



Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 02:05 pm BST

PDB ID : 3T8S
Title : Apo and InsP3-bound Crystal Structures of the Ligand-Binding Domain of an InsP3 Receptor
Authors : Lin, C.; Baek, K.; Lu, Z.
Deposited on : 2011-08-01
Resolution : 3.77 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) : 1.13
EDS : 2.11
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) : 2.11

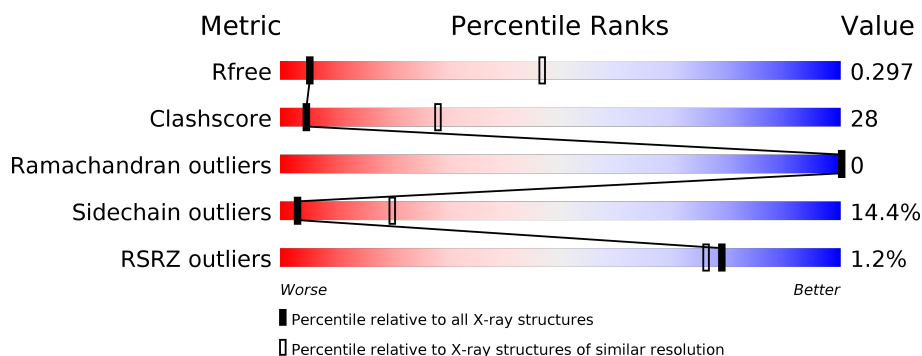
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.77 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}	130704	1038 (3.96-3.60)
Clashscore	141614	1100 (3.96-3.60)
Ramachandran outliers	138981	1062 (3.96-3.60)
Sidechain outliers	138945	1058 (3.96-3.60)
RSRZ outliers	127900	1009 (3.98-3.58)

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 $\leq 5\%$. 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	585	
1	B	585	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7386 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.

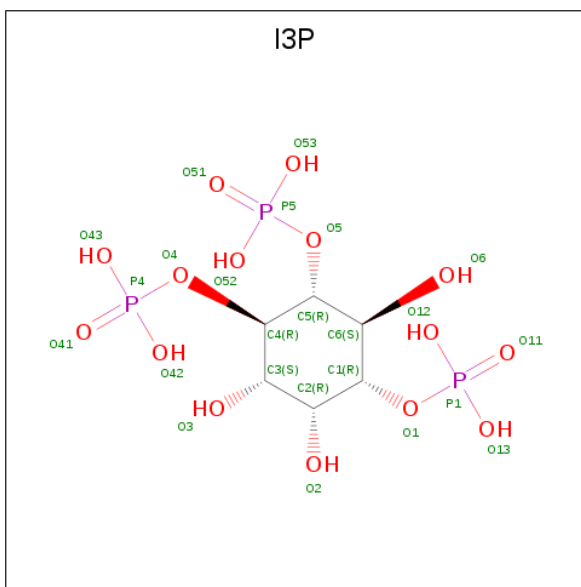
- Molecule 1 is a protein called Inositol 1,4,5-trisphosphate receptor type 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	501	Total	C	N	O	S	0	0	0
			3742	2368	644	715	15			
1	B	482	Total	C	N	O	S	23	0	0
			3620	2281	630	694	15			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	3	GLY	-	EXPRESSION TAG	UNP P29994-2
A	4	SER	-	EXPRESSION TAG	UNP P29994-2
A	5	GLU	-	EXPRESSION TAG	UNP P29994-2
A	6	PHE	-	EXPRESSION TAG	UNP P29994-2
B	3	GLY	-	EXPRESSION TAG	UNP P29994-2
B	4	SER	-	EXPRESSION TAG	UNP P29994-2
B	5	GLU	-	EXPRESSION TAG	UNP P29994-2
B	6	PHE	-	EXPRESSION TAG	UNP P29994-2

- Molecule 2 is D-MYO-INOSITOL-1,4,5-TRIPHOSPHATE (three-letter code: I3P) (formula: $C_6H_{15}O_{15}P_3$).



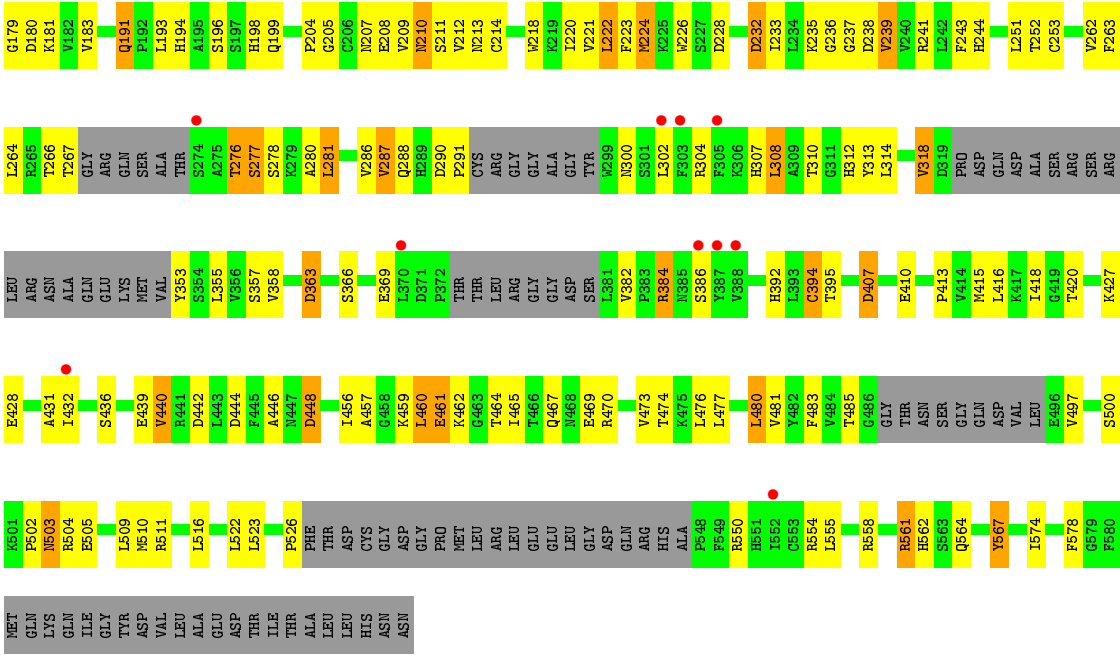
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	O	P	0	0
			24	6	15	3		

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 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 ($\text{RSRZ} > 2$). 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.

- Chain A: 46% 35% 5% 14%

Position	Amino Acid	Information Content (bits)
1	ASP	0.15
2	THR	0.15
3	ILE	0.15
4	PRO	0.15
5	ALA	0.15
6	LEU	0.15
7	LEU	0.15
8	ASP	0.15
9	CYS	0.15
10	ASN	0.15
11	ASN	0.15
12	PRO	0.15
13	MET	0.15
14	LEU	0.15
15	ARG	0.15
16	LEU	0.15
17	GLU	0.15
18	GLU	0.15
19	LEU	0.15
20	GLY	0.15
21	PRO	0.15
22	MET	0.15
23	LEU	0.15
24	ARG	0.15
25	LEU	0.15
26	GLU	0.15
27	GLU	0.15
28	GLY	0.15
29	ASP	0.15
30	GLN	0.15
31	GLN	0.15
32	GLN	0.15
33	GLN	0.15
34	GLN	0.15
35	GLN	0.15
36	GLN	0.15
37	GLN	0.15
38	GLN	0.15
39	GLN	0.15
40	GLN	0.15
41	GLN	0.15
42	GLN	0.15
43	GLN	0.15
44	GLN	0.15
45	GLN	0.15
46	GLN	0.15
47	GLN	0.15
48	GLN	0.15
49	GLN	0.15
50	GLN	0.15
51	GLN	0.15
52	GLN	0.15
53	GLN	0.15
54	GLN	0.15
55	GLN	0.15
56	GLN	0.15
57	GLN	0.15
58	GLN	0.15
59	GLN	0.15
60	GLN	0.15
61	GLN	0.15
62	GLN	0.15
63	GLN	0.15
64	GLN	0.15
65	GLN	0.15
66	GLN	0.15
67	GLN	0.15
68	GLN	0.15
69	GLN	0.15
70	GLN	0.15
71	GLN	0.15
72	GLN	0.15
73	GLN	0.15
74	GLN	0.15
75	GLN	0.15
76	GLN	0.15
77	GLN	0.15
78	GLN	0.15
79	GLN	0.15
80	GLN	0.15
81	GLN	0.15
82	GLN	0.15
83	GLN	0.15
84	GLN	0.15
85	GLN	0.15
86	GLN	0.15
87	GLN	0.15
88	GLN	0.15
89	GLN	0.15
90	GLN	0.15
91	GLN	0.15
92	GLN	0.15
93	GLN	0.15
94	GLN	0.15
95	GLN	0.15
96	GLN	0.15
97	GLN	0.15
98	GLN	0.15
99	GLN	0.15
100	GLN	0.15

- Chain B:
-
- | Amino Acid | Percentage |
|------------|------------|
| GLY | 2% |
| SER | 47% |
| GLU | 29% |
| ALA | 6% |
| PHE | 18% |
| S7 | |
| F8 | |
| L9 | |
| H10 | |
| I11 | |
| G12 | |
| D13 | |
| I14 | |
| C15 | |
| S16 | |
| A19 | |
| E20 | |
| M24 | |
| I27 | |
| S28 | |
| T29 | |
| L30 | |
| G31 | |
| D35 | |
| R36 | |
| C37 | |
| V38 | |
| P41 | |
| E42 | |
| L45 | |
| M47 | |
| P48 | |
| P49 | |
| K52 | |
| D55 | |
| F58 | |
| K59 | |
| L60 | |
| C61 | |
| D62 | |
| P63 | |
| M64 | |
| R65 | |
| K70 | |
| Q71 | |
| F72 | |
| W73 | |
| K74 | |
| ALA | |
| LYS | |



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	159.83Å 84.88Å 95.09Å 90.00° 116.92° 90.00°	Depositor
Resolution (Å)	41.45 – 3.77 41.45 – 3.77	Depositor EDS
% Data completeness (in resolution range)	99.1 (41.45-3.77) 99.0 (41.45-3.77)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.82 (at 3.76Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.277 , 0.292 0.273 , 0.297	Depositor DCC
R_{free} test set	540 reflections (4.71%)	wwPDB-VP
Wilson B-factor (Å ²)	132.9	Xtriage
Anisotropy	0.033	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 118.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	7386	wwPDB-VP
Average B, all atoms (Å ²)	144.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.00% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: I3P

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	0.46	0/3815	0.61	0/5196
1	B	0.44	1/3690 (0.0%)	0.60	3/5028 (0.1%)
All	All	0.45	1/7505 (0.0%)	0.61	3/10224 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	502	PRO	C-N	-5.21	1.22	1.34

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	567	TYR	N-CA-C	-8.12	89.09	111.00
1	B	384	ARG	N-CA-CB	-6.93	98.12	110.60
1	B	166	PHE	N-CA-C	5.24	125.15	111.00

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	3742	0	3483	243	0
1	B	3620	0	3346	155	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	24	0	9	3	0
All	All	7386	0	6838	398	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 28.

All (398) 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:38:VAL:HB	1:A:206:CYS:SG	1.75	1.25
1:A:298:TYR:CB	1:A:383:PRO:HD3	1.75	1.17
1:A:249:LYS:HE3	1:A:416:LEU:HD12	1.25	1.13
1:A:249:LYS:HD3	1:A:266:THR:HG22	1.15	1.13
1:A:249:LYS:HD3	1:A:266:THR:CG2	1.79	1.12
1:B:288:GLN:HB2	1:B:290:ASP:O	1.49	1.10
1:A:298:TYR:HB3	1:A:383:PRO:CD	1.83	1.08
1:B:503:ASN:HD21	1:B:505:GLU:HG2	1.21	1.04
1:A:231:ASP:HB2	1:A:232:ASP:HA	1.41	1.02
1:A:301:SER:O	1:A:369:GLU:HG3	1.61	1.01
1:A:444:ASP:O	1:A:448:ASP:HB2	1.66	0.96
1:A:488:THR:HB	1:A:497:VAL:HG11	1.50	0.92
1:B:550:ARG:O	1:B:554:ARG:HB2	1.70	0.92
1:A:16:SER:OG	1:A:221:VAL:HG22	1.70	0.91
1:B:444:ASP:O	1:B:448:ASP:HB2	1.72	0.90
1:A:296:ALA:HB2	1:A:382:VAL:HG13	1.54	0.90
1:A:298:TYR:HB3	1:A:383:PRO:HD3	0.91	0.89
1:A:38:VAL:CB	1:A:206:CYS:SG	2.60	0.88
1:B:191:GLN:HA	1:B:191:GLN:HE21	1.39	0.88
1:A:373:THR:CB	1:A:389:ARG:HH11	1.87	0.88
1:A:90:ASN:HA	1:A:93:HIS:CE1	2.08	0.88
1:A:298:TYR:HD1	1:A:382:VAL:HA	1.38	0.87
1:B:241:ARG:NH2	1:B:276:THR:HG23	1.89	0.87
1:A:296:ALA:CB	1:A:382:VAL:HG13	2.06	0.86
1:B:241:ARG:NH2	1:B:276:THR:CG2	2.39	0.85
1:A:15:CYS:HB2	1:A:221:VAL:O	1.77	0.85
1:A:520:PHE:O	1:A:523:LEU:HG	1.78	0.83
1:B:503:ASN:ND2	1:B:505:GLU:HG2	1.92	0.82
1:A:551:HIS:O	1:A:555:LEU:HG	1.80	0.82
1:A:230:LYS:O	1:A:235:LYS:CE	2.28	0.82
1:A:64:ASN:HB2	1:A:66:TYR:CE1	2.15	0.81
1:A:66:TYR:HE1	1:A:122:GLN:HE22	1.28	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:441:ARG:HH11	1:A:441:ARG:HG3	1.44	0.81
1:B:253:CYS:HB3	1:B:307:HIS:HD2	1.47	0.80
1:A:65:ARG:HB2	1:A:103:ASN:OD1	1.82	0.79
1:A:29:THR:HG21	1:A:151:LEU:HD11	1.63	0.78
1:A:364:ILE:HG22	1:A:394:CYS:HB2	1.66	0.78
1:B:11:ILE:HG21	1:B:62:PRO:HG3	1.65	0.77
1:A:252:THR:HG22	1:A:280:ALA:HB2	1.64	0.77
1:A:64:ASN:CB	1:A:66:TYR:CE1	2.67	0.77
1:B:253:CYS:HB3	1:B:307:HIS:CD2	2.19	0.77
1:A:230:LYS:O	1:A:235:LYS:HE2	1.84	0.77
1:B:16:SER:OG	1:B:221:VAL:HB	1.85	0.76
1:A:389:ARG:HD3	1:A:429:ALA:HB2	1.68	0.76
1:A:298:TYR:HD1	1:A:382:VAL:CA	1.99	0.76
1:A:425:GLU:CB	1:A:428:GLU:HB2	2.16	0.76
1:A:486:GLY:O	1:A:497:VAL:HG13	1.85	0.75
1:B:31:GLY:HA2	1:B:448:ASP:OD2	1.85	0.75
1:A:287:VAL:HG11	1:A:302:LEU:HB2	1.68	0.74
1:A:133:THR:HA	1:A:158:GLY:O	1.88	0.74
1:B:288:GLN:CB	1:B:290:ASP:O	2.35	0.74
1:B:267:THR:HG23	2:B:603:I3P:O42	1.87	0.74
1:A:394:CYS:SG	1:A:395:THR:HG23	2.27	0.74
1:B:20:GLU:HA	1:B:24:ASN:OD1	1.89	0.73
1:A:233:ILE:CB	1:A:382:VAL:HG11	2.19	0.72
1:B:191:GLN:CA	1:B:191:GLN:HE21	2.02	0.72
1:A:495:LEU:O	1:A:499:PHE:CD2	2.42	0.72
1:A:487:GLY:HA3	1:A:488:THR:HG22	1.71	0.72
1:A:235:LYS:HB2	1:A:238:ASP:OD2	1.90	0.71
1:A:298:TYR:HB2	1:A:381:LEU:O	1.90	0.71
1:B:318:VAL:HA	1:B:353:TYR:HA	1.73	0.71
1:A:296:ALA:N	1:A:297:GLY:HA2	2.04	0.71
1:B:137:ARG:HG3	1:B:138:LEU:HG	1.73	0.70
1:A:91:LYS:O	1:A:94:HIS:ND1	2.25	0.69
1:B:194:HIS:HB2	1:B:214:CYS:SG	2.31	0.69
1:A:298:TYR:CB	1:A:381:LEU:O	2.41	0.69
1:A:232:ASP:CG	1:A:385:ASN:HD21	1.95	0.69
1:B:71:GLN:HE21	1:B:92:LEU:HD23	1.58	0.69
1:A:373:THR:OG1	1:A:389:ARG:NH1	2.26	0.69
1:B:191:GLN:HA	1:B:191:GLN:NE2	2.07	0.69
1:B:235:LYS:O	1:B:238:ASP:HB2	1.92	0.69
1:A:298:TYR:CD1	1:A:382:VAL:HA	2.24	0.69
1:B:71:GLN:HE21	1:B:92:LEU:CD2	2.06	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:64:ASN:HB2	1:B:122:GLN:OE1	1.94	0.68
1:B:497:VAL:O	1:B:500:SER:OG	2.09	0.68
1:B:89:LEU:O	1:B:93:HIS:HB2	1.93	0.68
1:A:58:PHE:HA	1:A:124:LEU:O	1.94	0.67
1:A:32:LEU:HD22	1:A:445:PHE:HB2	1.75	0.67
1:A:40:GLN:HB3	1:A:205:GLY:O	1.94	0.67
1:A:249:LYS:CD	1:A:266:THR:CG2	2.69	0.67
1:A:51:LYS:HE2	1:A:311:GLY:HA3	1.77	0.67
1:A:495:LEU:O	1:A:499:PHE:HD2	1.78	0.67
1:A:287:VAL:CG1	1:A:302:LEU:HB2	2.25	0.66
1:A:235:LYS:HD2	1:A:238:ASP:OD2	1.95	0.66
1:A:91:LYS:HA	1:A:94:HIS:ND1	2.11	0.66
1:A:170:ARG:NH1	1:A:180:ASP:OD2	2.29	0.65
1:A:497:VAL:HA	1:A:500:SER:HB3	1.78	0.65
1:A:389:ARG:NH2	1:A:425:GLU:O	2.29	0.65
1:A:231:ASP:HB3	1:A:235:LYS:NZ	2.10	0.65
1:B:29:THR:HG22	1:B:37:CYS:HA	1.79	0.65
1:B:122:GLN:HG2	1:B:159:SER:O	1.96	0.65
1:B:19:ALA:O	1:B:24:ASN:HA	1.96	0.65
1:A:249:LYS:HE3	1:A:416:LEU:CD1	2.15	0.65
1:B:241:ARG:HH21	1:B:276:THR:HG23	1.62	0.65
1:A:231:ASP:HB2	1:A:232:ASP:CA	2.23	0.64
1:B:14:ILE:HD13	1:B:126:LEU:HD13	1.78	0.64
1:A:487:GLY:CA	1:A:488:THR:HG22	2.27	0.64
1:A:486:GLY:HA2	1:A:506:ARG:NH1	2.11	0.64
1:B:164:GLN:HB2	1:B:183:VAL:HB	1.80	0.64
1:B:264:LEU:HG	1:B:418:ILE:HD11	1.80	0.64
1:A:389:ARG:CD	1:A:429:ALA:HB2	2.28	0.63
1:A:436:SER:O	1:A:439:GLU:HG2	1.99	0.63
1:B:19:ALA:HB2	1:B:218:TRP:CZ3	2.33	0.63
1:B:232:ASP:O	1:B:384:ARG:HG2	1.98	0.63
1:A:38:VAL:HB	1:A:206:CYS:HG	1.64	0.63
1:A:64:ASN:HB3	1:A:66:TYR:CE1	2.33	0.62
1:B:147:MET:HB2	1:B:211:SER:HB3	1.80	0.62
1:A:166:PHE:CE1	1:A:217:SER:HB3	2.34	0.62
1:A:444:ASP:O	1:A:448:ASP:CB	2.45	0.62
1:B:204:PRO:N	1:B:205:GLY:HA3	2.14	0.62
1:A:391:ARG:HB2	1:A:398:TRP:CZ3	2.35	0.62
1:A:91:LYS:HA	1:A:94:HIS:CE1	2.35	0.62
1:A:298:TYR:N	1:A:298:TYR:CD2	2.67	0.61
1:B:61:CYS:O	1:B:121:ILE:HB	1.99	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:310:THR:HB	1:B:312:HIS:HD2	1.65	0.61
1:A:481:VAL:HG22	1:A:559:VAL:HG22	1.81	0.61
1:B:65:ARG:HH12	1:B:103:ASN:HA	1.65	0.61
1:A:488:THR:CB	1:A:497:VAL:HG11	2.29	0.61
1:A:178:ILE:HD12	1:A:222:LEU:HB2	1.82	0.61
1:B:263:PHE:CZ	1:B:415:MET:HG2	2.36	0.60
1:B:314:LEU:HD11	1:B:355:LEU:HG	1.82	0.60
1:A:475:LYS:O	1:A:478:GLU:HG2	2.01	0.60
1:A:391:ARG:HB2	1:A:398:TRP:CH2	2.37	0.59
1:A:425:GLU:CB	1:A:428:GLU:CB	2.80	0.59
1:A:495:LEU:O	1:A:498:VAL:HB	2.03	0.59
1:A:122:GLN:HE21	1:A:160:TRP:HD1	1.51	0.59
1:A:297:GLY:O	1:A:383:PRO:HD2	2.02	0.58
1:A:390:LEU:HB2	1:A:399:VAL:CG2	2.32	0.58
1:A:231:ASP:CB	1:A:232:ASP:HA	2.16	0.58
1:A:84:THR:HG22	1:A:85:ASP:N	2.19	0.58
1:B:267:THR:HA	2:B:603:I3P:O42	2.02	0.58
1:A:249:LYS:HD3	1:A:266:THR:HG23	1.80	0.58
1:A:387:TYR:CD2	1:A:387:TYR:N	2.72	0.58
1:B:386:SER:O	1:B:432:ILE:HD12	2.04	0.58
1:A:375:LEU:N	1:A:375:LEU:HD12	2.19	0.58
1:B:503:ASN:HD22	1:B:504:ARG:N	2.02	0.57
1:A:234:LEU:O	1:A:296:ALA:HB1	2.04	0.57
1:A:316:ALA:HB3	1:A:392:HIS:CD2	2.38	0.57
1:A:400:HIS:HA	1:A:428:GLU:HG2	1.85	0.57
1:B:65:ARG:HB2	1:B:103:ASN:OD1	2.04	0.57
1:A:287:VAL:HG11	1:A:302:LEU:HD12	1.85	0.57
1:B:286:VAL:HG13	1:B:287:VAL:N	2.18	0.57
1:A:296:ALA:HB3	1:A:297:GLY:O	2.05	0.56
1:A:387:TYR:H	1:A:387:TYR:HD2	1.54	0.56
1:A:264:LEU:HG	1:A:418:ILE:HD11	1.87	0.56
1:A:391:ARG:HD3	1:A:398:TRP:CZ2	2.40	0.56
1:B:310:THR:HB	1:B:312:HIS:CD2	2.41	0.56
1:B:14:ILE:HD13	1:B:126:LEU:CD1	2.35	0.56
1:B:574:ILE:O	1:B:578:PHE:HB2	2.05	0.56
1:A:239:VAL:HG21	1:A:440:VAL:HG21	1.89	0.55
1:A:488:THR:HB	1:A:497:VAL:CG1	2.31	0.55
1:B:241:ARG:NH2	1:B:276:THR:HG21	2.17	0.55
1:B:436:SER:OG	1:B:439:GLU:HB2	2.07	0.55
1:A:298:TYR:CD1	1:A:382:VAL:CA	2.87	0.55
1:B:27:ILE:HD11	1:B:218:TRP:CH2	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:392:HIS:CE1	1:B:394:CYS:HB3	2.41	0.55
1:A:298:TYR:CD1	1:A:382:VAL:N	2.75	0.55
1:A:441:ARG:NH1	1:A:441:ARG:HG3	2.16	0.55
1:B:384:ARG:HD3	1:B:384:ARG:O	2.06	0.55
1:B:232:ASP:OD1	1:B:233:ILE:N	2.40	0.55
1:A:551:HIS:O	1:A:555:LEU:N	2.40	0.54
1:B:241:ARG:CZ	1:B:276:THR:OG1	2.55	0.54
1:B:193:LEU:HD11	1:B:209:VAL:HG12	1.89	0.54
1:A:231:ASP:HB3	1:A:235:LYS:HZ2	1.71	0.54
1:A:288:GLN:HE21	1:A:293:ARG:C	2.11	0.54
1:A:31:GLY:HA3	1:A:448:ASP:OD1	2.08	0.54
1:A:38:VAL:CG1	1:A:206:CYS:SG	2.96	0.54
1:A:365:SER:O	1:A:392:HIS:HE1	1.88	0.54
1:A:223:PHE:CD2	1:A:293:ARG:CB	2.90	0.54
1:A:40:GLN:NE2	1:A:205:GLY:O	2.36	0.54
1:A:233:ILE:CB	1:A:382:VAL:CG1	2.86	0.54
1:A:124:LEU:HD12	1:A:125:HIS:N	2.22	0.54
1:A:19:ALA:HB2	1:A:218:TRP:CZ3	2.42	0.54
1:A:298:TYR:CA	1:A:383:PRO:HD3	2.36	0.53
1:A:487:GLY:HA3	1:A:497:VAL:HG11	1.91	0.53
1:A:390:LEU:HB2	1:A:399:VAL:HG21	1.90	0.53
1:A:316:ALA:HB3	1:A:392:HIS:NE2	2.23	0.53
1:B:224:MET:CE	1:B:236:GLY:H	2.21	0.53
1:B:558:ARG:O	1:B:562:HIS:ND1	2.39	0.53
1:A:392:HIS:CD2	1:A:395:THR:HG23	2.44	0.52
1:B:194:HIS:HB3	1:B:210:ASN:ND2	2.23	0.52
1:A:301:SER:O	1:A:369:GLU:CG	2.48	0.52
1:B:304:ARG:NH1	1:B:366:SER:OG	2.41	0.52
1:A:117:TYR:HE1	1:A:170:ARG:CG	2.22	0.52
1:B:196:SER:HB2	1:B:198:HIS:HD2	1.74	0.52
1:B:457:ALA:O	1:B:461:GLU:HG3	2.10	0.52
1:A:489:ASN:O	1:A:494:VAL:CB	2.57	0.52
1:B:170:ARG:HH11	1:B:170:ARG:HB2	1.73	0.52
1:B:477:LEU:O	1:B:481:VAL:HG23	2.09	0.52
1:B:313:TYR:O	1:B:357:SER:HA	2.08	0.52
1:A:503:ASN:HB3	1:A:506:ARG:HB2	1.92	0.52
1:A:19:ALA:HB3	1:A:25:GLY:H	1.73	0.52
1:A:230:LYS:O	1:A:235:LYS:HE3	2.07	0.52
1:B:41:PRO:HG3	1:B:207:ASN:ND2	2.25	0.52
1:B:71:GLN:HG3	1:B:92:LEU:HD21	1.91	0.51
1:A:441:ARG:CG	1:A:441:ARG:HH11	2.20	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:487:GLY:HA3	1:A:488:THR:CG2	2.39	0.51
1:A:25:GLY:HA3	1:A:39:VAL:CG1	2.39	0.51
1:A:365:SER:O	1:A:392:HIS:CE1	2.64	0.51
1:A:64:ASN:HB2	1:A:66:TYR:HE1	1.71	0.51
1:B:241:ARG:HH22	1:B:276:THR:HG21	1.76	0.51
1:B:460:LEU:HD23	1:B:465:ILE:HD13	1.93	0.51
1:B:473:VAL:HA	1:B:476:LEU:HB3	1.92	0.51
1:B:65:ARG:NH1	1:B:103:ASN:HA	2.25	0.51
1:B:70:LYS:HA	1:B:73:TRP:CE3	2.45	0.51
1:A:310:THR:OG1	1:A:312:HIS:HB2	2.11	0.51
1:B:561:ARG:HG3	1:B:562:HIS:N	2.26	0.51
1:A:314:LEU:HG	1:A:368:PHE:CE1	2.47	0.50
1:A:373:THR:CB	1:A:389:ARG:NH1	2.68	0.50
1:A:15:CYS:HB3	1:A:222:LEU:HA	1.93	0.50
1:A:117:TYR:CE1	1:A:170:ARG:CG	2.94	0.50
1:A:307:HIS:ND1	1:A:308:LEU:N	2.60	0.50
1:B:72:PHE:HA	1:B:92:LEU:HD11	1.94	0.50
1:A:488:THR:HB	1:A:497:VAL:HG21	1.92	0.50
1:B:35:ASP:HB2	1:B:151:LEU:H	1.76	0.50
1:B:267:THR:CA	2:B:603:I3P:O42	2.60	0.49
1:B:467:GLN:HA	1:B:470:ARG:HH21	1.77	0.49
1:A:410:GLU:O	1:A:413:PRO:HG3	2.13	0.49
1:B:278:SER:HA	1:B:281:LEU:HD12	1.93	0.49
1:B:407:ASP:O	1:B:413:PRO:HB3	2.12	0.49
1:A:16:SER:OG	1:A:221:VAL:CG2	2.54	0.49
1:A:64:ASN:HB2	1:A:122:GLN:HE22	1.77	0.49
1:A:58:PHE:CD2	1:A:125:HIS:HA	2.48	0.49
1:A:194:HIS:HD2	1:A:216:THR:OG1	1.96	0.49
1:A:239:VAL:HG23	1:A:435:VAL:HB	1.95	0.49
1:B:196:SER:HB2	1:B:198:HIS:CD2	2.48	0.49
1:A:142:LEU:HD21	1:A:200:LEU:HD23	1.95	0.49
1:A:117:TYR:CE1	1:A:170:ARG:HG3	2.48	0.49
1:A:140:ALA:N	1:A:146:ALA:O	2.20	0.49
1:A:235:LYS:HA	1:A:296:ALA:O	2.13	0.49
1:A:354:SER:HA	1:A:419:GLY:HA2	1.93	0.49
1:A:447:ASN:ND2	1:A:513:GLN:OE1	2.46	0.49
1:B:470:ARG:O	1:B:474:THR:OG1	2.27	0.49
1:A:223:PHE:CE2	1:A:293:ARG:CB	2.96	0.48
1:A:373:THR:HG21	1:A:389:ARG:NH1	2.28	0.48
1:B:122:GLN:HE21	1:B:159:SER:HB3	1.79	0.48
1:B:286:VAL:HG22	1:B:287:VAL:H	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:389:ARG:HD3	1:A:429:ALA:CB	2.43	0.48
1:B:239:VAL:HG11	1:B:440:VAL:HG21	1.96	0.48
1:A:117:TYR:HE1	1:A:170:ARG:HG2	1.78	0.48
1:B:286:VAL:HG11	1:B:288:GLN:OE1	2.14	0.48
1:B:503:ASN:ND2	1:B:505:GLU:H	2.12	0.48
1:A:310:THR:C	1:A:312:HIS:H	2.18	0.47
1:A:385:ASN:N	1:A:385:ASN:OD1	2.47	0.47
1:B:224:MET:HE2	1:B:236:GLY:H	1.79	0.47
1:A:123:LEU:HB2	1:A:132:LEU:HD23	1.95	0.47
1:A:287:VAL:HG12	1:A:302:LEU:O	2.14	0.47
1:B:112:GLY:HA2	1:B:226:TRP:CE2	2.49	0.47
1:B:232:ASP:C	1:B:232:ASP:OD1	2.53	0.47
1:A:134:VAL:HG22	1:A:149:VAL:HG22	1.97	0.47
1:B:252:THR:HG22	1:B:280:ALA:HB2	1.96	0.47
1:A:122:GLN:NE2	1:A:160:TRP:CD1	2.82	0.47
1:B:251:LEU:HD11	1:B:262:VAL:HG12	1.97	0.47
1:A:384:ARG:C	1:A:385:ASN:OD1	2.53	0.47
1:B:204:PRO:CD	1:B:205:GLY:HA3	2.45	0.47
1:B:263:PHE:CE1	1:B:415:MET:HG2	2.50	0.47
1:A:231:ASP:HB3	1:A:235:LYS:HZ1	1.78	0.47
1:A:441:ARG:CG	1:A:441:ARG:NH1	2.77	0.47
1:B:277:SER:O	1:B:280:ALA:HB3	2.13	0.47
1:B:446:ALA:CB	1:B:509:LEU:HD23	2.44	0.47
1:A:16:SER:O	1:A:17:LEU:HD23	2.14	0.47
1:A:363:ASP:O	1:A:366:SER:OG	2.32	0.47
1:A:364:ILE:HD12	1:A:364:ILE:H	1.78	0.47
1:B:191:GLN:CA	1:B:191:GLN:NE2	2.70	0.47
1:A:84:THR:CG2	1:A:85:ASP:N	2.78	0.46
1:A:224:MET:CG	1:A:228:ASP:HB2	2.46	0.46
1:B:52:LYS:O	1:B:52:LYS:HG3	2.15	0.46
1:A:139:PRO:O	1:A:148:ARG:NH2	2.47	0.46
1:B:181:LYS:HA	1:B:218:TRP:O	2.15	0.46
1:B:236:GLY:HA3	1:B:237:GLY:HA3	1.68	0.46
1:A:66:TYR:HE1	1:A:122:GLN:NE2	2.05	0.46
1:A:405:PRO:HA	1:A:415:MET:O	2.16	0.46
1:A:487:GLY:HA3	1:A:488:THR:CB	2.46	0.46
1:B:193:LEU:CD1	1:B:209:VAL:HG12	2.45	0.46
1:A:64:ASN:ND2	1:A:122:GLN:OE1	2.41	0.46
1:A:263:PHE:HA	1:A:418:ILE:HD12	1.98	0.46
1:A:117:TYR:CE1	1:A:170:ARG:HG2	2.51	0.45
1:A:226:TRP:CG	1:A:227:SER:N	2.83	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:243:PHE:O	1:B:431:ALA:N	2.37	0.45
1:B:15:CYS:N	1:B:58:PHE:O	2.43	0.45
1:B:90:ASN:O	1:B:94:HIS:HB3	2.16	0.45
1:B:353:TYR:HB2	1:B:420:THR:OG1	2.16	0.45
1:A:133:THR:O	1:A:149:VAL:HA	2.17	0.45
1:A:193:LEU:HD12	1:A:209:VAL:HG12	1.98	0.45
1:B:139:PRO:HA	1:B:146:ALA:O	2.17	0.45
1:A:138:LEU:HB3	1:A:148:ARG:NH1	2.32	0.45
1:A:244:HIS:HB3	1:A:247:GLN:HB2	1.99	0.45
1:A:40:GLN:HE21	1:A:40:GLN:HB3	1.68	0.45
1:A:57:LEU:HB3	1:A:126:LEU:HD12	1.99	0.45
1:A:65:ARG:HH22	1:A:106:GLU:HB2	1.81	0.45
1:A:68:ALA:HB3	1:A:99:GLU:CD	2.36	0.45
1:B:481:VAL:O	1:B:485:THR:HG23	2.17	0.45
1:A:146:ALA:HB1	1:A:210:ASN:HB2	1.97	0.45
1:A:373:THR:HB	1:A:389:ARG:HH11	1.75	0.45
1:A:564:GLN:HE21	1:A:564:GLN:HB2	1.56	0.45
1:A:156:ASN:O	1:A:159:SER:N	2.50	0.44
1:A:288:GLN:HG3	1:A:292:CYS:O	2.17	0.44
1:A:549:PHE:O	1:A:553:CYS:HB3	2.17	0.44
1:A:163:ILE:HG23	1:A:163:ILE:O	2.17	0.44
1:A:167:TYR:HE2	1:A:181:LYS:HB2	1.83	0.44
1:B:510:MET:HB3	1:B:516:LEU:HG	2.00	0.44
1:A:256:HIS:HB3	1:A:261:HIS:ND1	2.33	0.44
1:A:486:GLY:HA2	1:A:506:ARG:HH11	1.83	0.44
1:B:28:SER:O	1:B:38:VAL:HG22	2.18	0.44
1:A:138:LEU:HD22	1:A:148:ARG:HH12	1.83	0.44
1:B:222:LEU:HD22	1:B:224:MET:N	2.32	0.44
1:B:459:LYS:HD3	1:B:469:GLU:OE1	2.17	0.44
1:B:263:PHE:HB2	1:B:416:LEU:O	2.18	0.44
1:A:481:VAL:HA	1:A:484:VAL:HG12	1.99	0.44
1:A:564:GLN:HG3	1:A:565:GLN:N	2.32	0.44
1:A:55:ASP:OD2	1:A:127:LYS:NZ	2.49	0.43
1:B:41:PRO:CG	1:B:207:ASN:ND2	2.81	0.43
1:A:364:ILE:CG2	1:A:394:CYS:HB2	2.40	0.43
1:B:191:GLN:HB2	1:B:212:VAL:CA	2.47	0.43
1:A:407:ASP:OD2	1:A:407:ASP:N	2.47	0.43
1:B:212:VAL:HG22	1:B:213:ASN:N	2.33	0.43
1:A:194:HIS:HB3	1:A:210:ASN:ND2	2.33	0.43
1:B:49:PRO:CG	1:B:291:PRO:HB3	2.49	0.43
1:B:473:VAL:HG23	1:B:476:LEU:HD23	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:244:HIS:HE1	1:B:427:LYS:O	2.01	0.43
1:B:8:PHE:N	1:B:8:PHE:CD1	2.86	0.43
1:A:19:ALA:O	1:A:24:ASN:HA	2.19	0.43
1:A:468:ASN:HA	1:A:471:ARG:HH21	1.83	0.43
1:A:494:VAL:O	1:A:497:VAL:N	2.51	0.43
1:B:307:HIS:ND1	1:B:308:LEU:N	2.67	0.43
1:A:13:ASP:OD1	1:A:226:TRP:HE3	2.02	0.43
1:A:412:LYS:N	1:A:413:PRO:HD3	2.33	0.43
1:A:561:ARG:HA	1:A:564:GLN:HG2	2.01	0.43
1:B:10:HIS:CD2	1:B:10:HIS:N	2.87	0.43
1:B:290:ASP:O	1:B:291:PRO:C	2.56	0.43
1:B:122:GLN:NE2	1:B:159:SER:HB3	2.34	0.43
1:B:177:VAL:O	1:B:180:ASP:CG	2.57	0.43
1:A:363:ASP:OD2	1:A:363:ASP:N	2.52	0.43
1:B:13:ASP:OD1	1:B:226:TRP:HB3	2.19	0.43
1:A:123:LEU:HD11	1:A:184:LEU:HD13	2.00	0.42
1:A:370:LEU:HD13	1:A:388:VAL:HG21	2.00	0.42
1:B:179:GLY:HA2	1:B:220:ILE:O	2.19	0.42
1:B:232:ASP:OD1	1:B:384:ARG:HG3	2.19	0.42
1:A:392:HIS:O	1:A:396:ASN:N	2.46	0.42
1:A:298:TYR:HB3	1:A:381:LEU:O	2.16	0.42
1:A:14:ILE:HG12	1:A:126:LEU:HD11	2.01	0.42
1:A:404:ILE:HA	1:A:405:PRO:HD3	1.89	0.42
1:B:300:ASN:HA	1:B:369:GLU:OE2	2.19	0.42
1:B:94:HIS:CE1	1:B:98:LEU:HD21	2.54	0.42
1:B:141:LEU:O	1:B:141:LEU:HD13	2.20	0.42
1:B:149:VAL:HG23	1:B:210:ASN:HA	2.02	0.42
1:B:194:HIS:CE1	1:B:196:SER:HA	2.55	0.42
1:A:235:LYS:CA	1:A:296:ALA:O	2.68	0.42
1:A:298:TYR:O	1:A:301:SER:HB2	2.20	0.42
1:B:392:HIS:ND1	1:B:395:THR:HG23	2.34	0.42
1:B:89:LEU:O	1:B:93:HIS:CB	2.63	0.42
1:A:200:LEU:HD12	1:A:206:CYS:SG	2.58	0.42
1:A:239:VAL:HG21	1:A:440:VAL:CG2	2.48	0.42
1:A:394:CYS:SG	1:A:395:THR:CG2	3.05	0.42
1:A:473:VAL:HA	1:A:476:LEU:HD23	2.02	0.42
1:A:10:HIS:HD2	1:A:13:ASP:OD2	2.02	0.41
1:A:318:VAL:HG13	1:A:318:VAL:O	2.20	0.41
1:A:84:THR:CG2	1:A:85:ASP:H	2.33	0.41
1:B:287:VAL:HG11	1:B:302:LEU:HB2	2.02	0.41
1:B:55:ASP:HB2	1:B:127:LYS:HD2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:222:LEU:HD22	1:B:223:PHE:N	2.35	0.41
1:B:304:ARG:NH1	1:B:363:ASP:O	2.47	0.41
1:B:480:LEU:O	1:B:483:PHE:HB3	2.20	0.41
1:A:390:LEU:HB2	1:A:399:VAL:HG23	2.01	0.41
1:B:29:THR:OG1	1:B:125:HIS:CE1	2.74	0.41
1:A:91:LYS:O	1:A:94:HIS:CE1	2.73	0.41
1:B:210:ASN:C	1:B:210:ASN:HD22	2.23	0.41
1:A:264:LEU:HB2	1:A:416:LEU:HB2	2.02	0.41
1:A:314:LEU:CD1	1:A:355:LEU:HG	2.50	0.41
1:A:58:PHE:CA	1:A:124:LEU:O	2.65	0.41
1:A:224:MET:HG2	1:A:228:ASP:HB2	2.01	0.41
1:B:142:LEU:HB2	1:B:208:GLU:CD	2.41	0.41
1:B:35:ASP:N	1:B:35:ASP:OD1	2.52	0.41
1:A:375:LEU:HD12	1:A:375:LEU:H	1.82	0.41
1:A:565:GLN:O	1:A:566:ASP:HB2	2.21	0.41
1:B:462:LYS:HA	1:B:462:LYS:HD3	1.79	0.41
1:B:503:ASN:HD21	1:B:505:GLU:CG	2.10	0.41
1:B:503:ASN:ND2	1:B:504:ARG:N	2.68	0.41
1:A:147:MET:HB2	1:A:211:SER:HB3	2.03	0.41
1:A:243:PHE:CZ	1:A:248:GLU:HA	2.56	0.41
1:A:255:GLU:HA	1:A:259:LYS:O	2.19	0.41
1:A:564:GLN:O	1:A:571:GLN:HG3	2.21	0.41
1:B:276:THR:HG22	1:B:276:THR:O	2.20	0.41
1:A:249:LYS:CD	1:A:266:THR:HG23	2.44	0.41
1:B:436:SER:OG	1:B:439:GLU:CG	2.69	0.41
1:A:39:VAL:N	1:A:207:ASN:O	2.37	0.41
1:A:95:ALA:HA	1:A:98:LEU:HD22	2.03	0.41
1:B:278:SER:C	1:B:280:ALA:H	2.24	0.41
1:A:296:ALA:N	1:A:297:GLY:CA	2.81	0.40
1:A:304:ARG:NH2	1:A:367:ILE:HD11	2.36	0.40
1:A:376:ARG:HA	1:A:377:GLY:C	2.40	0.40
1:B:12:GLY:HA3	1:B:111:LEU:HD22	2.03	0.40
1:A:91:LYS:HA	1:A:91:LYS:HD2	1.80	0.40
1:B:523:LEU:O	1:B:526:PRO:HD2	2.21	0.40
1:A:296:ALA:HB3	1:A:297:GLY:C	2.42	0.40
1:B:310:THR:C	1:B:312:HIS:H	2.23	0.40
1:A:246:GLU:HB2	1:A:427:LYS:HB3	2.02	0.40
1:B:312:HIS:HB3	1:B:357:SER:OG	2.21	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	487/585 (83%)	465 (96%)	22 (4%)	0	100	100
1	B	466/585 (80%)	450 (97%)	16 (3%)	0	100	100
All	All	953/1170 (82%)	915 (96%)	38 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	383/513 (75%)	333 (87%)	50 (13%)	4	23
1	B	373/513 (73%)	314 (84%)	59 (16%)	2	17
All	All	756/1026 (74%)	647 (86%)	109 (14%)	3	20

All (109) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	SER
1	A	10	HIS
1	A	32	LEU
1	A	40	GLN
1	A	47	ASN
1	A	56	CYS
1	A	65	ARG
1	A	71	GLN

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Mol	Chain	Res	Type
1	A	98	LEU
1	A	101	LYS
1	A	111	LEU
1	A	115	ILE
1	A	116	GLN
1	A	121	ILE
1	A	127	LYS
1	A	167	TYR
1	A	183	VAL
1	A	185	ASN
1	A	193	LEU
1	A	209	VAL
1	A	210	ASN
1	A	228	ASP
1	A	230	LYS
1	A	274	SER
1	A	298	TYR
1	A	302	LEU
1	A	373	THR
1	A	374	THR
1	A	375	LEU
1	A	385	ASN
1	A	387	TYR
1	A	389	ARG
1	A	394	CYS
1	A	396	ASN
1	A	409	GLU
1	A	410	GLU
1	A	428	GLU
1	A	441	ARG
1	A	476	LEU
1	A	480	LEU
1	A	488	THR
1	A	509	LEU
1	A	510	MET
1	A	558	ARG
1	A	561	ARG
1	A	563	SER
1	A	564	GLN
1	A	565	GLN
1	A	566	ASP
1	A	567	TYR

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Mol	Chain	Res	Type
1	B	8	PHE
1	B	10	HIS
1	B	14	ILE
1	B	28	SER
1	B	35	ASP
1	B	42	GLU
1	B	46	LEU
1	B	47	ASN
1	B	59	LYS
1	B	65	ARG
1	B	84	THR
1	B	85	ASP
1	B	92	LEU
1	B	94	HIS
1	B	105	THR
1	B	116	GLN
1	B	121	ILE
1	B	138	LEU
1	B	141	LEU
1	B	153	GLU
1	B	170	ARG
1	B	178	ILE
1	B	191	GLN
1	B	199	GLN
1	B	210	ASN
1	B	222	LEU
1	B	224	MET
1	B	228	ASP
1	B	232	ASP
1	B	239	VAL
1	B	266	THR
1	B	276	THR
1	B	277	SER
1	B	281	LEU
1	B	287	VAL
1	B	308	LEU
1	B	318	VAL
1	B	358	VAL
1	B	363	ASP
1	B	382	VAL
1	B	394	CYS
1	B	407	ASP

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Mol	Chain	Res	Type
1	B	410	GLU
1	B	428	GLU
1	B	440	VAL
1	B	442	ASP
1	B	448	ASP
1	B	456	ILE
1	B	460	LEU
1	B	461	GLU
1	B	464	THR
1	B	480	LEU
1	B	503	ASN
1	B	511	ARG
1	B	522	LEU
1	B	555	LEU
1	B	561	ARG
1	B	564	GLN
1	B	567	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	HIS
1	A	47	ASN
1	A	93	HIS
1	A	135	ASN
1	A	194	HIS
1	A	199	GLN
1	A	210	ASN
1	A	288	GLN
1	A	392	HIS
1	A	396	ASN
1	A	507	GLN
1	A	564	GLN
1	B	71	GLN
1	B	94	HIS
1	B	102	GLN
1	B	191	GLN
1	B	194	HIS
1	B	210	ASN
1	B	213	ASN
1	B	312	HIS
1	B	447	ASN

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Mol	Chain	Res	Type
1	B	503	ASN
1	B	551	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

1 ligand is 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	$\# Z > 2$
2	I3P	B	603	-	24,24,24	0.89	2 (8%)	36,39,39	1.01	1 (2%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	I3P	B	603	-	-	4/15/39/39	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	603	I3P	P1-O1	2.24	1.63	1.59
2	B	603	I3P	P5-O5	2.10	1.63	1.59

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	603	I3P	C6-C1-C2	2.37	114.27	110.85

There are no chirality outliers.

All (4) torsion outliers are listed below:

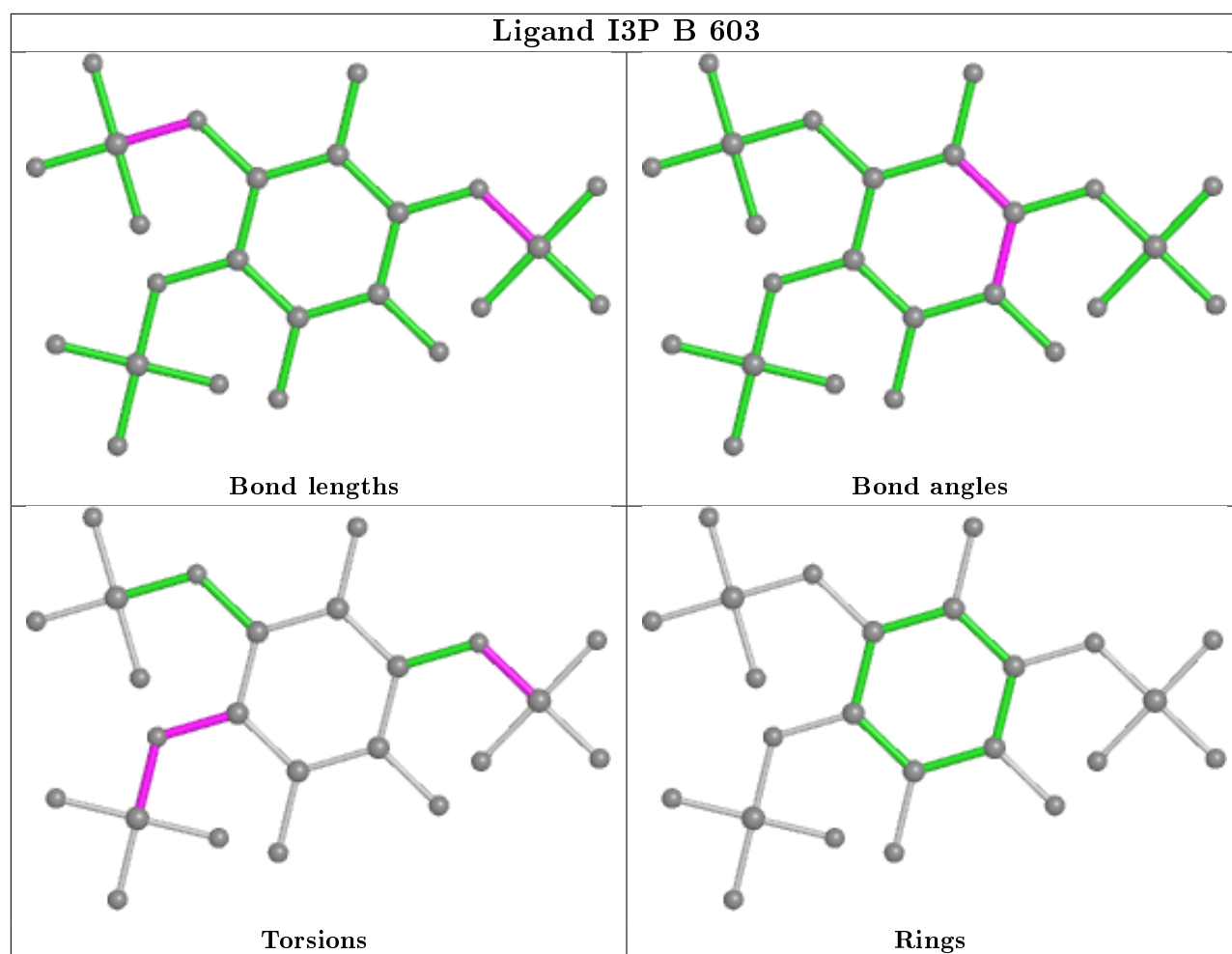
Mol	Chain	Res	Type	Atoms
2	B	603	I3P	C3-C4-O4-P4
2	B	603	I3P	C5-C4-O4-P4
2	B	603	I3P	C4-O4-P4-O42
2	B	603	I3P	C1-O1-P1-O11

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	603	I3P	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 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 [i](#)

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	501/585 (85%)	-0.28	2 (0%) 92 92	54, 131, 219, 312	0
1	B	479/585 (81%)	-0.22	10 (2%) 63 59	60, 146, 236, 390	2 (0%)
All	All	980/1170 (83%)	-0.25	12 (1%) 79 76	54, 140, 230, 390	2 (0%)

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	370	LEU	3.7
1	B	386	SER	3.4
1	B	387	TYR	3.1
1	B	274	SER	2.7
1	B	303	PHE	2.6
1	A	374	THR	2.6
1	B	305	PHE	2.5
1	B	302	LEU	2.4
1	B	388	VAL	2.4
1	A	141	LEU	2.2
1	B	432	ILE	2.1
1	B	552	ILE	2.1

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](#)

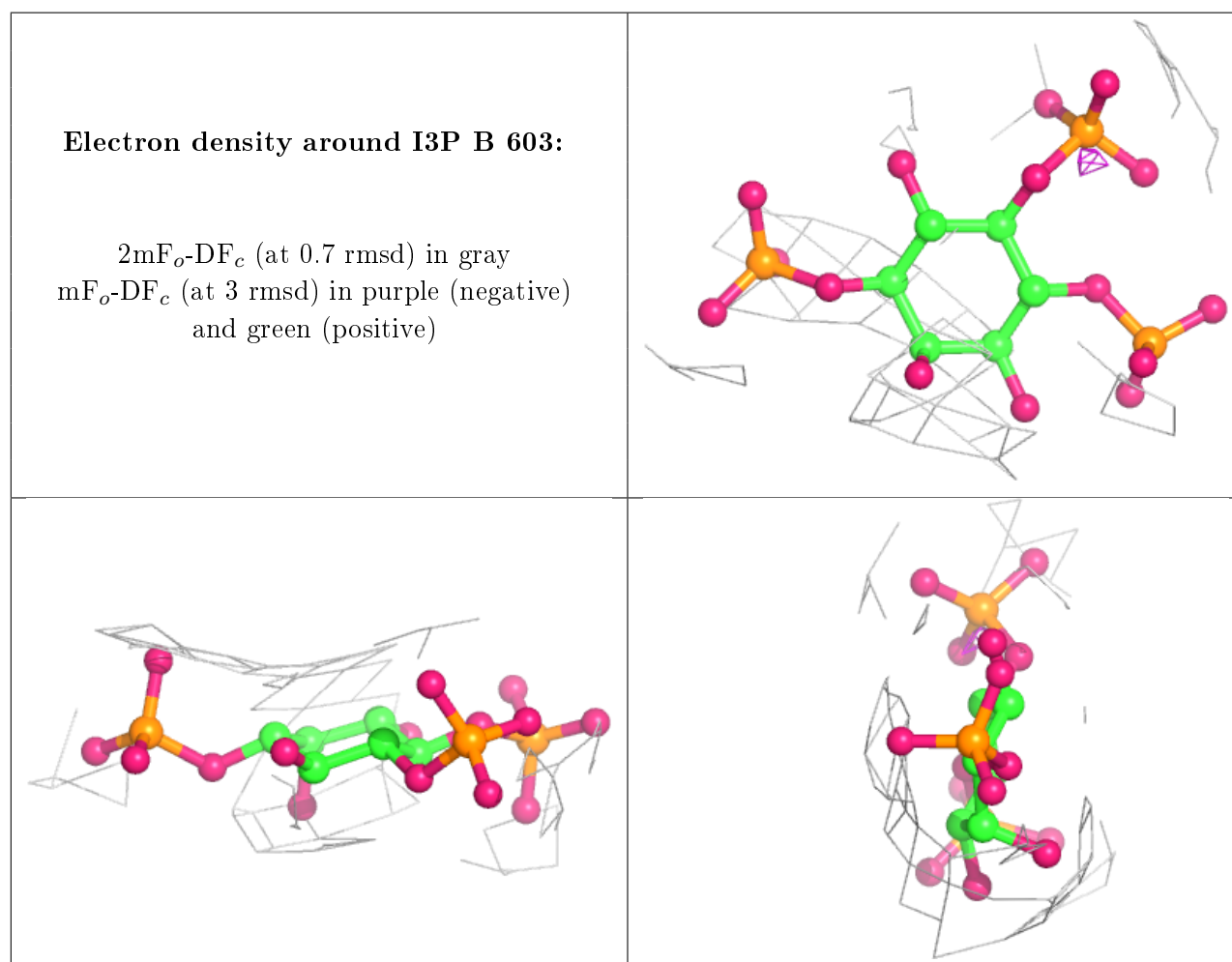
There are no carbohydrates in this entry.

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(\AA^2)	Q<0.9
2	I3P	B	603	24/24	0.95	0.14	60,92,114,118	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.