WORLDWIDE wwPDB PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report (i)

Aug 22, 2023 – 04:26 AM EDT

PDB ID	:	2Q5J
Title	:	X-ray structure of phenylpyruvate decarboxylase in complex with 3-deaza-ThDP
Authors	:	Versees, W.; Spaepen, S.; Wood, M.D.; Leeper, F.J.; Vanderleyden, J.; Steyaert, J.
Deposited on	:	2007-06-01
Resolution	:	3.20 Å(reported)

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

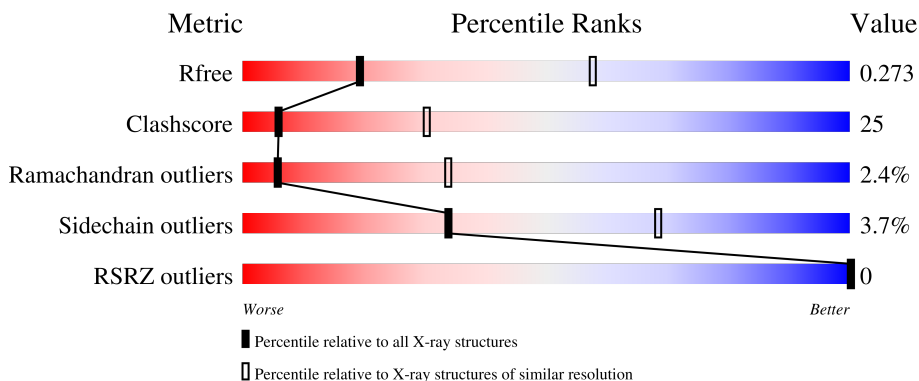|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 3.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.

Metric	Percentile Ranks	Value
Rfree		0.273
Clashscore		25
Ramachandran outliers		2.4%
Sidechain outliers		3.7%
RSRZ outliers		0

Worse   *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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 <=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	565	52% 38% • 7%
1	B	565	55% 36% •• 6%

2 Entry composition ⓘ

There are 4 unique types of molecules in this entry. The entry contains 8008 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 Phenylpyruvate decarboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	523	Total 3884	C 2459	N 678	O 724	S 23	0	0	0
1	B	530	Total 3935	C 2488	N 687	O 737	S 23	0	0	0

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP P51852
A	-18	GLY	-	expression tag	UNP P51852
A	-17	SER	-	expression tag	UNP P51852
A	-16	SER	-	expression tag	UNP P51852
A	-15	HIS	-	expression tag	UNP P51852
A	-14	HIS	-	expression tag	UNP P51852
A	-13	HIS	-	expression tag	UNP P51852
A	-12	HIS	-	expression tag	UNP P51852
A	-11	HIS	-	expression tag	UNP P51852
A	-10	HIS	-	expression tag	UNP P51852
A	-9	SER	-	expression tag	UNP P51852
A	-8	SER	-	expression tag	UNP P51852
A	-7	GLY	-	expression tag	UNP P51852
A	-6	LEU	-	expression tag	UNP P51852
A	-5	VAL	-	expression tag	UNP P51852
A	-4	PRO	-	expression tag	UNP P51852
A	-3	ARG	-	expression tag	UNP P51852
A	-2	GLY	-	expression tag	UNP P51852
A	-1	SER	-	expression tag	UNP P51852
A	0	HIS	-	expression tag	UNP P51852
A	155	GLN	LEU	expression tag	UNP P51852
A	327	ARG	GLY	SEE REMARK 999	UNP P51852
B	-19	MET	-	expression tag	UNP P51852
B	-18	GLY	-	expression tag	UNP P51852
B	-17	SER	-	expression tag	UNP P51852

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	-16	SER	-	expression tag	UNP P51852
B	-15	HIS	-	expression tag	UNP P51852
B	-14	HIS	-	expression tag	UNP P51852
B	-13	HIS	-	expression tag	UNP P51852
B	-12	HIS	-	expression tag	UNP P51852
B	-11	HIS	-	expression tag	UNP P51852
B	-10	HIS	-	expression tag	UNP P51852
B	-9	SER	-	expression tag	UNP P51852
B	-8	SER	-	expression tag	UNP P51852
B	-7	GLY	-	expression tag	UNP P51852
B	-6	LEU	-	expression tag	UNP P51852
B	-5	VAL	-	expression tag	UNP P51852
B	-4	PRO	-	expression tag	UNP P51852
B	-3	ARG	-	expression tag	UNP P51852
B	-2	GLY	-	expression tag	UNP P51852
B	-1	SER	-	expression tag	UNP P51852
B	0	HIS	-	expression tag	UNP P51852
B	155	GLN	LEU	expression tag	UNP P51852
B	327	ARG	GLY	SEE REMARK 999	UNP P51852

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 3 is 2-{4-[(4-AMINO-2-METHYLPYRIMIDIN-5-YL)METHYL]-3-METHYL THIOPHEN-2-YL}ETHYL TRIHYDROGEN DIPHOSPHATE (three-letter code: TPW) (formula: $C_{13}H_{19}N_3O_7P_2S$).
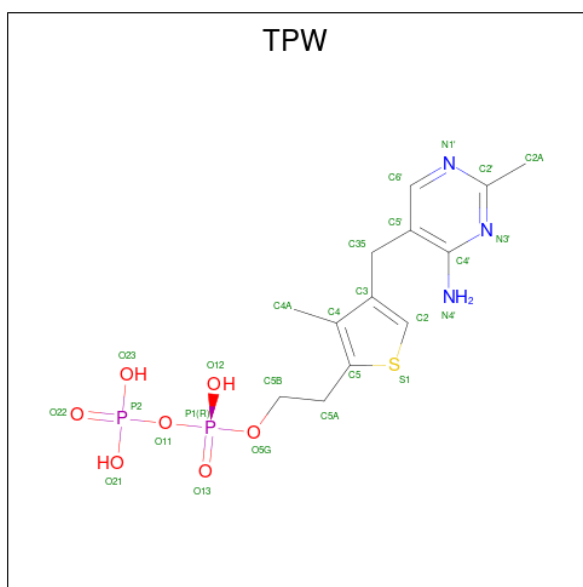
TPW

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	S	0	0
			26	13	3	7	2	1		
3	B	1	Total	C	N	O	P	S	0	0
			26	13	3	7	2	1		

• Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	56	Total	O	0	0
			56	56		
4	B	79	Total	O	0	0
			79	79		

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.
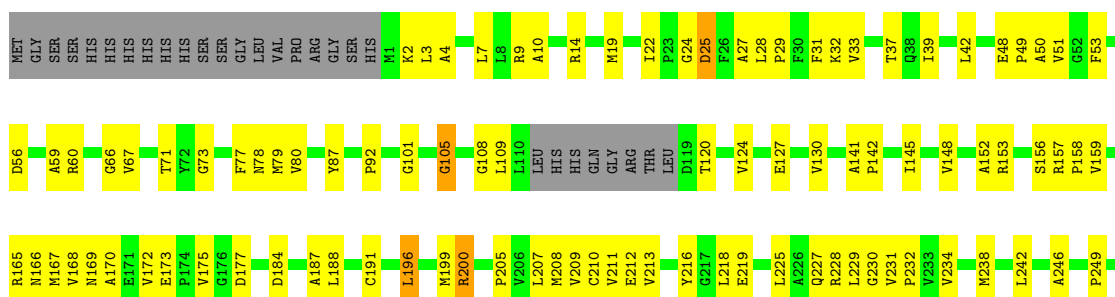
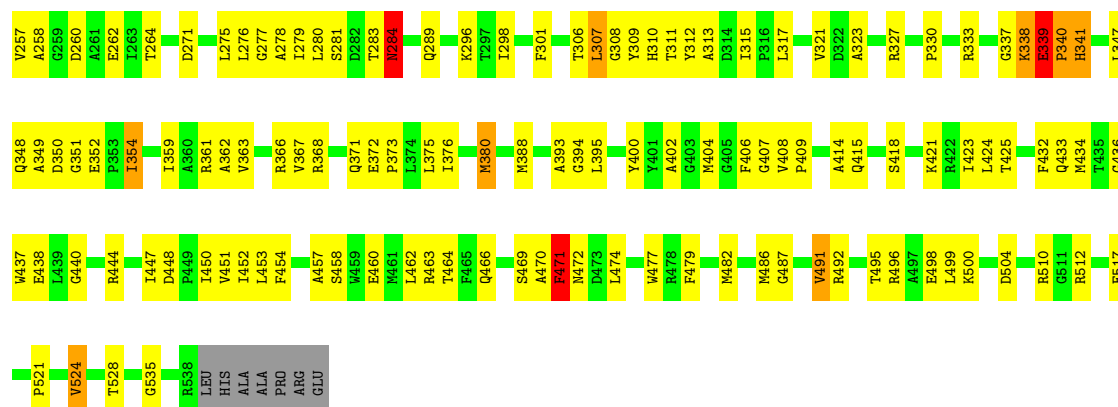- Molecule 1: Phenylpyruvate decarboxylase

Chain A:
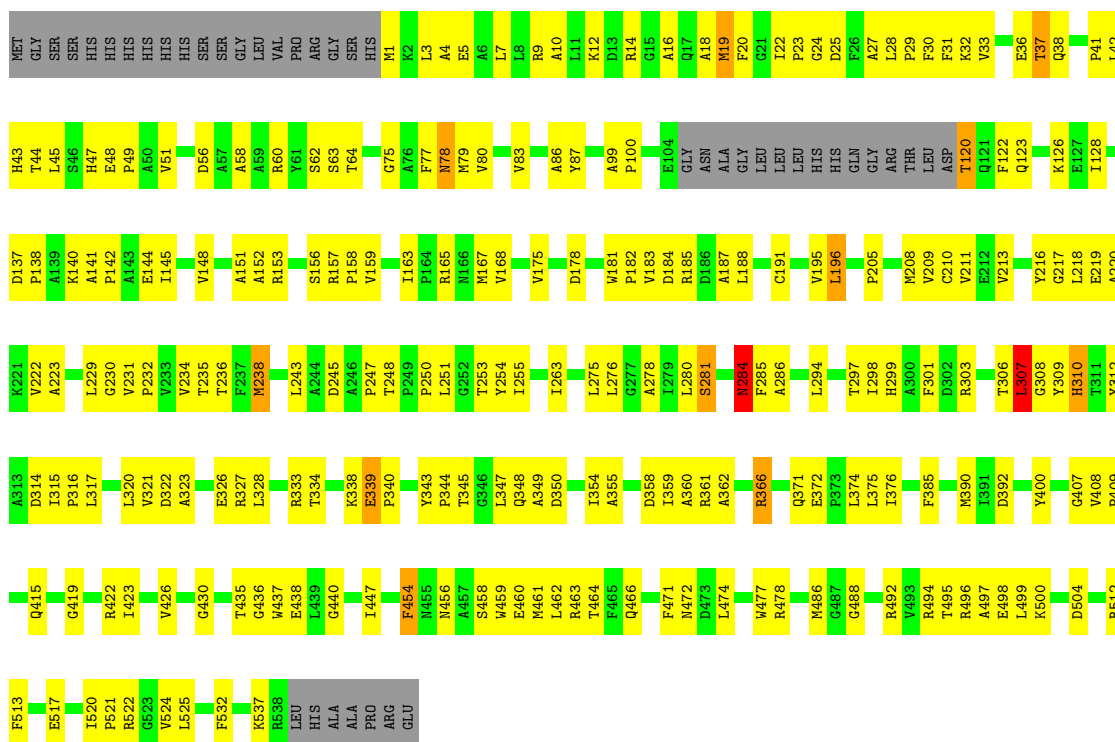
- Molecule 1: Phenylpyruvate decarboxylase

Chain B:

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	100.54Å 179.81Å 121.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.20 36.81 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.4 (50.00-3.20) 96.7 (36.81-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.16	Depositor
$< I/\sigma(I) >$ [1]	2.55 (at 3.18Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.176 , 0.289 0.162 , 0.273	Depositor DCC
R_{free} test set	911 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å^2)	62.0	Xtriage
Anisotropy	0.146	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 46.6	EDS
L-test for twinning[2]	$< |L| > = 0.48, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.013 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.030 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	8008	wwPDB-VP
Average B, all atoms (Å^2)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.53% of the height of the origin peak. No significant pseudotranslation is detected.*

---

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: MG, TPW

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	0.35	0/3959	0.62	0/5383
1	B	0.36	0/4010	0.63	1/5452 (0.0%)
All	All	0.35	0/7969	0.62	1/10835 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	105	GLY	N-CA-C	7.99	133.06	113.10

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	3884	0	3876	202	0
1	B	3935	0	3921	203	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	26	0	16	2	0
3	B	26	0	16	3	0
4	A	56	0	0	6	0
4	B	79	0	0	2	0

Continued on next page...

WORLD WIDE
wwPDB
PROTEIN DATA BANK

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	8008	0	7829	392	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 25.

All (392) 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:18:ALA:HA	1:A:41:PRO:HD2	1.41	1.00
1:A:120:THR:HG22	1:A:123:GLN:H	1.35	0.91
1:A:14:ARG:HD3	1:A:153:ARG:HD2	1.54	0.89
1:A:366:ARG:HB3	1:A:371:GLN:HE21	1.36	0.89
1:A:458:SER:HA	1:A:474:LEU:HG	1.55	0.88
1:A:462:LEU:HB2	1:A:472:ASN:HD21	1.44	0.83
1:A:196:LEU:HD21	1:A:328:LEU:HD21	1.61	0.82
1:A:12:LYS:HA	1:A:16:ALA:HB3	1.60	0.82
1:A:1:MET:CE	1:A:9:ARG:HE	1.93	0.81
1:A:354:ILE:HG13	1:A:494:ARG:O	1.80	0.81
1:B:458:SER:HB2	1:B:472:ASN:O	1.79	0.81
1:B:366:ARG:HB3	1:B:371:GLN:NE2	1.96	0.81
1:A:408:VAL:HB	1:A:409:PRO:HD3	1.62	0.80
1:A:415:GLN:HE21	1:A:422:ARG:HA	1.49	0.78
1:B:246:ALA:O	1:B:249:PRO:HD3	1.83	0.78
1:A:303:ARG:NH1	1:A:316:PRO:HB3	2.00	0.77
1:A:366:ARG:HB3	1:A:371:GLN:NE2	2.00	0.77
1:B:348:GLN:HB2	1:B:496:ARG:HH11	1.52	0.75
1:B:327:ARG:HG3	1:B:327:ARG:HH11	1.51	0.74
1:A:77:PHE:O	1:A:80:VAL:HG23	1.86	0.74
1:B:196:LEU:HD22	1:B:200:ARG:HD2	1.68	0.74
1:B:260:ASP:OD2	1:B:262:GLU:HB3	1.88	0.74
1:B:22:ILE:HG13	1:B:51:VAL:HG21	1.67	0.73
1:A:14:ARG:HB3	1:A:153:ARG:NH1	2.04	0.73
1:B:521:PRO:O	1:B:524:VAL:HG23	1.89	0.72
1:B:354:ILE:HD12	1:B:499:LEU:HD22	1.71	0.71
1:A:251:LEU:O	1:A:263:ILE:HD11	1.89	0.71
1:A:312:TYR:HB3	1:A:315:ILE:HD11	1.72	0.71
1:A:187:ALA:HB1	1:A:312:TYR:HD1	1.56	0.71
1:B:366:ARG:HE	1:B:371:GLN:NE2	1.88	0.70
1:A:213:VAL:HG13	1:A:222:VAL:HG21	1.73	0.70
1:A:462:LEU:HB2	1:A:472:ASN:ND2	2.06	0.70
1:B:375:LEU:HG	1:B:394:GLY:O	1.91	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1:MET:HE1	1:A:9:ARG:HE	1.58	0.69
1:B:228:ARG:HD3	1:B:330:PRO:HA	1.74	0.69
1:B:281:SER:HA	1:B:289:GLN:HE22	1.58	0.69
1:B:366:ARG:HB3	1:B:371:GLN:HE21	1.57	0.69
1:B:338:LYS:HG2	1:B:339:GLU:H	1.56	0.69
1:B:408:VAL:HB	1:B:409:PRO:HD3	1.75	0.69
1:B:352:GLU:O	1:B:496:ARG:HG3	1.93	0.69
1:A:408:VAL:HG21	1:A:436:GLY:HA2	1.74	0.68
1:A:230:GLY:HA2	1:A:333:ARG:NH2	2.09	0.68
1:A:255:ILE:HB	1:A:285:PHE:HD1	1.56	0.68
1:A:299:HIS:CE1	1:A:301:PHE:HB2	2.28	0.68
1:B:200:ARG:HG3	1:B:200:ARG:HH11	1.57	0.68
1:A:209:VAL:HG13	1:A:213:VAL:HG21	1.76	0.68
1:B:212:GLU:HB2	1:B:277:GLY:HA3	1.74	0.68
1:B:298:ILE:HD12	1:B:298:ILE:N	2.08	0.68
1:A:79:MET:O	1:A:79:MET:HG2	1.93	0.67
1:A:238:MET:HG3	1:A:400:TYR:CE2	2.29	0.67
1:A:236:THR:O	1:A:253:THR:HG23	1.95	0.67
1:B:348:GLN:O	1:B:350:ASP:N	2.26	0.67
1:B:283:THR:HG21	1:B:400:TYR:O	1.95	0.66
1:B:77:PHE:HA	1:B:80:VAL:HG23	1.76	0.66
1:A:28:LEU:HB2	1:A:29:PRO:HD3	1.78	0.65
1:A:31:PHE:HB3	1:B:471:PHE:CE2	2.32	0.65
1:B:33:VAL:O	1:B:37:THR:HG23	1.97	0.65
1:A:210:CYS:SG	1:A:211:VAL:HG12	2.37	0.65
1:A:188:LEU:HD13	1:A:315:ILE:HG23	1.80	0.64
1:A:210:CYS:HB3	1:A:278:ALA:HA	1.78	0.64
1:A:512:ARG:NH2	4:A:2046:HOH:O	2.30	0.64
1:A:477:TRP:CH2	1:B:440:GLY:HA3	2.33	0.64
1:A:488:GLY:HA3	1:A:513:PHE:CZ	2.33	0.64
1:A:345:THR:O	1:A:361:ARG:HD3	1.98	0.64
1:A:4:ALA:HB3	1:A:33:VAL:HG11	1.80	0.64
1:A:32:LYS:HB2	1:B:466:GLN:NE2	2.13	0.64
1:A:137:ASP:OD2	1:A:140:LYS:HG3	1.97	0.63
1:A:182:PRO:HB2	1:A:314:ASP:OD1	1.97	0.63
1:A:327:ARG:HH11	1:A:327:ARG:HG3	1.63	0.63
1:A:371:GLN:HG2	1:A:372:GLU:N	2.12	0.63
1:A:495:THR:OG1	1:A:498:GLU:HG3	1.98	0.63
1:B:205:PRO:O	1:B:232:PRO:HD2	1.99	0.63
1:B:363:VAL:O	1:B:367:VAL:HG23	1.97	0.63
1:A:306:THR:C	1:A:307:LEU:HG	2.19	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:4:ALA:HB2	1:B:168:VAL:HG13	1.81	0.62
1:B:380:MET:HG3	1:B:402:ALA:HA	1.81	0.62
1:B:347:LEU:HD11	1:B:496:ARG:HB3	1.80	0.62
1:B:440:GLY:HA2	1:B:486:MET:HB3	1.82	0.62
1:A:48:GLU:HB3	1:A:79:MET:HB2	1.82	0.62
1:A:374:LEU:HD22	1:A:422:ARG:O	1.98	0.62
1:A:284:ASN:HB2	4:A:2008:HOH:O	2.00	0.61
1:B:37:THR:OG1	1:B:39:ILE:HG12	2.00	0.61
1:B:283:THR:HG21	1:B:400:TYR:C	2.20	0.61
1:B:327:ARG:HG3	1:B:327:ARG:NH1	2.13	0.61
1:B:200:ARG:HH11	1:B:200:ARG:CG	2.13	0.61
1:A:7:LEU:HD13	1:A:145:ILE:HD13	1.82	0.61
1:B:257:VAL:HG13	1:B:258:ALA:H	1.65	0.61
1:B:458:SER:HA	1:B:474:LEU:HG	1.83	0.61
1:B:108:GLY:O	1:B:109:LEU:HD23	2.01	0.61
1:A:347:LEU:HD22	1:A:362:ALA:HB2	1.83	0.60
1:B:424:LEU:HD12	1:B:450:ILE:O	2.02	0.60
1:A:141:ALA:HB3	1:A:142:PRO:HD3	1.84	0.60
1:A:366:ARG:HE	1:A:371:GLN:NE2	2.00	0.60
1:B:177:ASP:HB3	4:B:2031:HOH:O	2.01	0.60
1:A:27:ALA:HB1	1:A:31:PHE:CE1	2.36	0.59
1:A:191:CYS:O	1:A:195:VAL:HG23	2.01	0.59
1:A:471:PHE:CE2	1:B:31:PHE:HB3	2.37	0.59
1:A:255:ILE:HB	1:A:285:PHE:CD1	2.36	0.59
1:A:440:GLY:HA3	1:B:477:TRP:CH2	2.36	0.59
1:B:348:GLN:C	1:B:350:ASP:H	2.06	0.59
1:A:415:GLN:NE2	1:A:422:ARG:HA	2.16	0.59
1:B:359:ILE:O	1:B:362:ALA:HB3	2.02	0.59
1:A:99:ALA:HB1	1:A:100:PRO:CD	2.31	0.59
1:B:348:GLN:HB2	1:B:496:ARG:NH1	2.18	0.59
1:A:366:ARG:CB	1:A:371:GLN:NE2	2.64	0.59
1:B:306:THR:OG1	1:B:311:THR:HG23	2.02	0.58
1:B:216:TYR:HB2	1:B:218:LEU:HG	1.85	0.58
1:B:521:PRO:HD2	1:B:524:VAL:HG21	1.84	0.58
1:A:312:TYR:HB3	1:A:315:ILE:CD1	2.32	0.58
1:A:415:GLN:NE2	1:A:423:ILE:H	2.00	0.58
1:A:220:ALA:O	1:A:223:ALA:HB3	2.04	0.58
1:B:238:MET:HG2	1:B:400:TYR:CE2	2.39	0.58
1:B:308:GLY:O	1:B:309:TYR:HB2	2.03	0.58
1:A:456:ASN:HA	1:A:520:ILE:O	2.04	0.57
1:B:317:LEU:O	1:B:321:VAL:HG23	2.04	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:404:MET:HB2	3:B:1001:TPW:N3'	2.20	0.57
1:A:148:VAL:CG1	1:A:159:VAL:HB	2.34	0.57
1:A:208:MET:HA	1:A:234:VAL:O	2.05	0.57
1:A:306:THR:O	1:A:307:LEU:HG	2.04	0.57
1:A:345:THR:N	1:A:361:ARG:HH11	2.02	0.57
1:B:2:LYS:HD3	1:B:169:ASN:OD1	2.05	0.57
1:A:4:ALA:HB2	1:A:168:VAL:HG13	1.87	0.56
1:B:433:GLN:HE22	1:B:474:LEU:HD13	1.71	0.56
1:B:458:SER:CB	1:B:463:ARG:HH21	2.18	0.56
1:A:48:GLU:HB2	1:A:78:ASN:HD22	1.69	0.56
1:B:152:ALA:HB2	1:B:159:VAL:HG13	1.86	0.56
1:B:323:ALA:O	1:B:327:ARG:NH1	2.39	0.56
1:B:460:GLU:O	1:B:464:THR:HG23	2.06	0.56
1:A:62:SER:O	1:A:63:SER:C	2.44	0.56
1:A:463:ARG:NH2	1:A:522:ARG:HD3	2.21	0.56
1:A:56:ASP:O	1:A:60:ARG:HG3	2.06	0.56
1:B:366:ARG:NE	1:B:371:GLN:NE2	2.54	0.56
1:B:444:ARG:HB3	1:B:444:ARG:NH1	2.21	0.56
1:B:199:MET:CE	1:B:199:MET:HA	2.35	0.56
1:A:375:LEU:HD23	1:A:376:ILE:N	2.21	0.56
1:A:123:GLN:O	1:A:126:LYS:HG2	2.06	0.55
1:A:62:SER:HB2	1:A:64:THR:HG22	1.88	0.55
1:A:338:LYS:O	1:A:339:GLU:C	2.44	0.55
1:B:406:PHE:O	1:B:409:PRO:HD2	2.06	0.55
1:B:19:MET:O	1:B:42:LEU:HD12	2.07	0.55
1:B:152:ALA:HB2	1:B:159:VAL:CG1	2.37	0.55
1:A:294:LEU:HA	1:A:297:THR:OG1	2.07	0.55
1:B:500:LYS:NZ	1:B:504:ASP:OD1	2.40	0.54
1:A:99:ALA:HB1	1:A:100:PRO:HD2	1.88	0.54
1:A:298:ILE:N	1:A:298:ILE:HD12	2.23	0.54
1:B:228:ARG:HD3	1:B:330:PRO:CA	2.38	0.54
1:A:245:ASP:HB2	4:A:2034:HOH:O	2.06	0.54
1:A:415:GLN:HE21	1:A:423:ILE:H	1.54	0.54
1:A:460:GLU:OE2	1:A:463:ARG:HD2	2.06	0.54
1:A:345:THR:N	1:A:361:ARG:NH1	2.56	0.54
1:B:196:LEU:HD21	1:B:200:ARG:NH1	2.22	0.54
1:B:500:LYS:O	1:B:500:LYS:HD3	2.06	0.54
1:A:77:PHE:C	1:A:79:MET:H	2.10	0.54
1:A:219:GLU:HG3	1:A:243:LEU:HD12	1.88	0.54
1:A:309:TYR:N	4:A:2040:HOH:O	2.39	0.54
1:A:355:ALA:O	1:A:358:ASP:HB2	2.07	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:366:ARG:HE	1:A:371:GLN:HE21	1.56	0.54
1:A:32:LYS:O	1:A:36:GLU:HG3	2.08	0.54
1:A:278:ALA:O	1:A:301:PHE:CD1	2.61	0.54
1:B:219:GLU:OE1	1:B:242:LEU:HD23	2.07	0.54
1:A:488:GLY:HA3	1:A:513:PHE:CE2	2.43	0.54
1:A:306:THR:HG22	1:A:307:LEU:N	2.22	0.54
1:A:210:CYS:CB	1:A:278:ALA:HA	2.37	0.53
1:A:205:PRO:O	1:A:232:PRO:HD2	2.08	0.53
1:B:14:ARG:HD3	1:B:153:ARG:HD2	1.89	0.53
1:B:49:PRO:HD3	1:B:78:ASN:ND2	2.24	0.53
1:B:50:ALA:CB	1:B:438:GLU:HG3	2.39	0.53
1:B:108:GLY:C	1:B:109:LEU:HD23	2.29	0.53
1:B:184:ASP:HB3	1:B:187:ALA:HB3	1.89	0.53
1:B:50:ALA:HB2	1:B:438:GLU:HG3	1.91	0.53
1:B:152:ALA:O	1:B:156:SER:HA	2.08	0.53
1:A:415:GLN:OE1	1:A:447:ILE:HB	2.09	0.53
1:B:141:ALA:HB3	1:B:142:PRO:HD3	1.89	0.53
1:B:120:THR:O	1:B:124:VAL:HG23	2.08	0.53
1:A:348:GLN:HB2	1:A:496:ARG:NH2	2.23	0.53
1:A:366:ARG:HG2	4:A:2047:HOH:O	2.09	0.52
1:B:7:LEU:O	1:B:10:ALA:HB3	2.09	0.52
1:A:188:LEU:HD11	1:A:320:LEU:HA	1.92	0.52
1:B:210:CYS:HB3	1:B:278:ALA:HA	1.90	0.52
1:A:275:LEU:HB3	1:A:278:ALA:HB3	1.92	0.52
1:A:408:VAL:CB	1:A:409:PRO:HD3	2.38	0.52
1:B:207:LEU:HD12	1:B:208:MET:N	2.24	0.52
1:B:340:PRO:O	1:B:341:HIS:HB2	2.10	0.52
1:A:210:CYS:SG	1:A:211:VAL:N	2.80	0.51
1:A:486:MET:HG3	1:B:482:MET:CE	2.40	0.51
1:B:228:ARG:CD	1:B:330:PRO:HA	2.40	0.51
1:B:73:GLY:HA3	4:B:2046:HOH:O	2.09	0.51
1:B:230:GLY:HA2	1:B:333:ARG:NH2	2.25	0.51
1:A:5:GLU:HG3	1:A:37:THR:HG21	1.93	0.51
1:A:19:MET:HG2	1:A:42:LEU:HD12	1.93	0.51
1:A:181:TRP:O	1:A:183:VAL:HG23	2.10	0.51
1:A:360:ALA:HA	1:A:390:MET:HE2	1.91	0.51
1:B:124:VAL:O	1:B:127:GLU:HB2	2.11	0.50
1:B:130:VAL:HG11	1:B:157:ARG:HB2	1.93	0.50
1:A:24:GLY:HA2	1:B:462:LEU:HD21	1.93	0.50
1:B:298:ILE:HA	1:B:307:LEU:HB3	1.93	0.50
1:A:229:LEU:HG	1:A:231:VAL:HG22	1.93	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:165:ARG:C	1:B:167:MET:H	2.14	0.50
1:B:373:PRO:HB2	1:B:393:ALA:HB2	1.93	0.50
1:B:375:LEU:HD23	1:B:376:ILE:N	2.25	0.50
1:A:349:ALA:HB1	1:A:497:ALA:HA	1.94	0.50
1:A:360:ALA:HA	1:A:390:MET:CE	2.42	0.50
1:B:130:VAL:CG1	1:B:157:ARG:HB2	2.41	0.50
1:B:24:GLY:O	1:B:25:ASP:C	2.49	0.49
1:B:487:GLY:C	1:B:512:ARG:HH21	2.14	0.49
1:A:23:PRO:O	3:B:1001:TPW:H351	2.12	0.49
1:B:3:LEU:HD23	1:B:3:LEU:O	2.12	0.49
1:B:275:LEU:HB3	1:B:278:ALA:HB3	1.93	0.49
1:A:30:PHE:HA	1:A:168:VAL:HG11	1.94	0.49
1:B:14:ARG:HG3	1:B:14:ARG:HH11	1.78	0.49
1:B:48:GLU:O	1:B:51:VAL:HB	2.12	0.49
1:A:459:TRP:HB2	1:A:472:ASN:HD22	1.77	0.49
1:B:229:LEU:HD23	1:B:231:VAL:HG22	1.93	0.49
1:A:437:TRP:CD1	1:B:437:TRP:CD1	3.01	0.49
1:B:33:VAL:O	1:B:37:THR:CG2	2.61	0.49
1:A:280:LEU:O	1:A:281:SER:HB2	2.13	0.48
1:A:284:ASN:ND2	1:A:532:PHE:CE1	2.81	0.48
1:A:297:THR:C	1:A:298:ILE:HD12	2.33	0.48
1:B:209:VAL:HG13	1:B:213:VAL:HG21	1.96	0.48
1:B:200:ARG:CG	1:B:200:ARG:NH1	2.76	0.48
1:B:371:GLN:HG2	1:B:372:GLU:O	2.13	0.48
1:B:477:TRP:HB2	1:B:479:PHE:CZ	2.48	0.48
1:A:338:LYS:O	1:A:339:GLU:O	2.31	0.48
1:B:212:GLU:HB2	1:B:277:GLY:CA	2.42	0.48
1:B:298:ILE:N	1:B:298:ILE:CD1	2.75	0.48
1:B:212:GLU:OE1	1:B:301:PHE:HA	2.13	0.48
1:A:77:PHE:O	1:A:79:MET:N	2.47	0.48
1:B:28:LEU:HB2	1:B:29:PRO:HD3	1.94	0.48
1:B:56:ASP:O	1:B:59:ALA:HB3	2.14	0.48
1:B:199:MET:HA	1:B:199:MET:HE2	1.94	0.48
1:A:14:ARG:HG3	1:A:14:ARG:HH11	1.78	0.48
1:B:491:VAL:HG22	1:B:491:VAL:O	2.13	0.48
1:B:457:ALA:O	1:B:474:LEU:HB2	2.13	0.47
1:A:322:ASP:O	1:A:326:GLU:HG3	2.14	0.47
1:A:152:ALA:O	1:A:156:SER:HA	2.15	0.47
1:A:276:LEU:CD1	1:A:317:LEU:HD11	2.45	0.47
1:A:426:VAL:HG23	1:A:426:VAL:O	2.13	0.47
1:B:148:VAL:CG1	1:B:159:VAL:HB	2.45	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:247:PRO:HA	1:A:334:THR:HG23	1.96	0.47
1:A:163:ILE:N	1:A:163:ILE:HD12	2.30	0.47
1:A:376:ILE:CD1	1:A:392:ASP:HB3	2.45	0.47
1:A:458:SER:HB2	1:A:472:ASN:O	2.15	0.47
1:B:87:TYR:HA	1:B:158:PRO:CD	2.44	0.47
1:B:101:GLY:HA2	1:B:166:ASN:OD1	2.15	0.47
1:B:196:LEU:HD22	1:B:200:ARG:CD	2.39	0.47
1:B:280:LEU:HD22	1:B:289:GLN:HG3	1.96	0.47
1:B:351:GLY:HA2	1:B:495:THR:HB	1.96	0.46
1:A:49:PRO:HD3	1:A:78:ASN:ND2	2.29	0.46
1:B:19:MET:HG3	1:B:67:VAL:HG12	1.98	0.46
1:B:500:LYS:HD3	1:B:500:LYS:C	2.36	0.46
1:A:235:THR:HG23	1:A:250:PRO:HB3	1.97	0.46
1:B:77:PHE:HA	1:B:80:VAL:CG2	2.45	0.46
1:B:367:VAL:HA	1:B:371:GLN:HB3	1.96	0.46
1:B:210:CYS:SG	1:B:211:VAL:N	2.86	0.46
1:B:257:VAL:HG13	1:B:258:ALA:N	2.31	0.46
1:A:218:LEU:O	1:A:222:VAL:HG23	2.15	0.46
1:B:440:GLY:CA	1:B:486:MET:HB3	2.46	0.46
1:A:20:PHE:HA	1:A:43:HIS:O	2.16	0.46
1:B:9:ARG:HG2	1:B:9:ARG:HH11	1.80	0.46
1:B:19:MET:HE1	1:B:42:LEU:HD13	1.98	0.46
1:B:340:PRO:HG2	1:B:341:HIS:H	1.80	0.46
1:A:32:LYS:HB2	1:B:466:GLN:HE22	1.81	0.46
1:B:495:THR:OG1	1:B:498:GLU:HG3	2.16	0.46
1:A:354:ILE:HG22	1:A:355:ALA:N	2.31	0.46
1:A:137:ASP:HA	1:A:138:PRO:HD2	1.78	0.45
1:A:3:LEU:C	1:A:3:LEU:HD23	2.36	0.45
1:A:44:THR:O	1:A:45:LEU:HD23	2.17	0.45
1:A:3:LEU:HD13	1:A:167:MET:O	2.17	0.45
1:A:430:GLY:N	3:A:1002:TPW:O13	2.47	0.45
1:A:80:VAL:HG13	1:A:128:ILE:CD1	2.46	0.45
1:A:230:GLY:HA2	1:A:333:ARG:HH21	1.81	0.45
1:A:144:GLU:HA	1:A:144:GLU:OE2	2.16	0.45
1:A:359:ILE:HD13	1:A:499:LEU:HD21	1.98	0.45
1:B:338:LYS:O	1:B:339:GLU:O	2.34	0.45
1:A:48:GLU:HG2	1:A:75:GLY:O	2.16	0.45
1:A:87:TYR:HA	1:A:158:PRO:CD	2.47	0.45
1:B:313:ALA:O	1:B:315:ILE:HG12	2.17	0.45
1:B:470:ALA:O	1:B:472:ASN:N	2.50	0.45
1:A:47:HIS:CD2	1:B:434:MET:HB3	2.52	0.45

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3:LEU:HD23	1:B:3:LEU:C	2.38	0.45
1:A:492:ARG:HE	1:A:517:GLU:CD	2.20	0.45
1:B:48:GLU:HB2	1:B:78:ASN:HD22	1.81	0.45
1:B:388:MET:CE	1:B:528:THR:HG21	2.46	0.45
1:B:380:MET:CG	1:B:402:ALA:HA	2.45	0.44
1:A:28:LEU:CB	1:A:29:PRO:HD3	2.47	0.44
1:B:172:VAL:HG23	1:B:173:GLU:O	2.18	0.44
1:B:208:MET:HA	1:B:234:VAL:O	2.16	0.44
1:A:148:VAL:HG13	1:A:159:VAL:HB	2.00	0.44
1:A:460:GLU:O	1:A:464:THR:HG23	2.17	0.44
1:B:361:ARG:HG2	1:B:361:ARG:HH11	1.82	0.44
1:B:448:ASP:OD2	1:B:510:ARG:HA	2.18	0.44
1:A:45:LEU:HD12	1:A:51:VAL:HA	1.98	0.44
1:A:22:ILE:HG13	1:A:51:VAL:HG21	2.00	0.44
1:A:347:LEU:HD11	1:A:496:ARG:HB3	2.00	0.44
1:B:28:LEU:N	1:B:29:PRO:CD	2.80	0.44
1:B:276:LEU:HD12	1:B:317:LEU:HD11	1.98	0.44
1:A:321:VAL:O	1:A:322:ASP:C	2.56	0.44
1:B:279:ILE:HD12	1:B:400:TYR:HD2	1.81	0.44
1:B:452:ILE:HG22	1:B:454:PHE:CE2	2.53	0.44
1:A:213:VAL:CG1	1:A:222:VAL:HG21	2.45	0.44
1:A:345:THR:O	1:A:361:ARG:NH1	2.51	0.44
1:B:165:ARG:HA	1:B:168:VAL:HG23	2.00	0.44
1:B:311:THR:HG22	1:B:312:TYR:N	2.32	0.44
1:B:418:SER:HB2	1:B:421:LYS:HB2	2.00	0.44
1:B:432:PHE:CD1	1:B:436:GLY:HA3	2.53	0.44
1:A:486:MET:HG3	1:B:482:MET:HE3	2.00	0.43
1:A:120:THR:HG23	1:A:122:PHE:H	1.83	0.43
1:A:409:PRO:CG	1:A:435:THR:HB	2.48	0.43
1:B:56:ASP:O	1:B:60:ARG:HG3	2.18	0.43
1:B:337:GLY:O	1:B:338:LYS:C	2.56	0.43
1:B:448:ASP:OD1	1:B:510:ARG:NH2	2.50	0.43
1:A:327:ARG:HG3	1:A:327:ARG:NH1	2.32	0.43
1:B:339:GLU:OE2	1:B:339:GLU:N	2.51	0.43
1:B:408:VAL:O	1:B:409:PRO:C	2.57	0.43
1:A:208:MET:HE1	1:A:254:TYR:HB3	2.01	0.43
1:B:49:PRO:O	1:B:53:PHE:CD2	2.72	0.43
1:B:463:ARG:HG3	1:B:463:ARG:HH11	1.83	0.43
1:A:253:THR:HG22	1:A:255:ILE:HG23	2.00	0.43
1:A:366:ARG:HB3	1:A:366:ARG:HE	1.40	0.43
1:B:142:PRO:HA	1:B:175:VAL:HG22	1.99	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:10:ALA:HB2	1:A:175:VAL:HG21	2.00	0.43
1:A:151:ALA:O	1:A:152:ALA:C	2.57	0.43
1:A:182:PRO:O	1:A:314:ASP:HB3	2.19	0.43
1:A:20:PHE:HE2	1:A:58:ALA:HB2	1.82	0.43
1:A:210:CYS:SG	1:A:278:ALA:HA	2.59	0.43
1:B:79:MET:O	1:B:79:MET:CG	2.66	0.43
1:B:87:TYR:HA	1:B:158:PRO:HD2	2.00	0.43
1:B:170:ALA:O	1:B:172:VAL:HG13	2.19	0.42
1:B:415:GLN:NE2	1:B:423:ILE:H	2.17	0.42
1:B:477:TRP:HB2	1:B:479:PHE:CE2	2.54	0.42
1:B:425:THR:HG22	1:B:451:VAL:HG13	2.01	0.42
1:A:188:LEU:HD13	1:A:315:ILE:CG2	2.48	0.42
1:A:343:TYR:HA	1:A:344:PRO:HD2	1.83	0.42
1:B:337:GLY:O	1:B:338:LYS:O	2.37	0.42
1:A:216:TYR:O	1:A:217:GLY:C	2.57	0.42
1:A:276:LEU:HD12	1:A:317:LEU:HD11	2.00	0.42
1:A:286:ALA:HA	1:A:400:TYR:CE1	2.54	0.42
1:A:320:LEU:O	1:A:323:ALA:HB3	2.19	0.42
1:B:225:LEU:C	1:B:227:GLN:N	2.72	0.42
1:A:284:ASN:HB3	1:A:285:PHE:H	1.70	0.42
1:B:415:GLN:HG2	1:B:447:ILE:HB	2.01	0.42
1:B:492:ARG:HB2	1:B:517:GLU:OE1	2.18	0.42
1:A:153:ARG:NE	1:A:178:ASP:OD2	2.51	0.42
1:A:454:PHE:N	1:A:454:PHE:CD2	2.87	0.42
1:A:477:TRP:CZ2	1:B:440:GLY:HA3	2.55	0.42
1:B:347:LEU:HD12	1:B:348:GLN:N	2.34	0.42
1:B:271:ASP:O	1:B:296:LYS:HB3	2.19	0.42
1:B:339:GLU:OE2	1:B:339:GLU:CA	2.67	0.42
1:A:187:ALA:HB1	1:A:312:TYR:CD1	2.46	0.42
1:A:345:THR:H	1:A:361:ARG:NH1	2.17	0.42
1:A:359:ILE:HD13	1:A:499:LEU:CD2	2.50	0.42
1:B:49:PRO:HD3	1:B:78:ASN:HD22	1.84	0.42
1:B:27:ALA:HB2	1:B:71:THR:HA	2.01	0.42
1:B:452:ILE:HG22	1:B:454:PHE:HE2	1.85	0.42
1:B:19:MET:HA	1:B:67:VAL:HB	2.02	0.41
1:A:466:GLN:OE1	1:B:32:LYS:HD2	2.19	0.41
1:A:238:MET:CG	1:A:400:TYR:CE2	3.02	0.41
1:B:368:ARG:HD3	1:B:368:ARG:HA	1.90	0.41
1:B:3:LEU:C	1:B:3:LEU:CD2	2.89	0.41
1:B:14:ARG:HG3	1:B:14:ARG:NH1	2.35	0.41
1:B:188:LEU:O	1:B:191:CYS:HB3	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:492:ARG:HA	1:B:517:GLU:HB3	2.02	0.41
1:A:339:GLU:HA	1:A:340:PRO:HD2	1.87	0.41
1:B:19:MET:HG3	1:B:67:VAL:CG1	2.50	0.41
1:A:285:PHE:HZ	1:A:385:PHE:CE1	2.39	0.41
1:A:307:LEU:HD12	1:A:310:HIS:HB3	2.02	0.41
1:A:500:LYS:HD3	1:A:504:ASP:OD2	2.20	0.41
1:A:520:ILE:HA	1:A:521:PRO:HD3	1.95	0.41
1:B:257:VAL:HG21	1:B:535:GLY:HA3	2.02	0.41
1:B:306:THR:HG23	1:B:310:HIS:O	2.21	0.41
1:B:338:LYS:HG2	1:B:339:GLU:N	2.29	0.41
1:B:415:GLN:HE21	1:B:415:GLN:HB2	1.71	0.41
1:B:59:ALA:HB2	1:B:66:GLY:HA3	2.03	0.41
1:B:210:CYS:CB	1:B:278:ALA:HA	2.50	0.41
1:A:524:VAL:O	1:A:525:LEU:HD23	2.20	0.41
1:A:77:PHE:C	1:A:79:MET:N	2.73	0.41
1:A:284:ASN:HD22	1:A:284:ASN:HA	1.68	0.41
1:A:454:PHE:N	1:A:454:PHE:HD2	2.19	0.41
1:A:462:LEU:CB	1:A:472:ASN:HD21	2.23	0.41
3:A:1002:TPW:N1'	1:B:48:GLU:OE2	2.53	0.41
1:B:276:LEU:CD1	1:B:317:LEU:HD11	2.51	0.41
1:B:284:ASN:OD1	1:B:284:ASN:N	2.54	0.41
1:A:83:VAL:O	1:A:86:ALA:HB3	2.21	0.41
1:B:7:LEU:HD13	1:B:145:ILE:HD13	2.03	0.41
1:B:59:ALA:HB2	1:B:66:GLY:CA	2.51	0.41
1:A:156:SER:O	1:A:157:ARG:HG2	2.21	0.40
1:A:409:PRO:HG3	1:A:438:GLU:HG3	2.02	0.40
1:A:12:LYS:HG3	4:A:2053:HOH:O	2.21	0.40
1:A:303:ARG:HH12	1:A:316:PRO:HB3	1.82	0.40
1:A:152:ALA:HB2	1:A:159:VAL:CG1	2.51	0.40
1:B:404:MET:HE3	3:B:1001:TPW:H5B2	2.03	0.40
1:B:444:ARG:HB3	1:B:444:ARG:CZ	2.51	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	519/565 (92%)	443 (85%)	64 (12%)	12 (2%)	6	34
1	B	526/565 (93%)	439 (84%)	74 (14%)	13 (2%)	5	32
All	All	1045/1130 (92%)	882 (84%)	138 (13%)	25 (2%)	6	34

All (25) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	105	GLY
1	B	340	PRO
1	B	349	ALA
1	B	407	GLY
1	A	38	GLN
1	A	78	ASN
1	A	307	LEU
1	A	308	GLY
1	A	407	GLY
1	B	25	ASP
1	B	338	LYS
1	B	339	GLU
1	B	341	HIS
1	B	471	PHE
1	A	37	THR
1	A	165	ARG
1	A	184	ASP
1	A	284	ASN
1	B	284	ASN
1	A	339	GLU
1	B	264	THR
1	B	414	ALA
1	A	281	SER
1	A	419	GLY
1	B	92	PRO

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	387/426 (91%)	371 (96%)	16 (4%)	30	66
1	B	392/426 (92%)	379 (97%)	13 (3%)	38	71
All	All	779/852 (91%)	750 (96%)	29 (4%)	34	68

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	MET
1	A	25	ASP
1	A	120	THR
1	A	185	ARG
1	A	196	LEU
1	A	238	MET
1	A	248	THR
1	A	284	ASN
1	A	307	LEU
1	A	310	HIS
1	A	350	ASP
1	A	366	ARG
1	A	454	PHE
1	A	461	MET
1	A	478	ARG
1	A	537	LYS
1	B	196	LEU
1	B	200	ARG
1	B	284	ASN
1	B	307	LEU
1	B	339	GLU
1	B	354	ILE
1	B	380	MET
1	B	395	LEU
1	B	453	LEU
1	B	469	SER
1	B	471	PHE
1	B	491	VAL
1	B	524	VAL

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

Mol	Chain	Res	Type
1	A	47	HIS
1	A	78	ASN
1	A	284	ASN
1	A	289	GLN
1	A	299	HIS
1	A	371	GLN
1	A	472	ASN
1	A	536	GLN
1	B	289	GLN
1	B	371	GLN
1	B	433	GLN
1	B	534	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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	TPW	A	1002	2	23,27,27	1.88	7 (30%)	30,40,40	2.53	8 (26%)
3	TPW	B	1001	2	23,27,27	1.55	4 (17%)	30,40,40	2.59	10 (33%)

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	TPW	A	1002	2	-	1/16/17/17	0/2/2/2
3	TPW	B	1001	2	-	1/16/17/17	0/2/2/2

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1002	TPW	C2-C3	-5.24	1.33	1.37
3	B	1001	TPW	C2-C3	-3.62	1.34	1.37
3	B	1001	TPW	P1-O13	2.73	1.60	1.50
3	A	1002	TPW	P1-O13	2.45	1.59	1.50
3	A	1002	TPW	C35-C5'	2.42	1.56	1.52
3	A	1002	TPW	C5A-C5	2.41	1.52	1.50
3	B	1001	TPW	C6'-C5'	2.33	1.42	1.37
3	A	1002	TPW	C6'-C5'	2.31	1.42	1.37
3	A	1002	TPW	C4'-N3'	2.21	1.38	1.35
3	A	1002	TPW	C5'-C4'	2.21	1.46	1.42
3	B	1001	TPW	C2-S1	2.03	1.73	1.70

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	1001	TPW	C3-C2-S1	-9.26	102.39	112.26
3	A	1002	TPW	C3-C2-S1	-8.72	102.97	112.26
3	B	1001	TPW	P1-O11-P2	-6.12	111.81	132.83
3	A	1002	TPW	P1-O11-P2	-5.91	112.54	132.83
3	A	1002	TPW	C2-C3-C4	3.59	119.57	110.34
3	B	1001	TPW	C2-C3-C4	3.56	119.48	110.34
3	A	1002	TPW	C6'-N1'-C2'	3.31	121.59	115.96
3	B	1001	TPW	C6'-N1'-C2'	3.15	121.33	115.96
3	A	1002	TPW	P1-O5G-C5B	-2.81	107.78	121.59
3	B	1001	TPW	N1'-C2'-N3'	-2.58	121.10	125.54
3	A	1002	TPW	N1'-C2'-N3'	-2.54	121.17	125.54
3	B	1001	TPW	C35-C3-C4	-2.34	122.31	126.49
3	B	1001	TPW	C2'-N3'-C4'	2.28	121.63	118.08
3	A	1002	TPW	C35-C3-C4	-2.27	122.43	126.49
3	B	1001	TPW	P1-O5G-C5B	-2.21	110.69	121.59
3	B	1001	TPW	C2A-C2'-N1'	2.16	119.51	117.14
3	B	1001	TPW	C5'-C6'-N1'	-2.16	120.22	123.82
3	A	1002	TPW	O21-P2-O11	2.13	111.79	104.64

There are no chirality outliers.
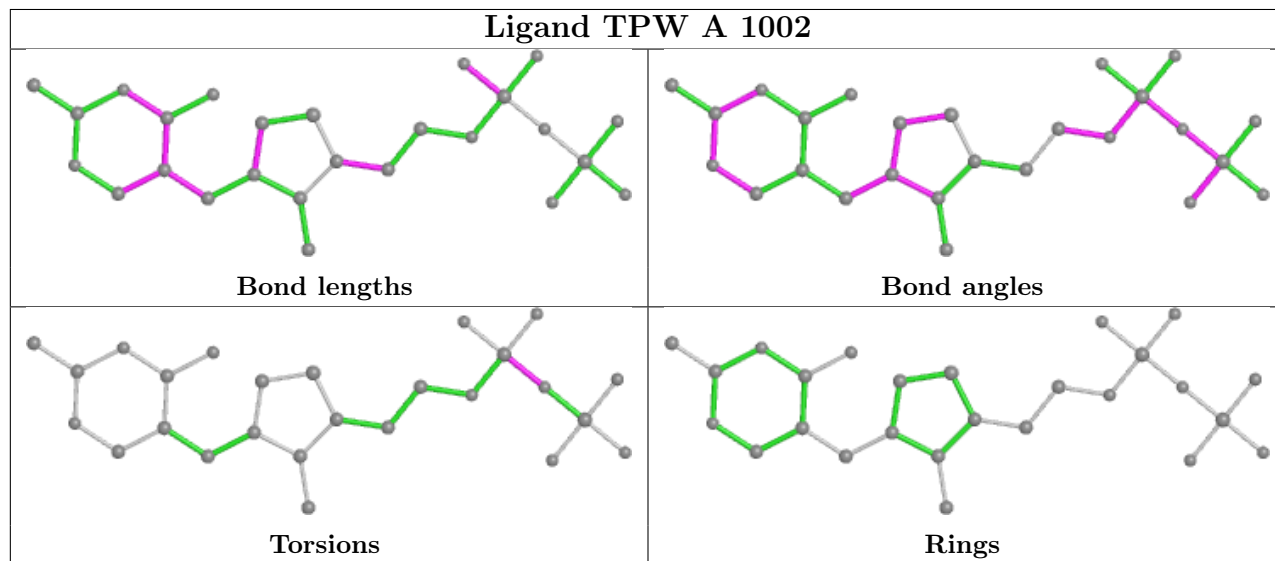
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1002	TPW	P2-O11-P1-O5G
3	B	1001	TPW	P2-O11-P1-O5G

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1002	TPW	2	0
3	B	1001	TPW	3	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 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.

Ligand TPW A 1002

Bond lengths

Bond angles

Torsions

Rings

Ligand TPW B 1001

Bond lengths

Bond angles

Torsions

Rings
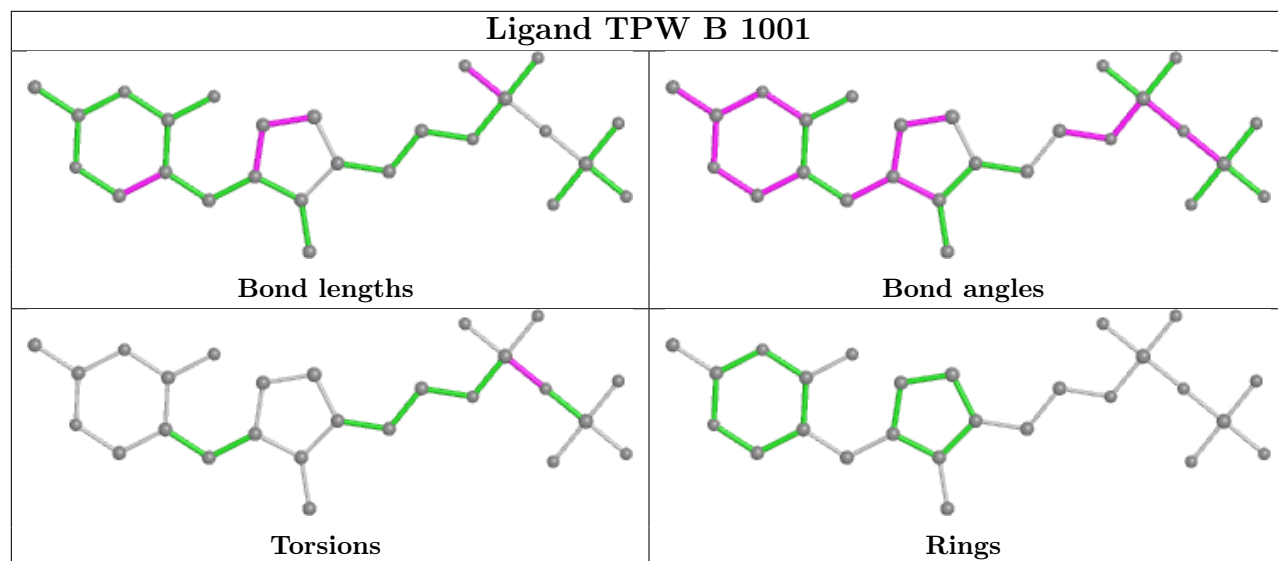
5.7 Other polymers ⓘ

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	523/565 (92%)	-0.61	0	100	100	10, 38, 66, 94	0
1	B	530/565 (93%)	-0.57	0	100	100	9, 39, 77, 99	0
All	All	1053/1130 (93%)	-0.59	0	100	100	9, 38, 72, 99	0

There are no RSRZ outliers to report.

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

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

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

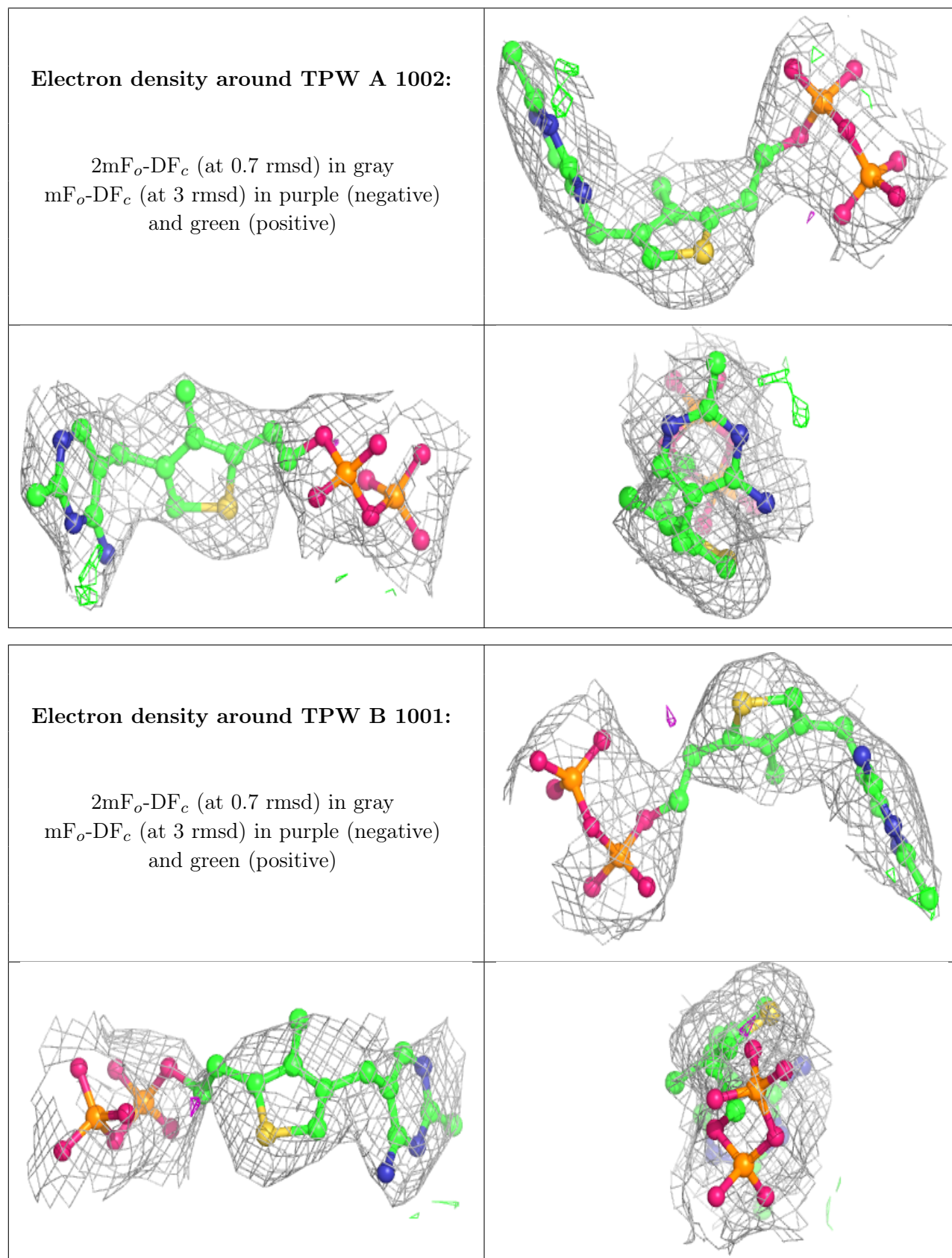## 6.4 Ligands ⓘ

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
2	MG	A	2002	1/1	0.98	0.20	50,50,50,50	0
2	MG	B	2001	1/1	0.98	0.14	22,22,22,22	0
3	TPW	A	1002	26/26	0.98	0.16	10,23,36,41	0
3	TPW	B	1001	26/26	0.98	0.16	9,32,47,50	0

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 TPW A 1002:

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

Electron density around TPW B 1001:

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

6.5 Other polymers (i)

There are no such residues in this entry.