP:HB2       1:B:1106:A	LU:HB2 LE:HD11 YS:HG2 RG:HB2 RG:HG3	1.74 1.77 1.80 1.80	0.69 0.67 0.63
1:B:1427:ALA:HB2       1:B:1436:II         1:A:1382:VAL:HG22       1:A:1389:L         1:A:1302:VAL:HG11       1:A:1342:A         1:A:1103:TRP:HB2       1:B:1106:A	E:HD11 YS:HG2 RG:HB2 RG:HG3	1.77 1.80 1.80	0.67 0.63
1:A:1382:VAL:HG22 1:A:1389:L 1:A:1302:VAL:HG11 1:A:1342:A 1:A:1103:TRP:HB2 1:B:1106:A	YS:HG2 RG:HB2 RG:HG3	1.80 1.80	0.63
1:A:1302:VAL:HG11 1:A:1342:A 1:A:1103:TRP:HB2 1:B:1106:A	RG:HB2 RG:HG3	1.80	
1:A:1103:TRP:HB2 1:B:1106:A	RG:HG3		0.63
		1.90	1
1 A 1010 ACD OD1 1 A 1010	ASP·N	1.00	0.63
1:A:1319:ASP:OD1 1:A:1319:	*****	2.31	0.63
1:B:1495:CYS:SG 1:B:1496:	VAL:N	2.72	0.63
1:B:1481:ILE:HG12 1:B:1506:TH	HR:HG22	1.84	0.58
1:A:1479:LEU:HD12 1:A:1507:LH	EU:HD22	1.84	0.58
1:B:1104:VAL:N 1:B:1116	:ILE:O	2.35	0.58
1:A:1154:GLU:O 1:A:1165:A	RG:NH2	2.39	0.56
1:A:1204:PRO:HG3 1:A:1417:S	SER:HA	1.90	0.54
1:B:1292:GLY:HA3 1:B:1360:L	EU:HA	1.90	0.54
1:B:1024:LEU:HA 1:B:1027:T	RP:HB3	1.89	0.54
1:A:1170:GLN:HE21 1:A:1275:L	EU:HB3	1.73	0.54
1:B:1344:ASP:OD2 1:B:1358:T	RP:NE1	2.40	0.54
1:A:1190:LEU:HD22 1:A:1223:T	THR:HB	1.89	0.52
1:A:1090:GLU:HB3 1:A:1093:F	HIS:HB3	1.90	0.52
1:B:1284:THR:HG22 1:B:1293:LH	EU:HD11	1.91	0.52
1:A:1073:VAL:HG22 1:A:1143:L	YS:HB3	1.90	0.52
1:A:1234:ARG:HH21 1:A:1512:T	YR:HA	1.74	0.52
1:A:1366:ARG:HH21 1:A:1382:V	AL:HG21	1.75	0.52
1:A:1430:MET:HG2 1:A:1496:VA	AL:HG12	1.93	0.50
1:B:1203:ILE:HD11 1:B:1283:M	ИЕТ:НА	1.93	0.50
1:B:1438:ASP:HA 1:B:1510:AI	RG:HH22	1.76	0.50
1:B:1489:LEU:HD13 1:B:1505:T	YR:HE1	1.77	0.50
1:B:1316:SER:O 1:B:1320:	LYS:N	2.41	0.50
1:A:1440:GLY:HA2 1:A:1510:AI	RG:HH22	1.78	0.49
1:A:1118:ILE:HD11 1:B:1118:II	E:HD11	1.94	0.49



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Atom-1	Atom-2	Interatomic	Clash
		$\operatorname{distance}\left(\mathrm{\AA}\right)$	overlap (Å)
1:B:1429:THR:OG1	1:B:1430:MET:N	2.45	0.48
1:A:1354:LYS:HA	1:A:1357:HIS:HB3	1.95	0.48
1:A:1397:ALA:HA	1:A:1401:LEU:HD13	1.95	0.48
1:B:1024:LEU:HD11	1:B:1232:SER:HB2	1.96	0.48
1:A:1106:ARG:NH1	1:A:1108:GLY:O	2.48	0.47
1:B:1297:PRO:HB3	1:B:1405:LEU:HD22	1.97	0.47
1:A:1495:CYS:SG	1:A:1496:VAL:N	2.89	0.46
1:B:1198:GLU:HG2	1:B:1204:PRO:HA	1.96	0.46
1:A:1045:GLY:HA3	1:A:1165:ARG:HG3	1.98	0.45
1:A:1061:LYS:O	1:A:1065:ASP:HB2	2.17	0.45
1:B:1189:ILE:HG21	1:B:1273:TRP:CG	2.51	0.45
1:A:1052:TRP:HH2	1:A:1302:VAL:HG22	1.80	0.45
1:A:1415:ARG:NH1	1:A:1419:ASP:OD1	2.50	0.45
1:B:1193:TYR:HH	1:B:1273:TRP:HE3	1.65	0.45
1:A:1453:CYS:SG	1:A:1497:CYS:HB3	2.57	0.44
1:B:1368:GLU:HB2	1:B:1380:VAL:HG23	1.99	0.44
1:A:1308:PRO:HA	1:A:1369:VAL:HG23	1.98	0.44
1:B:1185:GLU:HA	1:B:1188:GLN:HG2	1.99	0.44
1:B:1224:THR:HB	1:B:1240:THR:HG22	1.99	0.44
1:B:1039:GLU:HB3	1:B:1048:ILE:HB	2.00	0.44
1:A:1080:MET:HE2	1:A:1080:MET:HB2	1.75	0.43
1:B:1105:THR:O	1:B:1111:GLU:HG3	2.18	0.43
1:B:1210:LYS:HG3	1:B:1214:GLU:HB2	2.01	0.43
1:B:1170:GLN:HE21	1:B:1275:LEU:HB3	1.84	0.43
1:B:1373:ASP:HA	1:B:1376:SER:HB3	2.00	0.43
1:A:1127:TYR:HA	1:A:1130:TYR:HB2	2.01	0.42
1:A:1192:LEU:HD13	1:A:1192:LEU:HA	1.89	0.42
1:A:1178:THR:HB	1:A:1181:GLU:HB2	2.01	0.42
1:B:1197:TYR:CZ	1:B:1279:THR:HG22	2.55	0.42
1:A:1446:PRO:O	1:A:1496:VAL:HG23	2.19	0.42
1:A:1147:TRP:CE3	1:A:1170:GLN:HB3	2.55	0.42
1:A:1325:ALA:O	1:A:1329:ASP:N	2.52	0.42
1:A:1397:ALA:O	1:A:1401:LEU:HB2	2.20	0.41
1:B:1198:GLU:HB3	1:B:1413:PHE:CZ	2.55	0.41
1:B:1304:VAL:O	1:B:1341:VAL:HA	2.20	0.41
1:B:1216:PHE:HB2	1:B:1242:HIS:CE1	2.54	0.41
1:A:1234:ARG:NH2	1:A:1512:TYR:HA	2.34	0.41
1:B:1097:PHE:O	1:B:1101:VAL:HG23	2.20	0.41
1:B:1425:VAL:HG23	1:B:1436:ILE:HD12	2.02	0.41
1:A:1203:ILE:HD11	1:A:1283:MET:HA	2.03	0.41
1:B:1186:VAL:HG21	1:B:1243:HIS:HB2	2.03	0.41



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Atom-1	Atom-2	$egin{array}{ll}  ext{Interatomic} \  ext{distance} \ ( ext{\AA}) \end{array}$	Clash overlap (Å)
1:A:1157:HIS:HA	1:A:1158:PRO:HD3	1.95	0.41
1:A:1287:HIS:ND1	1:A:1412:LEU:HD12	2.36	0.41
1:A:1358:TRP:O	1:A:1363:VAL:HG12	2.21	0.41
1:B:1190:LEU:HD22	1:B:1223:THR:HB	2.03	0.41
1:A:1186:VAL:HG21	1:A:1243:HIS:HB2	2.03	0.41
1:A:1503:LYS:HE2	1:A:1503:LYS:HB3	1.91	0.41
1:A:1039:GLU:HB3	1:A:1048:ILE:HB	2.04	0.40
1:B:1423:HIS:CD2	1:B:1441:LYS:HG3	2.56	0.40
1:B:1494:LYS:HA	1:B:1501:PRO:HA	2.02	0.40
1:A:1304:VAL:HG22	1:A:1365:ILE:HB	2.02	0.40
1:B:1138:ARG:H	1:B:1138:ARG:HD2	1.86	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	n Analysed Favoured Allowed		Outliers	Perce	$\mathbf{ntiles}$	
1	A	$492/512 \; (96\%)$	484 (98%)	8 (2%)	0	100	100
1	В	$477/512 \; (93\%)$	458 (96%)	18 (4%)	1 (0%)	47	67
All	All	969/1024~(95%)	942 (97%)	26 (3%)	1 (0%)	51	71

### All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type	
1	В	1022	$\operatorname{GLU}$	

### 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	381/437 (87%)	370 (97%)	11 (3%)	42 67		
1	В	364/437~(83%)	353 (97%)	11 (3%)	41 66		
All	All	745/874 (85%)	723 (97%)	22 (3%)	42 66		

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type	
1	A	1065	ASP	
1	A	1082	VAL	
1	A	1169	TRP	
1	A	1180	GLU	
1	A	1273	TRP	
1	A	1319	ASP	
1	A	1348	ASN	
1	1 A		VAL	
1	1 A		ARG	
1	1 A 14 1 A 15		ASP	
			TYR	
1	В	1021	$\operatorname{GLU}$	
1	В	1023	ASN	
1	В	1087	LEU	
1	В	1138	ARG	
1	В	1169	TRP	
1	В	1178	THR	
1	В	1273	TRP	
1	В	1369	VAL	
1	В	1419	ASP	
1	В	1504	TYR	
1	В	1510	ARG	

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

Mol	Chain	Res	Type
1	A	1170	GLN
1	A	1266	GLN
1	В	1023	ASN
1	В	1093	HIS
1	В	1135	GLN



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Mol	Chain	Res	Type
1	В	1170	GLN
1	1 B 1246		GLN
1	В	1247	ASN
1	В	1428	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 monosaccharides in this entry.

### 5.6 Ligand geometry (i)

Of 10 ligands modelled in this entry, 6 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	Pos	Res Link	Bond lengths		Bond angles			
MIOI	Type	Chain	nes		Counts	RMSZ	# Z  > 2	Counts	RMSZ	$\mid \# Z  > 2 \mid$
2	PRO	В	1601	_	5,8,8	0.53	0	6,10,10	1.00	0
3	0W4	A	1602	_	28,28,28	0.18	0	36,37,37	0.29	0
2	PRO	A	1601	_	5,8,8	0.57	0	6,10,10	1.00	0
3	0W4	В	1602	_	28,28,28	0.17	0	36,37,37	0.29	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	$\mathbf{Type}$	Chain	$\operatorname{Res}$	Link	Chirals	${f Torsions}$	Rings
2	PRO	В	1601	_	-	0/0/11/11	0/1/1/1
3	0W4	A	1602	_	-	0/14/14/14	0/3/3/3
2	PRO	A	1601	-	-	0/0/11/11	0/1/1/1
3	0W4	В	1602	-	-	3/14/14/14	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

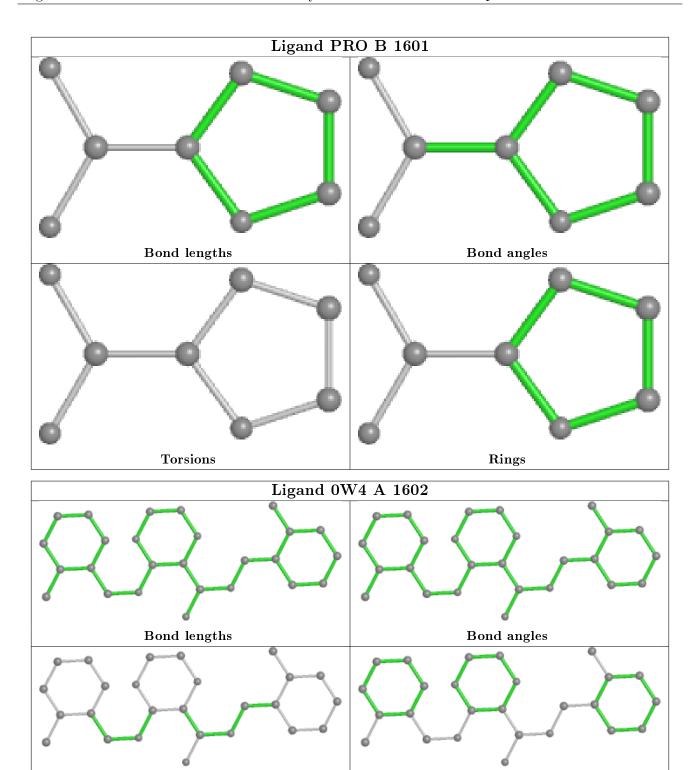
Mol	Chain	Res	Type	Atoms
3	В	1602	0W4	C2-C3-N10-C11
3	В	1602	0W4	N4-C3-N10-C11
3	В	1602	0W4	C12-C11-N10-C3

There are no ring outliers.

No monomer is involved in short contacts.

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 then 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.

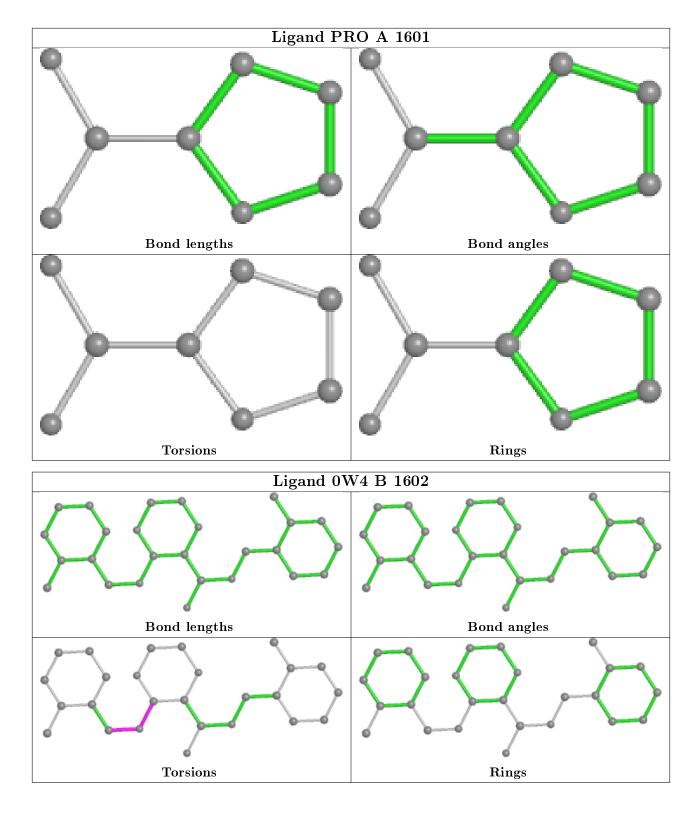






Rings

Torsions



# 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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

# 6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

### 6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

## 6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

