



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 02:21 AM UTC

PDB ID : 3CTL / pdb_00003ctl
Title : Crystal structure of D-Allulose 6-Phosphate 3-Epimerase from Escherichia coli K12 complexed with D-glucitol 6-phosphate and magnesium
Authors : Fedorov, A.A.; Fedorov, E.V.; Chan, K.K.; Gerlt, J.A.; Almo, S.C.
Deposited on : 2008-04-14
Resolution : 2.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

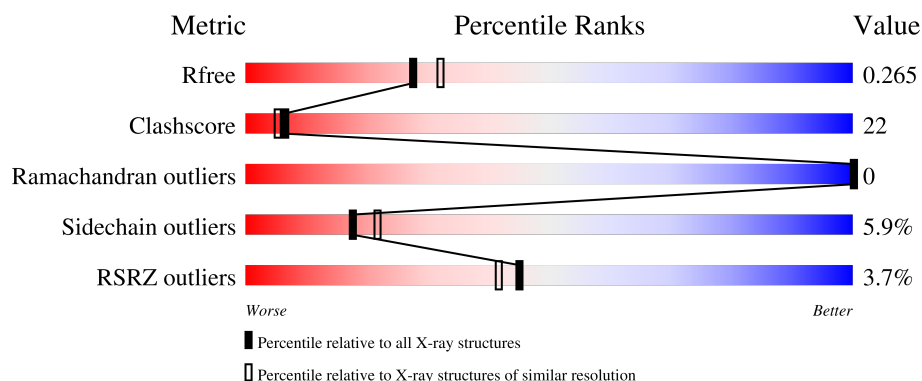
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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 $\leq 5\%$. 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	231	3% 62% 27% 5% 5%
1	B	231	3% 54% 36% 5%
1	C	231	3% 62% 27% 5% 5%
1	D	231	3% 60% 30% 5%
1	E	231	4% 61% 30% 5%

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Mol	Chain	Length	Quality of chain
1	F	231	4% 59% 31% • 5%

2 Entry composition [i](#)

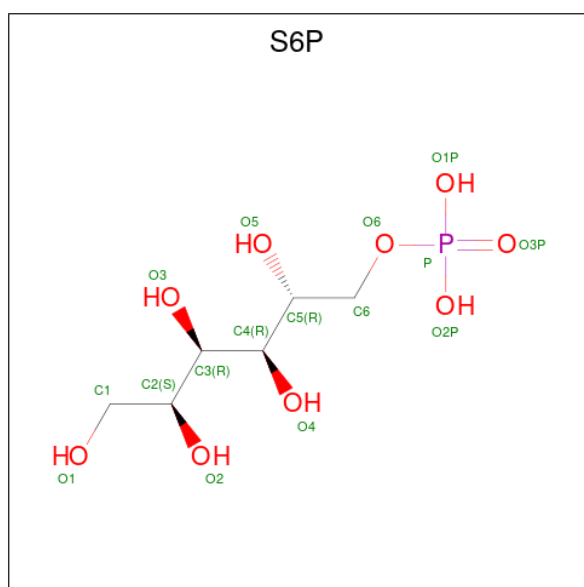
There are 4 unique types of molecules in this entry. The entry contains 10740 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 D-allulose-6-phosphate 3-epimerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	219	Total	C	N	O	S	0	0	0
			1744	1121	288	321	14			
1	B	219	Total	C	N	O	S	0	0	0
			1744	1121	288	321	14			
1	C	219	Total	C	N	O	S	0	0	0
			1744	1121	288	321	14			
1	D	219	Total	C	N	O	S	0	0	0
			1744	1121	288	321	14			
1	E	219	Total	C	N	O	S	0	0	0
			1744	1121	288	321	14			
1	F	219	Total	C	N	O	S	0	0	0
			1744	1121	288	321	14			

- Molecule 2 is D-SORBITOL-6-PHOSPHATE (CCD ID: S6P) (formula: $C_6H_{15}O_9P$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			16	6	9	1		
2	B	1	Total	C	O	P	0	0
			16	6	9	1		
2	C	1	Total	C	O	P	0	0
			16	6	9	1		
2	D	1	Total	C	O	P	0	0
			16	6	9	1		
2	E	1	Total	C	O	P	0	0
			16	6	9	1		
2	F	1	Total	C	O	P	0	0
			16	6	9	1		

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	B	1	Total	Mg	0	0
			1	1		
3	C	1	Total	Mg	0	0
			1	1		
3	D	1	Total	Mg	0	0
			1	1		
3	E	1	Total	Mg	0	0
			1	1		
3	F	1	Total	Mg	0	0
			1	1		

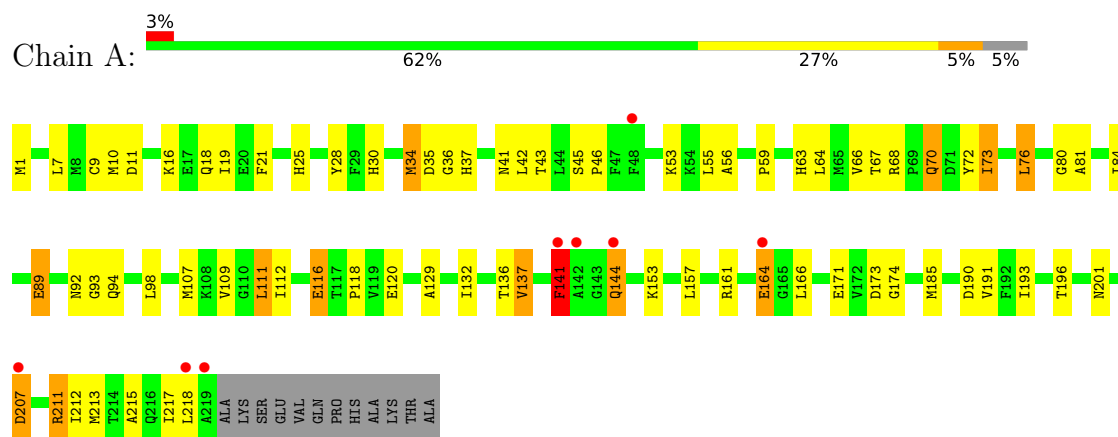
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	31	Total	O	0	0
			31	31		
4	B	23	Total	O	0	0
			23	23		
4	C	42	Total	O	0	0
			42	42		
4	D	20	Total	O	0	0
			20	20		
4	E	25	Total	O	0	0
			25	25		
4	F	33	Total	O	0	0
			33	33		

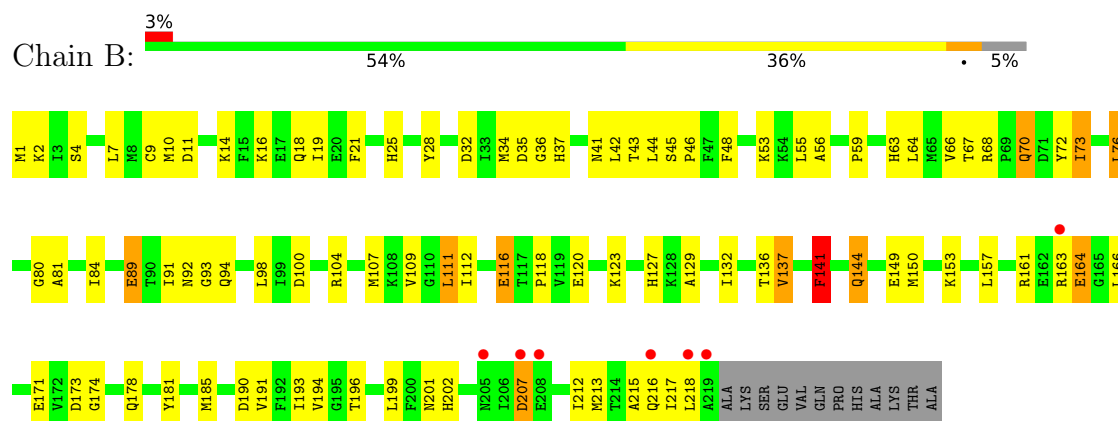
3 Residue-property plots [i](#)

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 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.

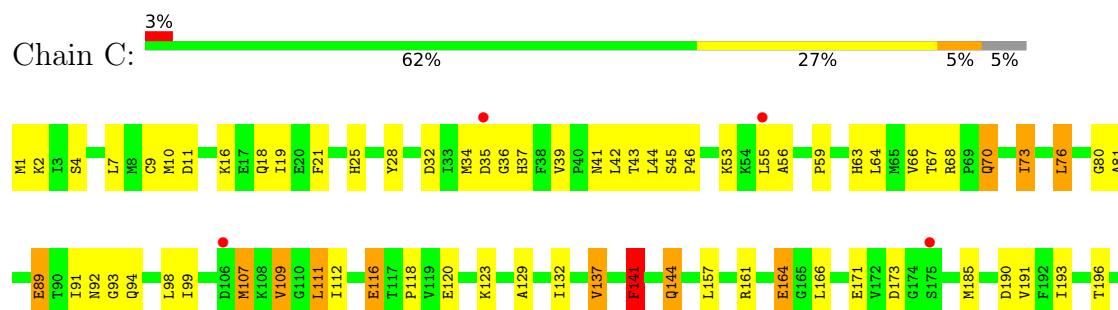
- Molecule 1: D-allulose-6-phosphate 3-epimerase

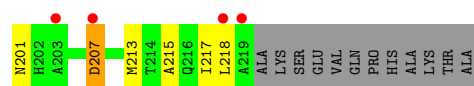


- Molecule 1: D-allulose-6-phosphate 3-epimerase

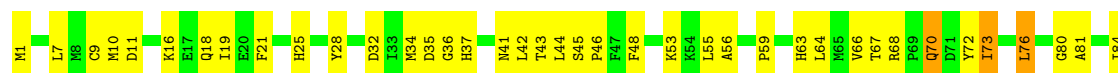


- Molecule 1: D-allulose-6-phosphate 3-epimerase

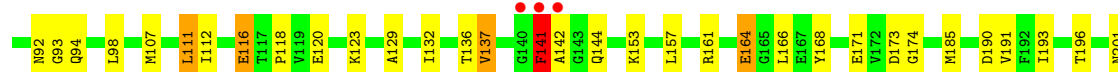
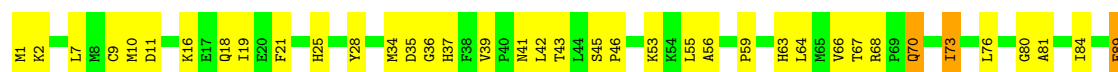




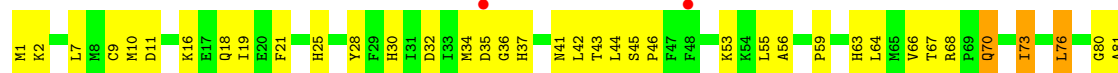
• Molecule 1: D-allulose-6-phosphate 3-epimerase



• Molecule 1: D-allulose-6-phosphate 3-epimerase



• Molecule 1: D-allulose-6-phosphate 3-epimerase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	75.71Å 129.04Å 154.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.96 – 2.20 24.96 – 2.20	Depositor EDS
% Data completeness (in resolution range)	96.5 (24.96-2.20) 96.5 (24.96-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.31 (at 2.20Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.243 , 0.265 0.243 , 0.265	Depositor DCC
R_{free} test set	3781 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	34.8	Xtriage
Anisotropy	0.328	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 29.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10740	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.05% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, S6P

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	0.45	1/1784 (0.1%)	0.98	6/2414 (0.2%)
1	B	0.44	0/1784	0.99	8/2414 (0.3%)
1	C	0.46	1/1784 (0.1%)	1.01	9/2414 (0.4%)
1	D	0.44	0/1784	0.99	6/2414 (0.2%)
1	E	0.44	0/1784	1.00	7/2414 (0.3%)
1	F	0.46	1/1784 (0.1%)	0.98	8/2414 (0.3%)
All	All	0.45	3/10704 (0.0%)	0.99	44/14484 (0.3%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	107	MET	SD-CE	-5.31	1.66	1.79
1	A	34	MET	SD-CE	-5.25	1.66	1.79
1	F	107	MET	SD-CE	-5.13	1.66	1.79

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	36	GLY	N-CA-C	-9.18	103.27	115.21
1	B	36	GLY	N-CA-C	-9.10	103.39	115.21
1	E	39	VAL	N-CA-C	-8.85	101.93	109.19
1	E	36	GLY	N-CA-C	-8.74	103.85	115.21
1	D	36	GLY	N-CA-C	-8.72	103.88	115.21
1	C	36	GLY	N-CA-C	-8.70	103.90	115.21
1	A	36	GLY	N-CA-C	-8.52	104.13	115.21
1	C	39	VAL	N-CA-C	-8.35	102.34	109.19
1	D	73	ILE	N-CA-C	6.76	116.91	110.42
1	C	73	ILE	N-CA-C	6.57	116.73	110.42
1	A	73	ILE	N-CA-C	6.47	116.63	110.42
1	F	73	ILE	N-CA-C	6.45	116.61	110.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	73	ILE	N-CA-C	6.35	116.52	110.42
1	E	73	ILE	N-CA-C	6.34	116.50	110.42
1	E	56	ALA	N-CA-C	6.24	120.23	110.32
1	F	56	ALA	N-CA-C	6.14	120.08	110.32
1	D	56	ALA	N-CA-C	6.13	120.07	110.32
1	C	123	LYS	N-CA-C	6.03	118.62	111.33
1	B	56	ALA	N-CA-C	6.00	119.86	110.32
1	C	56	ALA	N-CA-C	5.98	119.83	110.32
1	E	123	LYS	N-CA-C	5.83	118.39	111.33
1	F	123	LYS	N-CA-C	5.70	118.23	111.33
1	B	123	LYS	N-CA-C	5.70	118.23	111.33
1	A	56	ALA	N-CA-C	5.63	119.28	110.32
1	A	141	PHE	N-CA-C	5.53	116.65	108.86
1	E	141	PHE	N-CA-C	5.44	116.53	108.86
1	C	109	VAL	N-CA-C	5.39	116.07	108.36
1	D	109	VAL	N-CA-C	5.39	116.07	108.36
1	B	141	PHE	N-CA-C	5.38	116.44	108.86
1	C	141	PHE	N-CA-C	5.35	116.40	108.86
1	D	141	PHE	N-CA-C	5.34	116.39	108.86
1	A	109	VAL	N-CA-C	5.28	115.91	108.36
1	B	109	VAL	N-CA-C	5.27	115.89	108.36
1	C	64	LEU	N-CA-C	5.25	117.69	108.56
1	D	64	LEU	N-CA-C	5.25	117.69	108.56
1	A	64	LEU	N-CA-C	5.24	117.68	108.56
1	F	64	LEU	N-CA-C	5.22	117.64	108.56
1	B	64	LEU	N-CA-C	5.18	117.57	108.56
1	E	64	LEU	N-CA-C	5.17	117.56	108.56
1	F	138	ASP	CA-C-N	5.16	125.15	119.89
1	F	138	ASP	C-N-CA	5.16	125.15	119.89
1	F	141	PHE	N-CA-C	5.11	116.06	108.86
1	C	91	ILE	N-CA-C	5.10	117.29	111.88
1	B	91	ILE	N-CA-C	5.06	117.09	112.43

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	1744	0	1737	79	0
1	B	1744	0	1737	89	0
1	C	1744	0	1737	77	0
1	D	1744	0	1737	80	0
1	E	1744	0	1737	77	0
1	F	1744	0	1737	80	0
2	A	16	0	12	1	0
2	B	16	0	12	1	0
2	C	16	0	12	1	0
2	D	16	0	12	1	0
2	E	16	0	12	2	0
2	F	16	0	12	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
4	A	31	0	0	4	0
4	B	23	0	0	4	0
4	C	42	0	0	3	0
4	D	20	0	0	3	0
4	E	25	0	0	2	0
4	F	33	0	0	2	0
All	All	10740	0	10494	460	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 22.

All (460) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:127:HIS:HD2	4:B:619:HOH:O	1.37	1.06
1:D:7:LEU:HD22	1:D:10:MET:HE2	1.38	1.02
1:B:7:LEU:HD22	1:B:10:MET:HE2	1.40	1.02
1:C:7:LEU:HD22	1:C:10:MET:HE2	1.41	1.01
1:E:7:LEU:HD22	1:E:10:MET:HE2	1.40	1.00
1:F:7:LEU:HD22	1:F:10:MET:HE2	1.41	0.99
1:A:7:LEU:HD22	1:A:10:MET:HE2	1.39	0.97
1:B:68:ARG:HA	1:B:70:GLN:HE22	1.42	0.84
1:D:68:ARG:HA	1:D:70:GLN:HE22	1.44	0.82
1:C:68:ARG:HA	1:C:70:GLN:HE22	1.45	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:68:ARG:HA	1:A:70:GLN:HE22	1.45	0.82
1:E:68:ARG:HA	1:E:70:GLN:HE22	1.44	0.81
1:B:14:LYS:HE3	4:B:617:HOH:O	1.81	0.80
1:F:68:ARG:HA	1:F:70:GLN:HE22	1.46	0.80
1:A:196:THR:HG22	4:A:615:HOH:O	1.81	0.78
1:A:211:ARG:HB3	1:A:211:ARG:HH11	1.50	0.77
1:C:10:MET:HE1	1:C:19:ILE:HD11	1.67	0.74
1:F:10:MET:HE1	1:F:19:ILE:HD11	1.70	0.74
1:D:10:MET:HE1	1:D:19:ILE:HD11	1.70	0.73
1:D:53:LYS:HG3	1:D:80:GLY:HA3	1.71	0.73
1:E:10:MET:HE1	1:E:19:ILE:HD11	1.71	0.72
1:A:10:MET:HE1	1:A:19:ILE:HD11	1.71	0.72
1:F:53:LYS:HG3	1:F:80:GLY:HA3	1.70	0.72
1:C:53:LYS:HE2	4:C:620:HOH:O	1.89	0.71
1:B:10:MET:HE1	1:B:19:ILE:HD11	1.72	0.71
1:F:34:MET:CE	1:F:43:THR:HG23	2.21	0.71
1:F:70:GLN:H	1:F:70:GLN:NE2	1.90	0.70
1:C:70:GLN:H	1:C:70:GLN:NE2	1.88	0.70
1:E:70:GLN:H	1:E:70:GLN:NE2	1.89	0.70
1:B:70:GLN:H	1:B:70:GLN:NE2	1.90	0.70
1:F:34:MET:HE2	1:F:43:THR:HG23	1.73	0.69
1:D:70:GLN:H	1:D:70:GLN:NE2	1.90	0.69
1:E:53:LYS:HG3	1:E:80:GLY:HA3	1.74	0.69
1:A:28:TYR:HD1	1:A:59:PRO:HG2	1.57	0.69
1:A:70:GLN:H	1:A:70:GLN:NE2	1.91	0.69
1:B:53:LYS:HG3	1:B:80:GLY:HA3	1.74	0.69
1:C:34:MET:CE	1:C:43:THR:HG23	2.24	0.68
1:C:111:LEU:HD22	1:C:129:ALA:HB2	1.76	0.68
1:E:168:TYR:HD2	4:E:635:HOH:O	1.75	0.68
1:B:111:LEU:HD22	1:B:129:ALA:HB2	1.76	0.68
1:D:28:TYR:HD1	1:D:59:PRO:HG2	1.59	0.68
1:A:111:LEU:HD22	1:A:129:ALA:HB2	1.75	0.68
1:C:53:LYS:HG3	1:C:80:GLY:HA3	1.75	0.68
1:B:34:MET:CE	1:B:43:THR:HG23	2.24	0.67
1:E:111:LEU:HD22	1:E:129:ALA:HB2	1.76	0.67
1:B:28:TYR:HD1	1:B:59:PRO:HG2	1.58	0.67
1:F:28:TYR:HD1	1:F:59:PRO:HG2	1.60	0.67
1:A:30:HIS:HE1	4:A:612:HOH:O	1.76	0.67
1:E:34:MET:CE	1:E:43:THR:HG23	2.25	0.66
1:E:63:HIS:CE1	1:E:112:ILE:HD13	2.30	0.66
1:C:34:MET:HE2	1:C:43:THR:HG23	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:34:MET:HE2	1:D:43:THR:HG23	1.78	0.65
1:E:34:MET:HE2	1:E:43:THR:HG23	1.79	0.65
1:A:34:MET:CE	1:A:43:THR:HG23	2.26	0.65
1:F:111:LEU:HD22	1:F:129:ALA:HB2	1.77	0.65
1:A:53:LYS:HG3	1:A:80:GLY:HA3	1.77	0.65
1:B:81:ALA:C	1:B:107:MET:HE3	2.22	0.65
1:D:34:MET:CE	1:D:43:THR:HG23	2.26	0.64
1:E:81:ALA:C	1:E:107:MET:HE3	2.23	0.64
1:D:81:ALA:C	1:D:107:MET:HE3	2.22	0.64
1:D:211:ARG:HH11	1:D:211:ARG:HB3	1.61	0.64
1:A:81:ALA:C	1:A:107:MET:HE3	2.23	0.63
1:C:28:TYR:HD1	1:C:59:PRO:HG2	1.63	0.63
1:D:111:LEU:HD22	1:D:129:ALA:HB2	1.78	0.63
1:C:137:VAL:HG22	1:C:144:GLN:HB3	1.81	0.63
1:E:70:GLN:H	1:E:70:GLN:HE21	1.47	0.63
1:F:63:HIS:CE1	1:F:112:ILE:HD13	2.34	0.63
1:B:34:MET:HE2	1:B:43:THR:HG23	1.79	0.63
1:C:70:GLN:H	1:C:70:GLN:HE21	1.46	0.62
1:D:70:GLN:H	1:D:70:GLN:HE21	1.46	0.62
1:F:137:VAL:HG22	1:F:144:GLN:HB3	1.80	0.62
1:E:137:VAL:HG22	1:E:144:GLN:HB3	1.80	0.62
1:D:137:VAL:HG22	1:D:144:GLN:HB3	1.82	0.62
1:E:28:TYR:HD1	1:E:59:PRO:HG2	1.65	0.62
1:B:137:VAL:HG22	1:B:144:GLN:HB3	1.82	0.62
1:A:34:MET:HE2	1:A:43:THR:HG23	1.81	0.62
1:C:1:MET:HE3	1:C:185:MET:SD	2.40	0.61
1:D:63:HIS:CE1	1:D:112:ILE:HD13	2.35	0.61
1:F:81:ALA:C	1:F:107:MET:HE3	2.25	0.61
1:B:63:HIS:CE1	1:B:112:ILE:HD13	2.35	0.61
1:C:7:LEU:O	1:C:10:MET:HG2	2.00	0.61
1:A:137:VAL:HG22	1:A:144:GLN:HB3	1.81	0.60
1:C:81:ALA:C	1:C:107:MET:HE3	2.25	0.60
1:F:70:GLN:H	1:F:70:GLN:HE21	1.48	0.60
1:D:53:LYS:HE2	4:D:611:HOH:O	2.02	0.59
1:E:73:ILE:HD12	1:E:98:LEU:HD22	1.85	0.59
1:F:35:ASP:HB3	1:F:37:HIS:H	1.67	0.59
1:B:35:ASP:HB3	1:B:37:HIS:H	1.68	0.59
1:D:81:ALA:HB3	1:D:107:MET:HE1	1.85	0.59
1:B:10:MET:HE3	1:B:48:PHE:HZ	1.67	0.59
1:D:34:MET:HE3	1:D:41:ASN:C	2.28	0.59
1:A:34:MET:HE3	1:A:41:ASN:C	2.28	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:7:LEU:O	1:D:10:MET:HG2	2.03	0.58
1:E:7:LEU:O	1:E:10:MET:HG2	2.03	0.58
1:E:35:ASP:HB3	1:E:37:HIS:H	1.68	0.58
1:F:7:LEU:O	1:F:10:MET:HG2	2.03	0.58
1:F:73:ILE:HD12	1:F:98:LEU:HD22	1.86	0.58
1:F:34:MET:HE3	1:F:41:ASN:C	2.28	0.58
1:A:70:GLN:H	1:A:70:GLN:HE21	1.50	0.58
1:B:70:GLN:H	1:B:70:GLN:HE21	1.51	0.58
1:A:7:LEU:O	1:A:10:MET:HG2	2.03	0.58
1:A:63:HIS:CE1	1:A:112:ILE:HD13	2.38	0.58
1:B:1:MET:HE3	1:B:185:MET:SD	2.43	0.58
1:D:35:ASP:HB2	1:D:66:VAL:HA	1.86	0.58
1:B:7:LEU:O	1:B:10:MET:HG2	2.03	0.58
1:A:1:MET:HE3	1:A:185:MET:SD	2.43	0.57
1:C:63:HIS:CE1	1:C:112:ILE:HD13	2.38	0.57
1:D:7:LEU:HD22	1:D:10:MET:CE	2.25	0.57
1:A:70:GLN:CG	1:A:94:GLN:OE1	2.52	0.57
1:E:118:PRO:HB2	1:E:120:GLU:OE1	2.04	0.57
1:B:7:LEU:HB3	1:B:10:MET:HE3	1.87	0.57
1:B:34:MET:HE3	1:B:41:ASN:C	2.30	0.57
1:C:116:GLU:H	1:C:116:GLU:CD	2.13	0.57
1:F:211:ARG:NH1	1:F:211:ARG:HB3	2.20	0.57
1:E:34:MET:HE3	1:E:41:ASN:C	2.29	0.57
1:A:35:ASP:HB3	1:A:37:HIS:H	1.70	0.57
1:C:34:MET:HE3	1:C:41:ASN:C	2.30	0.57
1:C:35:ASP:HB3	1:C:37:HIS:H	1.69	0.56
1:A:116:GLU:H	1:A:116:GLU:CD	2.13	0.56
1:C:81:ALA:HB3	1:C:107:MET:HE1	1.86	0.56
1:F:70:GLN:CG	1:F:94:GLN:OE1	2.53	0.56
1:A:7:LEU:HD22	1:A:10:MET:CE	2.27	0.56
1:C:173:ASP:OD2	2:C:503:S6P:H3	2.05	0.56
1:A:70:GLN:HG2	1:A:94:GLN:OE1	2.05	0.56
1:E:67:THR:HG22	1:E:68:ARG:HG3	1.87	0.56
1:B:81:ALA:HB3	1:B:107:MET:HE1	1.87	0.56
1:D:53:LYS:CE	4:D:611:HOH:O	2.54	0.56
1:E:81:ALA:HB3	1:E:107:MET:HE1	1.88	0.56
1:D:183:LYS:HG3	4:D:607:HOH:O	2.06	0.55
1:E:116:GLU:CD	1:E:116:GLU:H	2.14	0.55
1:C:7:LEU:HB3	1:C:10:MET:HE3	1.88	0.55
1:B:67:THR:HG22	1:B:68:ARG:HG3	1.88	0.55
1:A:173:ASP:OD2	2:A:501:S6P:H3	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:11:ASP:H	1:C:18:GLN:HE22	1.54	0.55
1:D:118:PRO:HB2	1:D:120:GLU:OE1	2.06	0.55
1:E:7:LEU:HD22	1:E:10:MET:CE	2.26	0.55
1:F:213:MET:O	1:F:217:ILE:HG12	2.07	0.55
1:D:35:ASP:HB3	1:D:37:HIS:H	1.70	0.55
1:D:68:ARG:CA	1:D:70:GLN:HE22	2.18	0.55
1:A:30:HIS:CE1	4:A:612:HOH:O	2.54	0.55
1:E:70:GLN:CG	1:E:94:GLN:OE1	2.55	0.55
1:B:116:GLU:CD	1:B:116:GLU:H	2.15	0.54
1:B:173:ASP:OD2	2:B:502:S6P:H3	2.07	0.54
1:D:211:ARG:HB3	1:D:211:ARG:NH1	2.21	0.54
1:D:213:MET:O	1:D:217:ILE:HG12	2.07	0.54
1:A:213:MET:O	1:A:217:ILE:HG12	2.07	0.54
1:B:116:GLU:HG3	1:D:92:ASN:HA	1.89	0.54
1:B:118:PRO:HB2	1:B:120:GLU:OE1	2.08	0.54
1:D:73:ILE:HD12	1:D:98:LEU:HD22	1.88	0.54
1:F:81:ALA:HB3	1:F:107:MET:HE1	1.88	0.54
1:A:118:PRO:HB2	1:A:120:GLU:OE1	2.06	0.54
1:B:35:ASP:HB2	1:B:66:VAL:HA	1.88	0.54
1:C:35:ASP:HB2	1:C:66:VAL:HA	1.90	0.54
1:C:118:PRO:HB2	1:C:120:GLU:OE1	2.07	0.54
1:A:81:ALA:HB3	1:A:107:MET:HE1	1.88	0.54
1:D:81:ALA:O	1:D:107:MET:HE3	2.08	0.53
1:D:70:GLN:CG	1:D:94:GLN:OE1	2.56	0.53
1:F:70:GLN:HG2	1:F:94:GLN:OE1	2.08	0.53
1:F:182:GLU:HB3	4:F:622:HOH:O	2.09	0.53
1:E:7:LEU:HB3	1:E:10:MET:HE3	1.91	0.53
1:D:1:MET:HE3	1:D:185:MET:SD	2.49	0.53
1:A:35:ASP:HB2	1:A:66:VAL:HA	1.90	0.53
1:D:7:LEU:HB3	1:D:10:MET:HE3	1.91	0.53
1:E:70:GLN:HG2	1:E:94:GLN:OE1	2.08	0.53
1:E:213:MET:O	1:E:217:ILE:HG12	2.08	0.53
1:F:1:MET:HE3	1:F:185:MET:SD	2.48	0.53
1:F:67:THR:HG22	1:F:68:ARG:HG3	1.91	0.53
1:D:81:ALA:HB3	1:D:107:MET:CE	2.39	0.53
1:B:28:TYR:CD1	1:B:59:PRO:HG2	2.43	0.52
1:C:213:MET:O	1:C:217:ILE:HG12	2.10	0.52
1:F:9:CYS:SG	1:F:196:THR:HG23	2.49	0.52
1:A:67:THR:HG22	1:A:68:ARG:HG3	1.92	0.52
1:C:67:THR:HG22	1:C:68:ARG:HG3	1.91	0.52
1:E:68:ARG:CA	1:E:70:GLN:HE22	2.18	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:1:MET:HE3	1:E:185:MET:SD	2.49	0.52
1:E:92:ASN:HA	1:F:116:GLU:HG3	1.92	0.52
1:F:116:GLU:H	1:F:116:GLU:CD	2.16	0.52
1:A:7:LEU:HB3	1:A:10:MET:HE3	1.92	0.52
1:A:173:ASP:HB2	1:A:193:ILE:HD12	1.92	0.52
1:D:173:ASP:HB2	1:D:193:ILE:HD12	1.92	0.52
1:F:118:PRO:HB2	1:F:120:GLU:OE1	2.08	0.52
1:C:68:ARG:CA	1:C:70:GLN:HE22	2.19	0.52
1:D:173:ASP:OD2	2:D:504:S6P:H3	2.09	0.52
1:E:171:GLU:HG3	1:E:191:VAL:HB	1.92	0.52
1:E:11:ASP:H	1:E:18:GLN:HE22	1.57	0.51
1:F:35:ASP:HB2	1:F:66:VAL:HA	1.92	0.51
1:F:68:ARG:CA	1:F:70:GLN:HE22	2.20	0.51
1:B:213:MET:O	1:B:217:ILE:HG12	2.10	0.51
1:B:171:GLU:HG3	1:B:191:VAL:HB	1.92	0.51
1:C:171:GLU:HG3	1:C:191:VAL:HB	1.93	0.51
1:A:171:GLU:HG3	1:A:191:VAL:HB	1.93	0.51
1:C:7:LEU:HD22	1:C:10:MET:CE	2.28	0.51
1:E:173:ASP:HB2	1:E:193:ILE:HD12	1.93	0.51
1:F:45:SER:HB2	1:F:46:PRO:CD	2.41	0.51
1:F:171:GLU:HG3	1:F:191:VAL:HB	1.91	0.51
1:B:196:THR:O	1:B:201:ASN:HB2	2.09	0.51
1:D:70:GLN:HG2	1:D:94:GLN:OE1	2.10	0.51
1:D:196:THR:O	1:D:201:ASN:HB2	2.11	0.51
1:E:81:ALA:HB3	1:E:107:MET:CE	2.41	0.51
1:A:28:TYR:CD1	1:A:59:PRO:HG2	2.42	0.51
1:B:16:LYS:HG3	1:B:55:LEU:HD21	1.92	0.51
1:B:73:ILE:HD12	1:B:98:LEU:HD22	1.93	0.51
1:F:7:LEU:HB3	1:F:10:MET:HE3	1.92	0.51
1:F:45:SER:HB2	1:F:46:PRO:HD2	1.92	0.51
1:F:141:PHE:CD1	1:F:141:PHE:N	2.79	0.51
1:B:127:HIS:CD2	4:B:619:HOH:O	2.27	0.51
1:B:173:ASP:HB2	1:B:193:ILE:HD12	1.91	0.51
1:D:11:ASP:H	1:D:18:GLN:HE22	1.59	0.51
1:C:73:ILE:HD12	1:C:98:LEU:HD22	1.93	0.51
1:C:92:ASN:HA	1:D:116:GLU:HG3	1.93	0.51
1:D:67:THR:HG22	1:D:68:ARG:HG3	1.92	0.50
1:C:173:ASP:HB2	1:C:193:ILE:HD12	1.94	0.50
1:D:116:GLU:CD	1:D:116:GLU:H	2.18	0.50
1:F:196:THR:O	1:F:201:ASN:HB2	2.11	0.50
1:B:81:ALA:HB3	1:B:107:MET:CE	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:53:LYS:CG	1:E:80:GLY:HA3	2.41	0.50
1:E:196:THR:O	1:E:201:ASN:HB2	2.11	0.50
1:C:164:GLU:HB3	1:C:166:LEU:HG	1.93	0.50
1:D:45:SER:HB2	1:D:46:PRO:CD	2.42	0.50
1:E:164:GLU:HB3	1:E:166:LEU:HG	1.93	0.50
1:F:173:ASP:HB2	1:F:193:ILE:HD12	1.92	0.50
1:A:16:LYS:HG3	1:A:55:LEU:HD21	1.93	0.50
1:B:81:ALA:O	1:B:107:MET:HE3	2.11	0.50
1:E:45:SER:HB2	1:E:46:PRO:HD2	1.94	0.50
1:A:141:PHE:CD1	1:A:141:PHE:N	2.80	0.50
1:D:44:LEU:HD13	1:D:48:PHE:CD2	2.47	0.50
1:A:137:VAL:CG2	1:A:144:GLN:HB3	2.42	0.50
1:C:137:VAL:CG2	1:C:144:GLN:HB3	2.41	0.50
1:C:196:THR:O	1:C:201:ASN:HB2	2.11	0.50
1:A:196:THR:O	1:A:201:ASN:HB2	2.12	0.49
1:E:45:SER:HB2	1:E:46:PRO:CD	2.42	0.49
1:E:137:VAL:CG2	1:E:144:GLN:HB3	2.42	0.49
1:E:141:PHE:HB2	1:E:144:GLN:OE1	2.12	0.49
1:A:116:GLU:HG3	1:F:92:ASN:HA	1.93	0.49
1:B:164:GLU:HB3	1:B:166:LEU:HG	1.94	0.49
1:A:164:GLU:HB3	1:A:166:LEU:HG	1.94	0.49
1:B:11:ASP:H	1:B:18:GLN:HE22	1.60	0.49
1:B:68:ARG:CA	1:B:70:GLN:HE22	2.17	0.49
1:D:28:TYR:CD1	1:D:59:PRO:HG2	2.44	0.49
1:F:81:ALA:HB3	1:F:107:MET:CE	2.43	0.49
1:B:70:GLN:HG2	1:B:94:GLN:OE1	2.11	0.49
1:B:100:ASP:O	1:B:104:ARG:HG3	2.12	0.49
1:D:141:PHE:N	1:D:141:PHE:CD1	2.80	0.49
1:D:164:GLU:HB3	1:D:166:LEU:HG	1.94	0.49
1:A:211:ARG:HH12	1:A:212:ILE:CG1	2.25	0.49
1:C:141:PHE:N	1:C:141:PHE:CD1	2.81	0.49
1:A:81:ALA:HB3	1:A:107:MET:CE	2.43	0.49
1:B:178:GLN:HB2	1:B:216:GLN:NE2	2.27	0.49
1:D:45:SER:HB2	1:D:46:PRO:HD2	1.95	0.49
1:F:11:ASP:H	1:F:18:GLN:HE22	1.60	0.49
1:F:164:GLU:HB3	1:F:166:LEU:HG	1.94	0.49
1:D:137:VAL:CG2	1:D:144:GLN:HB3	2.43	0.49
1:A:92:ASN:HA	1:E:116:GLU:HG3	1.94	0.49
1:C:81:ALA:HB3	1:C:107:MET:CE	2.42	0.49
1:A:73:ILE:HD12	1:A:98:LEU:HD22	1.94	0.49
1:E:9:CYS:SG	1:E:196:THR:HG23	2.53	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:34:MET:HE1	1:B:43:THR:HG23	1.95	0.48
1:B:141:PHE:HB2	1:B:144:GLN:OE1	2.13	0.48
1:C:45:SER:HB2	1:C:46:PRO:HD2	1.95	0.48
1:C:81:ALA:O	1:C:107:MET:HE3	2.12	0.48
1:E:35:ASP:HB2	1:E:66:VAL:HA	1.95	0.48
1:C:16:LYS:HG3	1:C:55:LEU:HD21	1.95	0.48
1:C:45:SER:HB2	1:C:46:PRO:CD	2.44	0.48
1:E:173:ASP:OD2	2:E:505:S6P:H3	2.12	0.48
1:F:81:ALA:O	1:F:107:MET:HE3	2.13	0.48
1:E:10:MET:HB2	1:E:18:GLN:NE2	2.29	0.48
1:E:141:PHE:N	1:E:141:PHE:CD1	2.81	0.48
1:B:10:MET:HB2	1:B:18:GLN:NE2	2.29	0.48
1:B:92:ASN:HA	1:C:116:GLU:HG3	1.96	0.48
1:B:141:PHE:CD1	1:B:141:PHE:N	2.82	0.48
1:C:141:PHE:HB2	1:C:144:GLN:OE1	2.14	0.48
1:F:137:VAL:CG2	1:F:144:GLN:HB3	2.42	0.48
1:F:141:PHE:HB2	1:F:144:GLN:OE1	2.13	0.48
1:A:11:ASP:H	1:A:18:GLN:HE22	1.60	0.48
1:C:70:GLN:CG	1:C:94:GLN:OE1	2.62	0.48
1:F:28:TYR:CD1	1:F:59:PRO:HG2	2.45	0.48
1:D:141:PHE:HB2	1:D:144:GLN:OE1	2.14	0.48
1:E:73:ILE:CD1	1:E:98:LEU:HD22	2.42	0.48
1:E:81:ALA:O	1:E:107:MET:HE3	2.13	0.48
1:B:70:GLN:CG	1:B:94:GLN:OE1	2.62	0.47
1:B:137:VAL:CG2	1:B:144:GLN:HB3	2.44	0.47
1:D:10:MET:HB2	1:D:18:GLN:NE2	2.29	0.47
1:D:171:GLU:HG3	1:D:191:VAL:HB	1.95	0.47
1:A:9:CYS:SG	1:A:196:THR:HG23	2.54	0.47
1:A:81:ALA:O	1:A:107:MET:HE3	2.13	0.47
1:A:141:PHE:HB2	1:A:144:GLN:OE1	2.14	0.47
1:B:45:SER:HB2	1:B:46:PRO:CD	2.45	0.47
1:D:89:GLU:CD	1:D:89:GLU:H	2.22	0.47
1:D:215:ALA:O	1:D:218:LEU:HB2	2.14	0.47
1:F:16:LYS:HG3	1:F:55:LEU:HD21	1.96	0.47
1:B:46:PRO:HG3	1:B:76:LEU:HD13	1.96	0.47
1:D:9:CYS:SG	1:D:196:THR:HG23	2.55	0.47
1:A:45:SER:HB2	1:A:46:PRO:CD	2.45	0.47
1:C:34:MET:HE1	1:C:43:THR:HG23	1.96	0.47
1:D:161:ARG:NH2	1:D:190:ASP:OD1	2.48	0.47
1:E:16:LYS:HG3	1:E:55:LEU:HD21	1.97	0.47
1:A:10:MET:HB2	1:A:18:GLN:NE2	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:116:GLU:CG	1:D:92:ASN:HA	2.45	0.46
1:A:211:ARG:HH11	1:A:211:ARG:CB	2.25	0.46
1:C:53:LYS:CE	4:C:620:HOH:O	2.54	0.46
1:F:161:ARG:NH2	1:F:190:ASP:OD1	2.49	0.46
1:F:215:ALA:O	1:F:218:LEU:HB2	2.16	0.46
1:B:215:ALA:O	1:B:218:LEU:HB2	2.16	0.46
1:A:45:SER:HB2	1:A:46:PRO:HD2	1.97	0.46
1:C:28:TYR:CD1	1:C:59:PRO:HG2	2.47	0.46
1:F:10:MET:HB2	1:F:18:GLN:NE2	2.29	0.46
1:C:10:MET:HB2	1:C:18:GLN:NE2	2.30	0.46
1:F:153:LYS:HE3	4:F:612:HOH:O	2.16	0.46
1:A:46:PRO:HG3	1:A:76:LEU:HD13	1.98	0.46
1:B:163:ARG:NH2	4:B:623:HOH:O	2.47	0.46
1:D:132:ILE:HG22	1:D:157:LEU:HD21	1.98	0.46
1:C:215:ALA:O	1:C:218:LEU:HB2	2.16	0.46
1:E:92:ASN:HA	1:F:116:GLU:CG	2.46	0.46
1:D:16:LYS:HG3	1:D:55:LEU:HD21	1.98	0.45
1:B:7:LEU:HD22	1:B:10:MET:CE	2.28	0.45
1:B:45:SER:HB2	1:B:46:PRO:HD2	1.97	0.45
1:D:73:ILE:CD1	1:D:98:LEU:HD22	2.47	0.45
1:E:215:ALA:O	1:E:218:LEU:HB2	2.16	0.45
1:C:9:CYS:SG	1:C:196:THR:HG23	2.56	0.45
1:A:215:ALA:O	1:A:218:LEU:HB2	2.17	0.45
1:A:37:HIS:HE1	1:C:35:ASP:OD2	2.00	0.45
1:A:161:ARG:NH2	1:A:190:ASP:OD1	2.49	0.45
1:B:68:ARG:HA	1:B:70:GLN:NE2	2.22	0.45
1:C:161:ARG:NH2	1:C:190:ASP:OD1	2.50	0.45
1:B:181:TYR:CD1	1:B:217:ILE:HD13	2.52	0.45
1:C:2:LYS:HB2	1:C:191:VAL:HG22	1.99	0.45
1:C:89:GLU:H	1:C:89:GLU:CD	2.25	0.45
1:D:46:PRO:HG3	1:D:76:LEU:HD13	1.99	0.45
1:F:178:GLN:HB2	1:F:216:GLN:NE2	2.32	0.45
1:A:34:MET:HE1	1:A:43:THR:HG23	1.98	0.45
1:C:132:ILE:HG22	1:C:157:LEU:HD21	1.99	0.45
1:A:132:ILE:HG22	1:A:157:LEU:HD21	1.99	0.44
1:E:161:ARG:NH2	1:E:190:ASP:OD1	2.50	0.44
1:F:84:ILE:HG13	1:F:107:MET:CE	2.47	0.44
1:A:35:ASP:OD2	1:C:37:HIS:HE1	2.00	0.44
1:E:89:GLU:CD	1:E:89:GLU:H	2.25	0.44
1:F:34:MET:HE1	1:F:43:THR:HG23	1.94	0.44
1:B:116:GLU:CD	1:D:93:GLY:H	2.25	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:84:ILE:HG13	1:E:107:MET:CE	2.47	0.44
1:A:68:ARG:CA	1:A:70:GLN:HE22	2.20	0.44
1:D:68:ARG:HA	1:D:70:GLN:NE2	2.24	0.44
1:F:136:THR:OG1	1:F:174:GLY:O	2.35	0.44
1:B:2:LYS:HB2	1:B:191:VAL:HG22	1.99	0.44
1:F:202:HIS:HB3	1:F:212:ILE:HD12	1.99	0.44
1:B:89:GLU:CD	1:B:89:GLU:H	2.25	0.44
1:F:73:ILE:CD1	1:F:98:LEU:HD22	2.46	0.44
1:A:211:ARG:HH12	1:A:212:ILE:HG12	1.81	0.44
1:B:161:ARG:NH2	1:B:190:ASP:OD1	2.51	0.43
1:B:218:LEU:HD23	1:B:218:LEU:HA	1.88	0.43
1:F:211:ARG:HB3	1:F:211:ARG:HH11	1.81	0.43
1:B:149:GLU:OE1	1:D:127:HIS:HE1	2.02	0.43
1:F:173:ASP:OD2	2:F:506:S6P:H3	2.17	0.43
1:A:89:GLU:H	1:A:89:GLU:CD	2.26	0.43
1:B:9:CYS:SG	1:B:196:THR:HG23	2.58	0.43
1:C:46:PRO:HG3	1:C:76:LEU:HD13	2.00	0.43
1:D:44:LEU:HD13	1:D:48:PHE:CE2	2.54	0.43
1:A:116:GLU:CD	1:F:93:GLY:H	2.26	0.43
1:E:2:LYS:HB2	1:E:191:VAL:HG22	2.01	0.43
1:F:34:MET:HE2	1:F:43:THR:CG2	2.44	0.43
1:A:132:ILE:CG2	1:A:157:LEU:HD21	2.48	0.43
1:C:21:PHE:O	1:C:25:HIS:HD2	2.02	0.43
1:C:70:GLN:HG2	1:C:94:GLN:OE1	2.18	0.43
1:C:99:ILE:HG23	1:C:109:VAL:HG21	2.00	0.43
1:A:68:ARG:HA	1:A:70:GLN:NE2	2.24	0.43
1:E:153:LYS:HE3	4:E:621:HOH:O	2.17	0.43
1:C:93:GLY:H	1:D:116:GLU:CD	2.27	0.43
1:D:84:ILE:HG13	1:D:107:MET:CE	2.49	0.43
1:A:136:THR:OG1	1:A:174:GLY:O	2.37	0.43
1:B:149:GLU:OE1	1:D:127:HIS:CE1	2.72	0.43
1:C:34:MET:HE2	1:C:43:THR:CG2	2.47	0.43
1:D:132:ILE:CG2	1:D:157:LEU:HD21	2.49	0.43
1:E:34:MET:HE1	1:E:43:THR:HG23	1.97	0.43
1:E:132:ILE:HG22	1:E:157:LEU:HD21	2.01	0.43
1:E:207:ASP:N	1:E:207:ASP:OD2	2.51	0.43
1:F:89:GLU:CD	1:F:89:GLU:H	2.26	0.43
1:D:136:THR:OG1	1:D:174:GLY:O	2.35	0.42
1:F:70:GLN:HG3	1:F:94:GLN:OE1	2.19	0.42
1:D:34:MET:HE1	1:D:43:THR:HG23	1.99	0.42
1:E:136:THR:OG1	1:E:174:GLY:O	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:68:ARG:HA	1:C:70:GLN:NE2	2.25	0.42
1:B:93:GLY:H	1:C:116:GLU:CD	2.27	0.42
1:B:202:HIS:HB3	1:B:212:ILE:HD12	2.02	0.42
1:E:28:TYR:CD1	1:E:59:PRO:HG2	2.48	0.42
1:A:84:ILE:HG13	1:A:107:MET:CE	2.49	0.42
1:C:132:ILE:CG2	1:C:157:LEU:HD21	2.49	0.42
1:D:21:PHE:O	1:D:25:HIS:HD2	2.02	0.42
1:E:93:GLY:H	1:F:116:GLU:CD	2.28	0.42
1:F:7:LEU:HD22	1:F:10:MET:CE	2.29	0.42
1:F:132:ILE:HG22	1:F:157:LEU:HD21	2.01	0.42
1:A:116:GLU:CD	1:A:116:GLU:N	2.76	0.42
1:B:32:ASP:O	1:B:44:LEU:HB2	2.20	0.42
1:B:53:LYS:CG	1:B:80:GLY:HA3	2.48	0.42
1:C:70:GLN:HB3	4:C:632:HOH:O	2.19	0.42
1:D:53:LYS:CG	1:D:80:GLY:HA3	2.45	0.42
1:F:21:PHE:O	1:F:25:HIS:HD2	2.03	0.42
1:B:72:TYR:O	1:B:76:LEU:HB2	2.20	0.42
1:B:84:ILE:HG13	1:B:107:MET:CE	2.49	0.42
1:C:1:MET:HE3	1:C:185:MET:HG2	2.02	0.42
1:E:208:GLU:O	1:E:212:ILE:HG13	2.19	0.42
1:F:2:LYS:HB2	1:F:191:VAL:HG22	2.02	0.42
1:B:34:MET:HE2	1:B:43:THR:CG2	2.49	0.42
1:A:93:GLY:H	1:E:116:GLU:CD	2.27	0.41
1:D:34:MET:HE2	1:D:43:THR:CG2	2.49	0.41
1:E:11:ASP:H	1:E:18:GLN:NE2	2.18	0.41
1:E:21:PHE:O	1:E:25:HIS:HD2	2.02	0.41
1:E:63:HIS:NE2	1:E:112:ILE:HD13	2.34	0.41
1:A:207:ASP:N	1:A:207:ASP:OD2	2.53	0.41
1:B:92:ASN:HA	1:C:116:GLU:CG	2.50	0.41
1:B:207:ASP:N	1:B:207:ASP:OD2	2.53	0.41
1:F:218:LEU:HD23	1:F:218:LEU:HA	1.89	0.41
1:B:136:THR:OG1	1:B:174:GLY:O	2.36	0.41
1:E:68:ARG:C	1:E:70:GLN:NE2	2.79	0.41
1:F:132:ILE:CG2	1:F:157:LEU:HD21	2.51	0.41
1:B:35:ASP:C	1:B:37:HIS:H	2.29	0.41
1:B:116:GLU:CD	1:B:116:GLU:N	2.78	0.41
1:C:4:SER:O	1:C:193:ILE:HA	2.21	0.41
1:C:207:ASP:N	1:C:207:ASP:OD2	2.53	0.41
1:E:116:GLU:CD	1:E:116:GLU:N	2.78	0.41
1:F:53:LYS:CG	1:F:80:GLY:HA3	2.44	0.41
1:B:4:SER:O	1:B:193:ILE:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:21:PHE:O	1:B:25:HIS:HD2	2.03	0.41
1:B:132:ILE:HG22	1:B:157:LEU:HD21	2.02	0.41
1:E:34:MET:HE2	1:E:43:THR:CG2	2.48	0.41
1:E:35:ASP:C	1:E:37:HIS:H	2.29	0.41
1:E:68:ARG:HA	1:E:70:GLN:NE2	2.24	0.41
1:E:142:ALA:HA	2:E:505:S6P:H61	2.03	0.41
1:C:11:ASP:H	1:C:18:GLN:NE2	2.18	0.41
1:C:116:GLU:CD	1:C:116:GLU:N	2.78	0.41
1:D:68:ARG:C	1:D:70:GLN:NE2	2.79	0.41
1:F:116:GLU:CD	1:F:116:GLU:N	2.78	0.41
1:F:157:LEU:HD12	1:F:157:LEU:HA	1.94	0.41
1:A:72:TYR:HB3	1:A:76:LEU:HD22	2.03	0.41
1:A:153:LYS:HE3	4:A:603:HOH:O	2.21	0.41
1:B:7:LEU:HB3	1:B:10:MET:CE	2.50	0.41
1:B:194:VAL:CG2	1:B:199:LEU:HB2	2.51	0.41
1:C:68:ARG:C	1:C:70:GLN:NE2	2.79	0.41
1:C:73:ILE:CD1	1:C:98:LEU:HD22	2.50	0.41
1:D:11:ASP:H	1:D:18:GLN:NE2	2.19	0.41
1:D:218:LEU:HA	1:D:218:LEU:HD23	1.89	0.41
1:E:70:GLN:HG3	1:E:94:GLN:OE1	2.21	0.41
1:F:63:HIS:NE2	1:F:112:ILE:HD13	2.36	0.41
1:A:21:PHE:O	1:A:25:HIS:HD2	2.03	0.41
1:A:116:GLU:CG	1:F:92:ASN:HA	2.51	0.41
1:A:11:ASP:H	1:A:18:GLN:NE2	2.19	0.40
1:B:150:MET:SD	1:B:153:LYS:HE2	2.61	0.40
1:C:35:ASP:C	1:C:37:HIS:H	2.29	0.40
1:D:72:TYR:O	1:D:76:LEU:HB2	2.21	0.40
1:D:136:THR:HA	1:D:150:MET:HG3	2.03	0.40
1:A:72:TYR:O	1:A:76:LEU:HB2	2.21	0.40
1:A:70:GLN:HG3	1:A:94:GLN:OE1	2.21	0.40
1:F:76:LEU:HD12	1:F:76:LEU:HA	1.93	0.40
1:F:207:ASP:OD2	1:F:207:ASP:N	2.53	0.40
1:A:92:ASN:HA	1:E:116:GLU:CG	2.50	0.40
1:B:37:HIS:HE1	1:E:35:ASP:OD2	2.04	0.40
1:B:68:ARG:C	1:B:70:GLN:NE2	2.79	0.40
1:C:32:ASP:O	1:C:44:LEU:HB2	2.21	0.40
1:B:1:MET:HE3	1:B:185:MET:HG2	2.04	0.40
1:D:32:ASP:O	1:D:44:LEU:HB2	2.21	0.40
1:F:30:HIS:CE1	1:F:193:ILE:HD13	2.56	0.40
1:F:32:ASP:O	1:F:44:LEU:HB2	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	217/231 (94%)	209 (96%)	8 (4%)	0	100	100
1	B	217/231 (94%)	208 (96%)	9 (4%)	0	100	100
1	C	217/231 (94%)	209 (96%)	8 (4%)	0	100	100
1	D	217/231 (94%)	208 (96%)	9 (4%)	0	100	100
1	E	217/231 (94%)	208 (96%)	9 (4%)	0	100	100
1	F	217/231 (94%)	208 (96%)	9 (4%)	0	100	100
All	All	1302/1386 (94%)	1250 (96%)	52 (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	188/197 (95%)	176 (94%)	12 (6%)	16	19
1	B	188/197 (95%)	177 (94%)	11 (6%)	18	22
1	C	188/197 (95%)	177 (94%)	11 (6%)	18	22
1	D	188/197 (95%)	176 (94%)	12 (6%)	16	19
1	E	188/197 (95%)	178 (95%)	10 (5%)	20	26
1	F	188/197 (95%)	178 (95%)	10 (5%)	20	26
All	All	1128/1182 (95%)	1062 (94%)	66 (6%)	18	22

All (66) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	42	LEU
1	A	70	GLN
1	A	76	LEU
1	A	89	GLU
1	A	111	LEU
1	A	116	GLU
1	A	137	VAL
1	A	141	PHE
1	A	144	GLN
1	A	164	GLU
1	A	207	ASP
1	A	211	ARG
1	B	42	LEU
1	B	70	GLN
1	B	76	LEU
1	B	89	GLU
1	B	111	LEU
1	B	116	GLU
1	B	137	VAL
1	B	141	PHE
1	B	144	GLN
1	B	164	GLU
1	B	207	ASP
1	C	42	LEU
1	C	70	GLN
1	C	76	LEU
1	C	89	GLU
1	C	111	LEU
1	C	116	GLU
1	C	137	VAL
1	C	141	PHE
1	C	144	GLN
1	C	164	GLU
1	C	207	ASP
1	D	42	LEU
1	D	70	GLN
1	D	76	LEU
1	D	89	GLU
1	D	104	ARG
1	D	111	LEU
1	D	116	GLU
1	D	137	VAL

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Mol	Chain	Res	Type
1	D	141	PHE
1	D	144	GLN
1	D	164	GLU
1	D	207	ASP
1	E	42	LEU
1	E	70	GLN
1	E	76	LEU
1	E	89	GLU
1	E	111	LEU
1	E	116	GLU
1	E	137	VAL
1	E	141	PHE
1	E	164	GLU
1	E	207	ASP
1	F	42	LEU
1	F	70	GLN
1	F	76	LEU
1	F	89	GLU
1	F	111	LEU
1	F	116	GLU
1	F	137	VAL
1	F	141	PHE
1	F	164	GLU
1	F	207	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	GLN
1	A	37	HIS
1	A	70	GLN
1	A	216	GLN
1	B	18	GLN
1	B	37	HIS
1	B	70	GLN
1	B	216	GLN
1	C	18	GLN
1	C	37	HIS
1	C	70	GLN
1	C	127	HIS
1	C	216	GLN
1	D	18	GLN

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Mol	Chain	Res	Type
1	D	37	HIS
1	D	70	GLN
1	D	127	HIS
1	D	216	GLN
1	E	18	GLN
1	E	37	HIS
1	E	70	GLN
1	E	127	HIS
1	E	216	GLN
1	F	18	GLN
1	F	37	HIS
1	F	70	GLN
1	F	216	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 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	$\# Z > 2$
2	S6P	B	502	3	15,15,15	1.24	1 (6%)	20,21,21	0.98	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	S6P	A	501	3	15,15,15	1.23	1 (6%)	20,21,21	0.96	1 (5%)
2	S6P	D	504	3	15,15,15	1.28	1 (6%)	20,21,21	0.95	1 (5%)
2	S6P	E	505	3	15,15,15	1.26	1 (6%)	20,21,21	0.97	1 (5%)
2	S6P	F	506	3	15,15,15	1.28	1 (6%)	20,21,21	0.97	1 (5%)
2	S6P	C	503	3	15,15,15	1.26	1 (6%)	20,21,21	0.97	1 (5%)

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	S6P	B	502	3	-	0/20/20/20	-
2	S6P	A	501	3	-	0/20/20/20	-
2	S6P	D	504	3	-	0/20/20/20	-
2	S6P	E	505	3	-	0/20/20/20	-
2	S6P	F	506	3	-	0/20/20/20	-
2	S6P	C	503	3	-	0/20/20/20	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	502	S6P	P-O3P	3.74	1.62	1.50
2	C	503	S6P	P-O3P	3.73	1.62	1.50
2	F	506	S6P	P-O3P	3.64	1.61	1.50
2	D	504	S6P	P-O3P	3.62	1.61	1.50
2	A	501	S6P	P-O3P	3.61	1.61	1.50
2	E	505	S6P	P-O3P	3.52	1.61	1.50

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	502	S6P	O2P-P-O6	3.06	114.64	106.67
2	A	501	S6P	O2P-P-O6	3.06	114.64	106.67
2	F	506	S6P	O2P-P-O6	3.03	114.57	106.67
2	C	503	S6P	O2P-P-O6	3.03	114.56	106.67
2	E	505	S6P	O2P-P-O6	3.02	114.55	106.67
2	D	504	S6P	O2P-P-O6	2.98	114.45	106.67

There are no chirality outliers.

There are no torsion outliers.

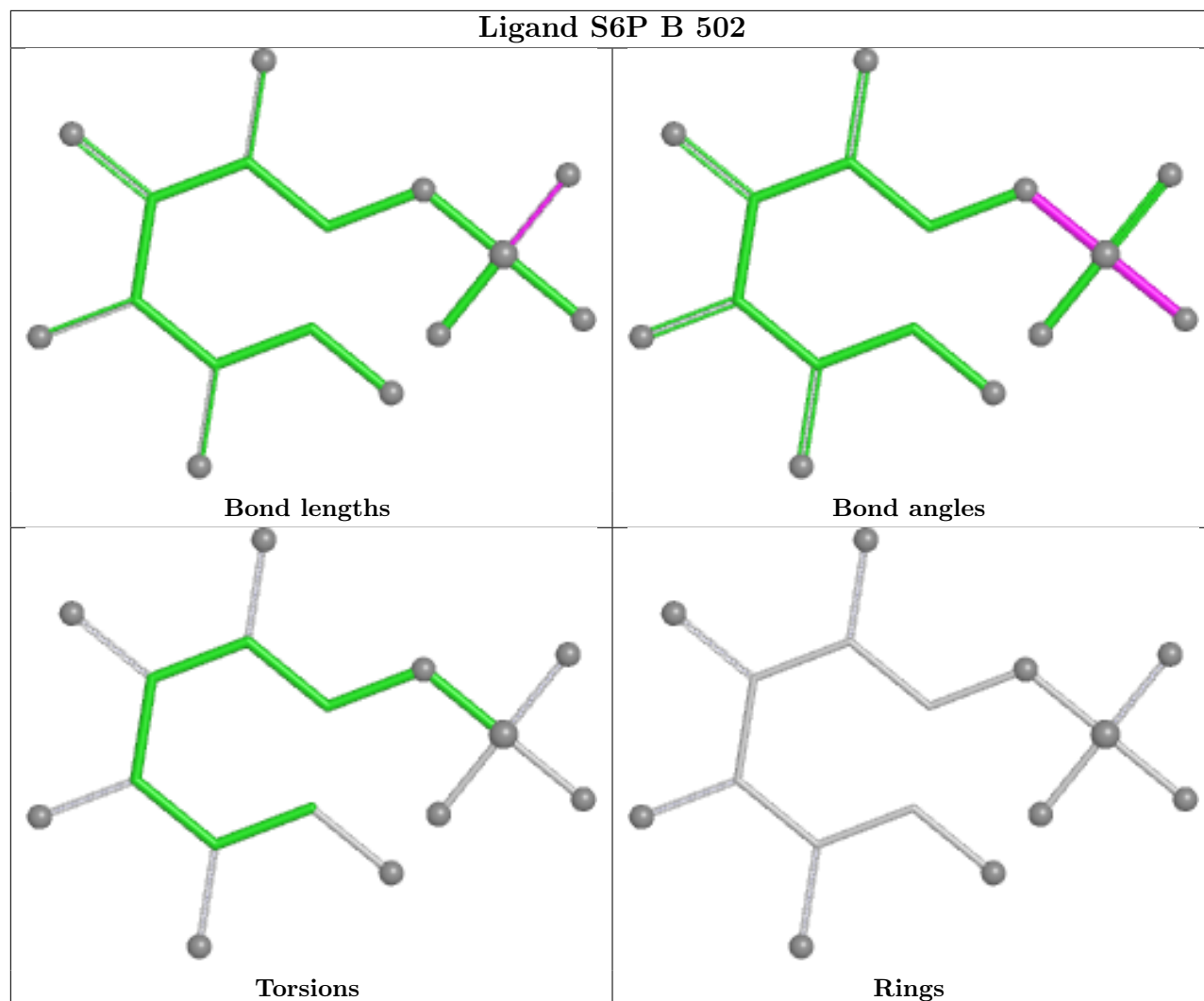
There are no ring outliers.

6 monomers are involved in 7 short contacts:

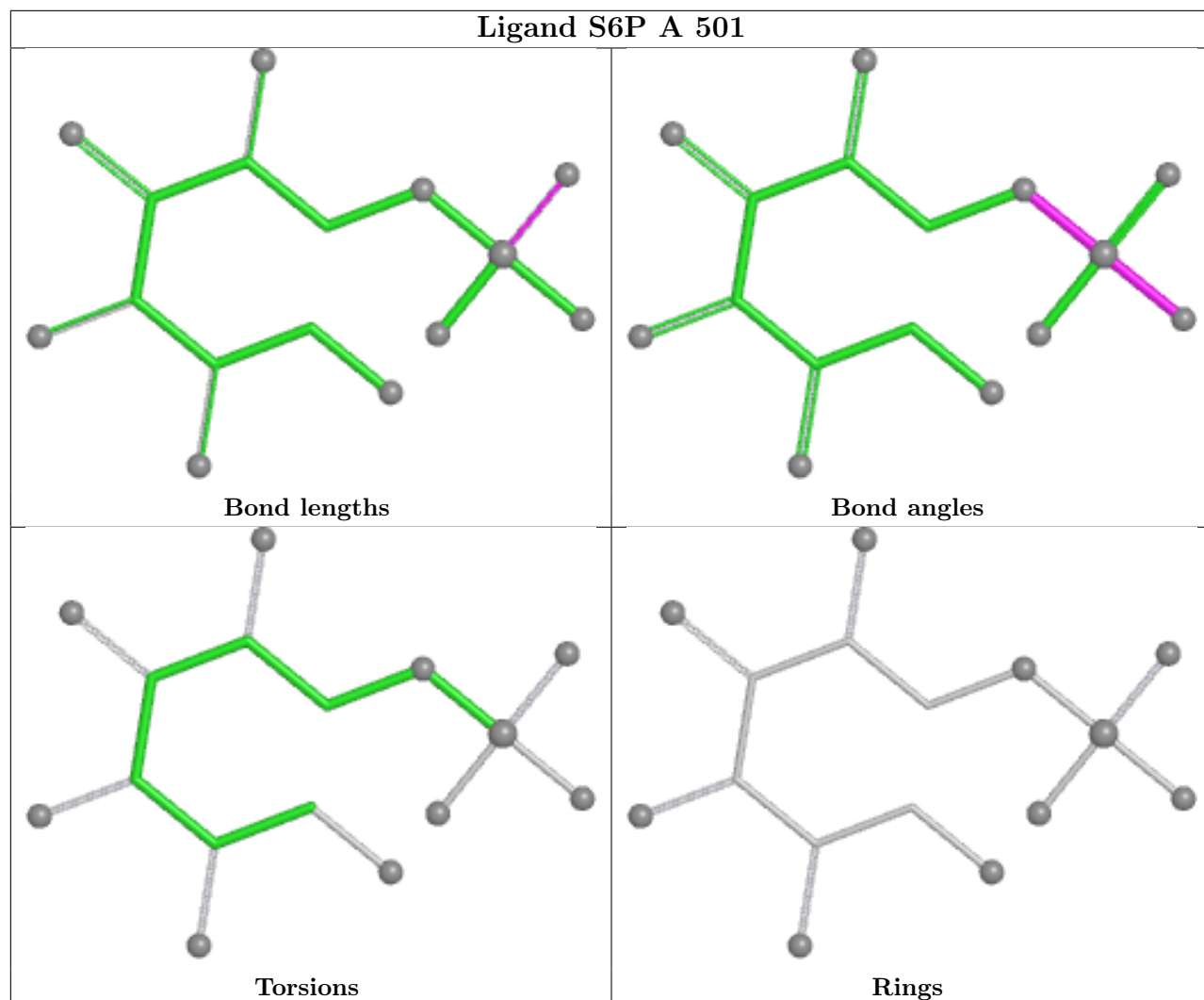
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	502	S6P	1	0
2	A	501	S6P	1	0
2	D	504	S6P	1	0
2	E	505	S6P	2	0
2	F	506	S6P	1	0
2	C	503	S6P	1	0

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.

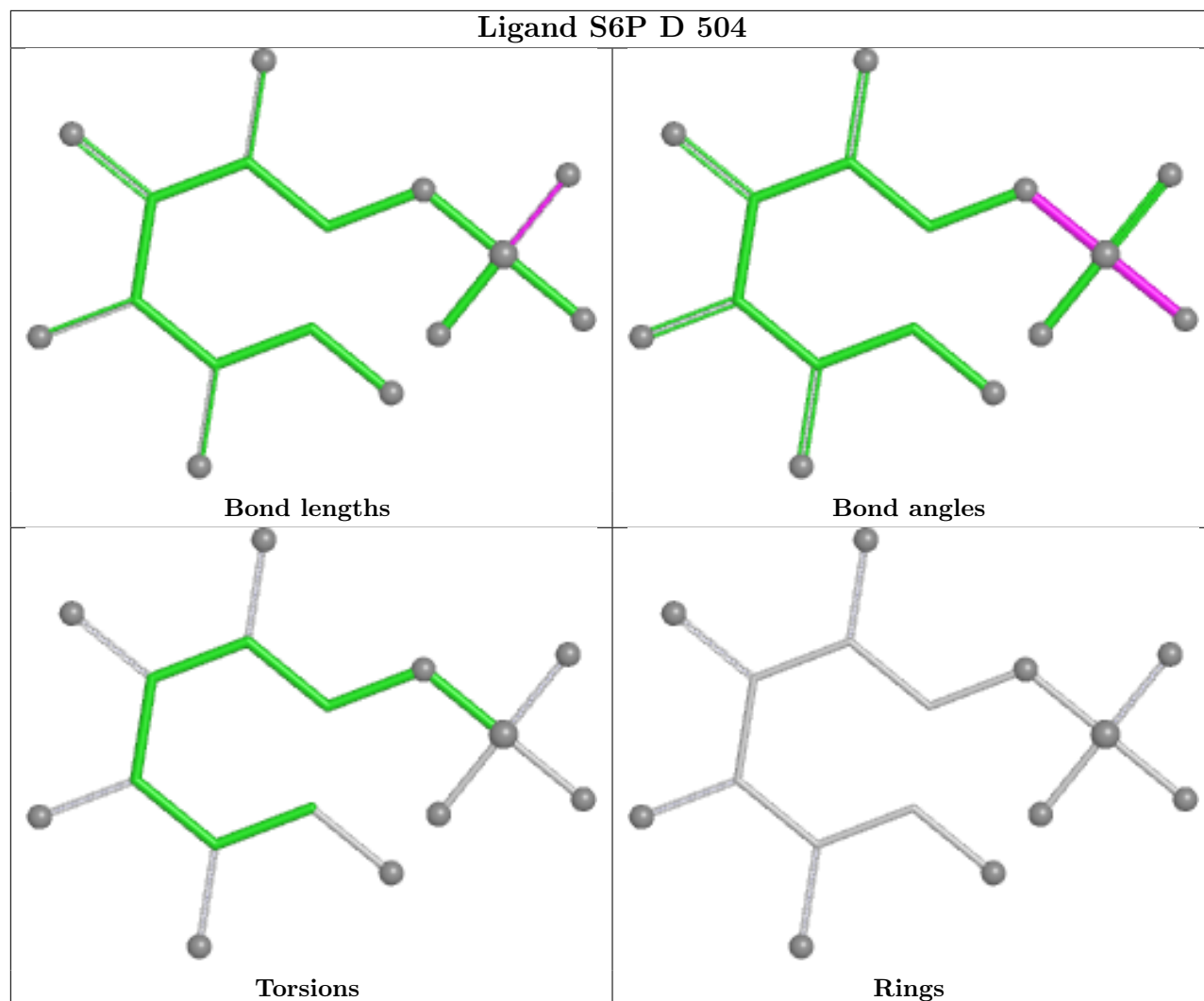
Ligand S6P B 502



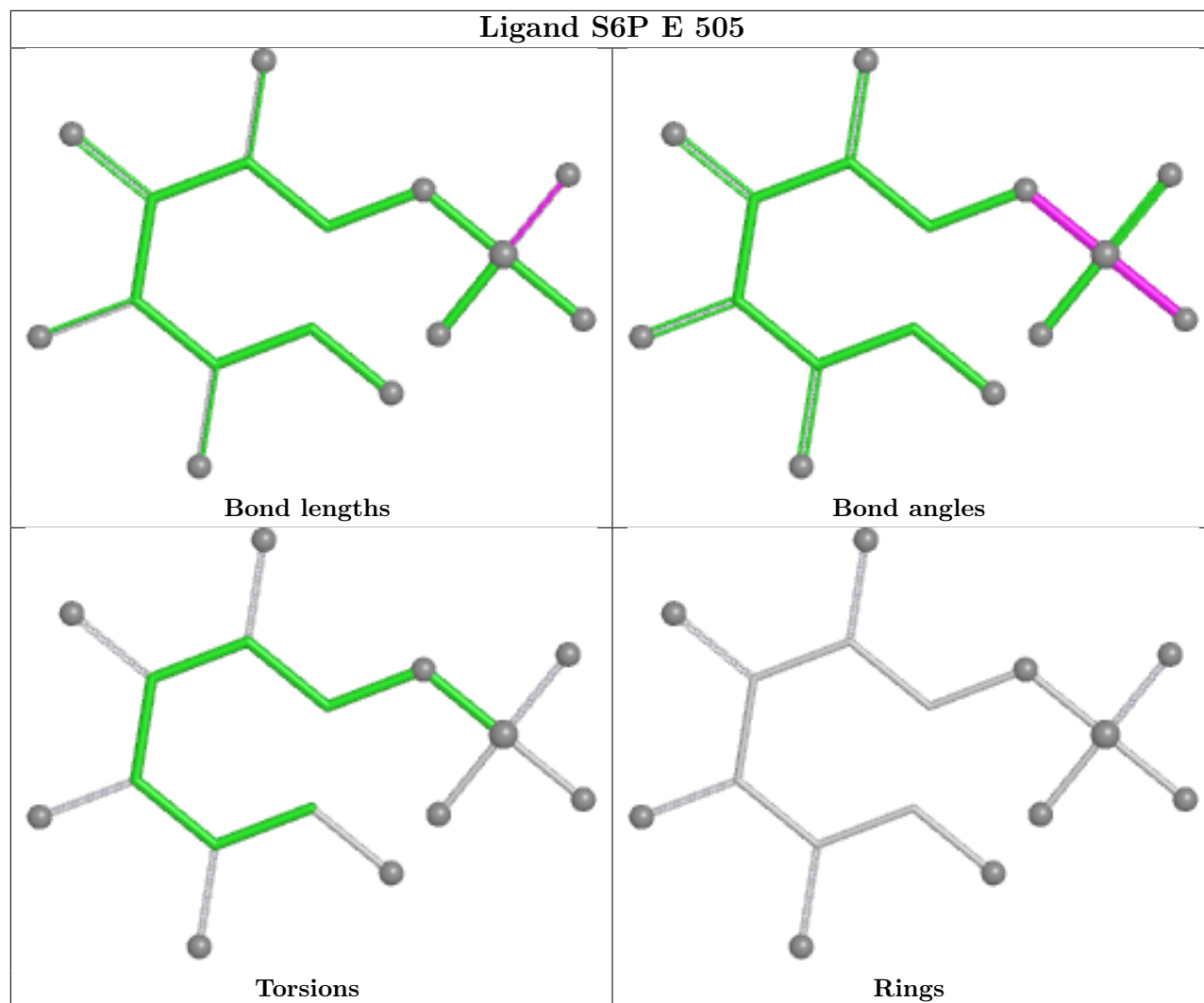
Ligand S6P A 501



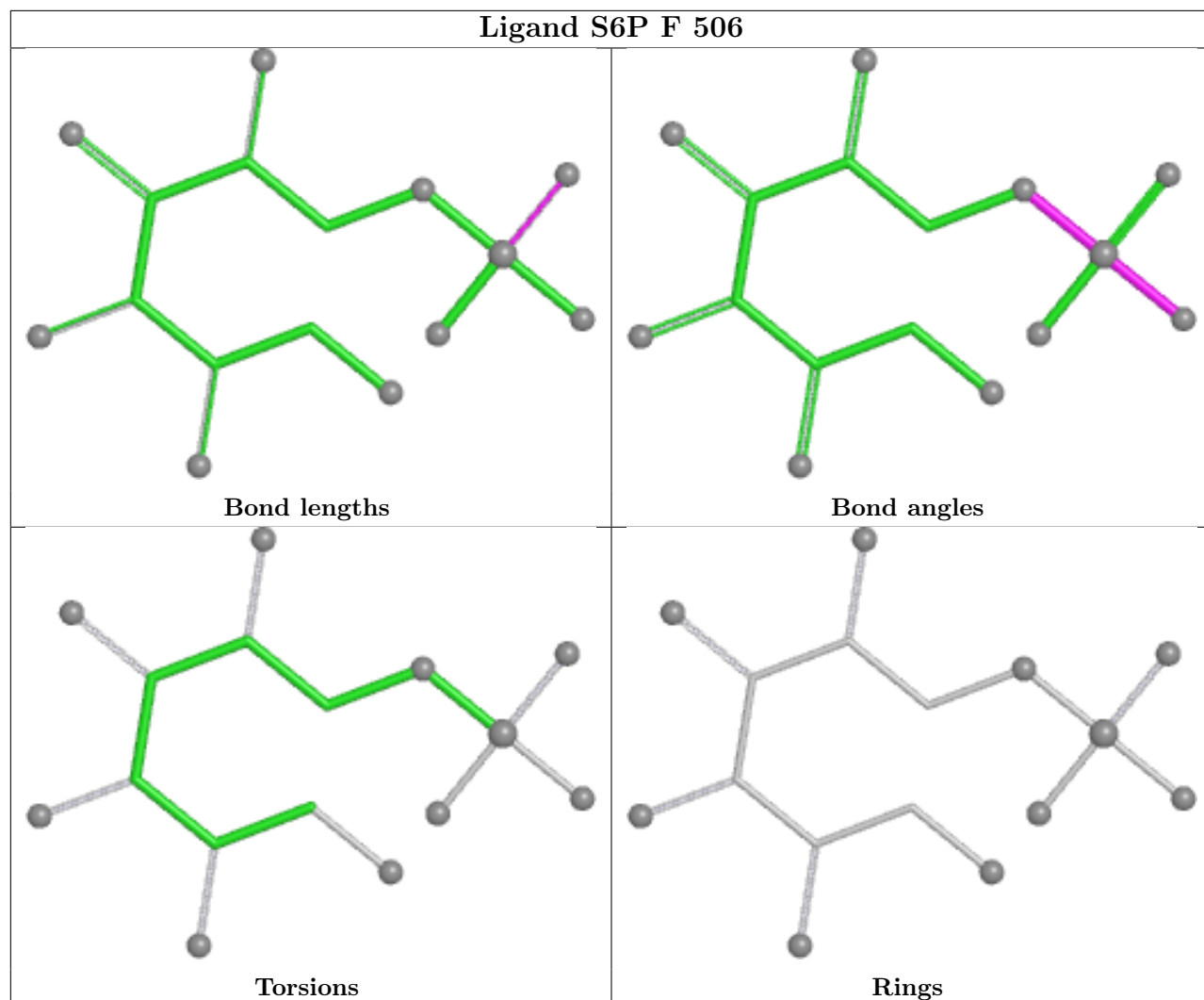
Ligand S6P D 504

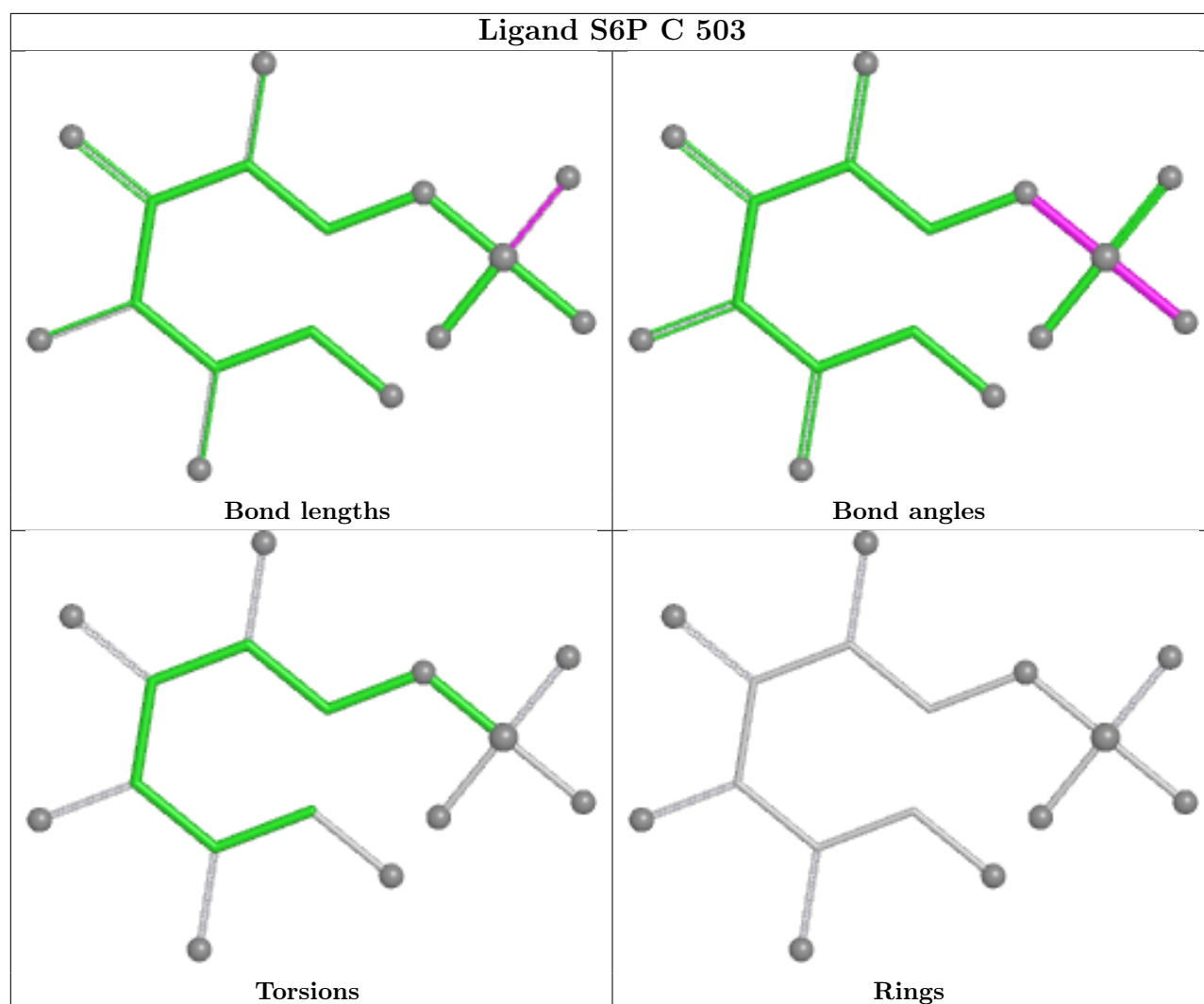


Ligand S6P E 505



Ligand S6P F 506





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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	219/231 (94%)	0.20	8 (3%)	45	42	25, 36, 55, 65	0
1	B	219/231 (94%)	0.44	7 (3%)	50	47	24, 39, 56, 70	0
1	C	219/231 (94%)	0.26	8 (3%)	45	42	21, 35, 58, 69	0
1	D	219/231 (94%)	0.37	7 (3%)	50	47	21, 40, 60, 77	0
1	E	219/231 (94%)	0.22	9 (4%)	41	38	21, 35, 62, 76	0
1	F	219/231 (94%)	0.32	9 (4%)	41	38	21, 38, 68, 79	0
All	All	1314/1386 (94%)	0.30	48 (3%)	45	42	21, 37, 60, 79	0

All (48) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	219	ALA	6.9
1	A	219	ALA	6.5
1	B	219	ALA	6.0
1	C	219	ALA	5.9
1	D	219	ALA	5.7
1	F	219	ALA	5.6
1	B	218	LEU	5.2
1	E	218	LEU	4.1
1	A	218	LEU	3.9
1	F	218	LEU	3.8
1	B	205	ASN	3.5
1	C	218	LEU	3.3
1	E	141	PHE	3.3
1	E	207	ASP	3.2
1	E	140	GLY	3.1
1	B	208	GLU	3.1
1	C	207	ASP	3.0
1	C	106	ASP	2.8
1	A	142	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
1	D	207	ASP	2.7
1	C	175	SER	2.7
1	F	206	ILE	2.6
1	F	48	PHE	2.6
1	F	207	ASP	2.6
1	D	205	ASN	2.6
1	B	163	ARG	2.6
1	D	218	LEU	2.5
1	A	207	ASP	2.5
1	A	141	PHE	2.4
1	A	48	PHE	2.4
1	E	211	ARG	2.4
1	F	175	SER	2.3
1	A	144	GLN	2.3
1	C	35	ASP	2.3
1	E	142	ALA	2.3
1	B	207	ASP	2.3
1	F	35	ASP	2.3
1	F	211	ARG	2.2
1	E	203	ALA	2.2
1	B	216	GLN	2.2
1	D	206	ILE	2.1
1	D	142	ALA	2.1
1	A	164	GLU	2.1
1	D	203	ALA	2.0
1	F	141	PHE	2.0
1	C	203	ALA	2.0
1	C	55	LEU	2.0
1	E	217	ILE	2.0

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 oligosaccharides in this entry.

6.4 Ligands

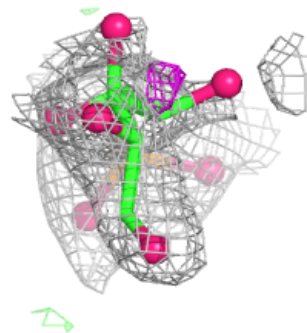
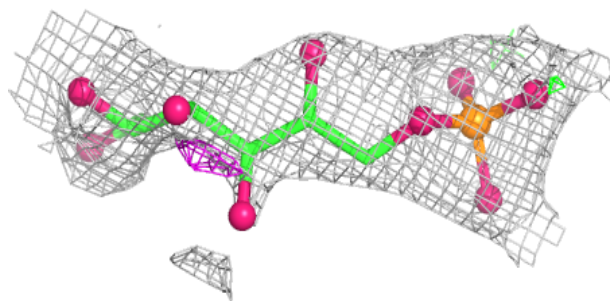
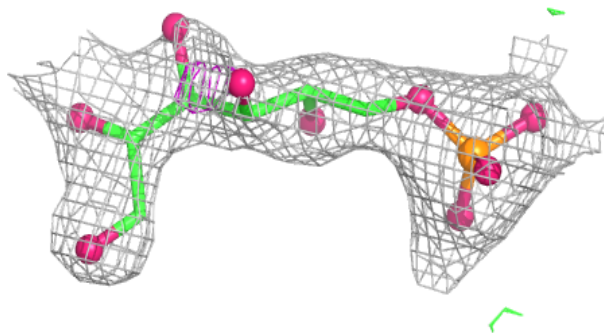
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	S6P	E	505	16/16	0.88	0.12	57,63,64,64	0
2	S6P	D	504	16/16	0.89	0.12	57,59,61,62	0
2	S6P	A	501	16/16	0.90	0.11	53,57,60,61	0
2	S6P	C	503	16/16	0.91	0.11	58,60,61,61	0
2	S6P	F	506	16/16	0.92	0.10	52,56,60,61	0
2	S6P	B	502	16/16	0.93	0.10	47,51,52,52	0
3	MG	B	602	1/1	0.94	0.06	41,41,41,41	0
3	MG	E	605	1/1	0.94	0.09	45,45,45,45	0
3	MG	F	606	1/1	0.94	0.06	46,46,46,46	0
3	MG	D	604	1/1	0.96	0.10	41,41,41,41	0
3	MG	C	603	1/1	0.97	0.04	45,45,45,45	0
3	MG	A	601	1/1	0.99	0.05	35,35,35,35	0

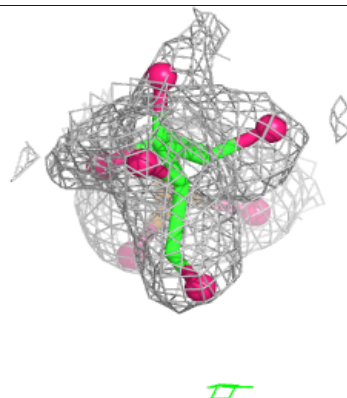
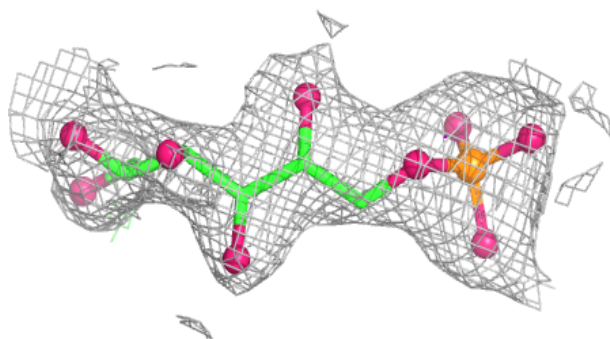
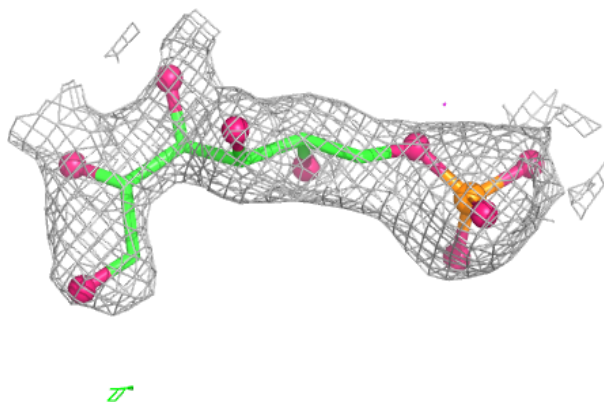
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around S6P E 505:

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

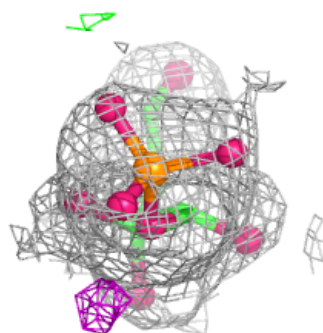
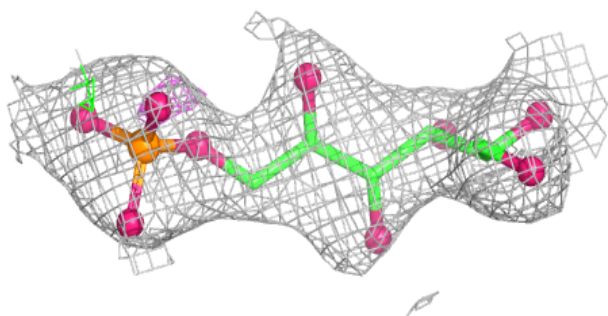
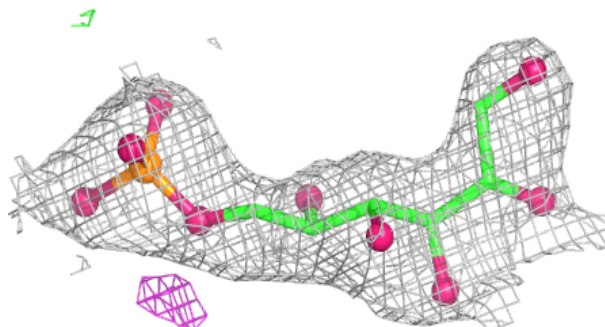
**Electron density around S6P D 504:**

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

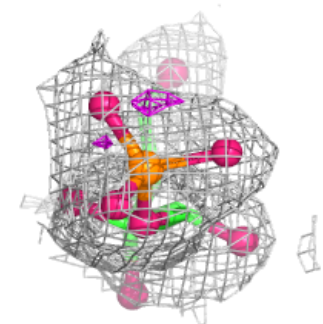
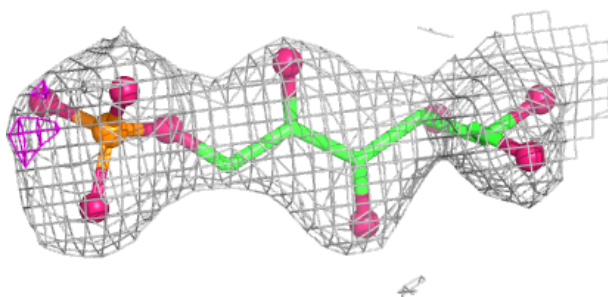
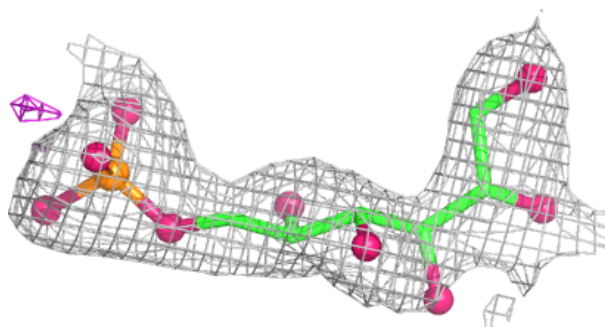


Electron density around S6P A 501:

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

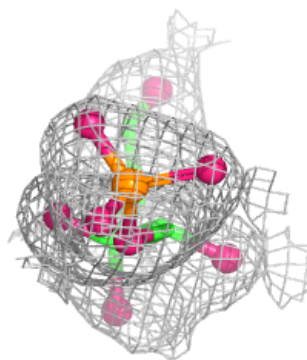
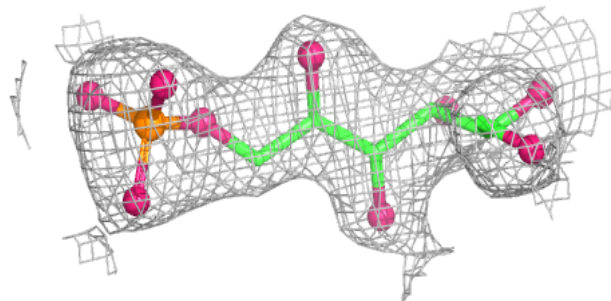
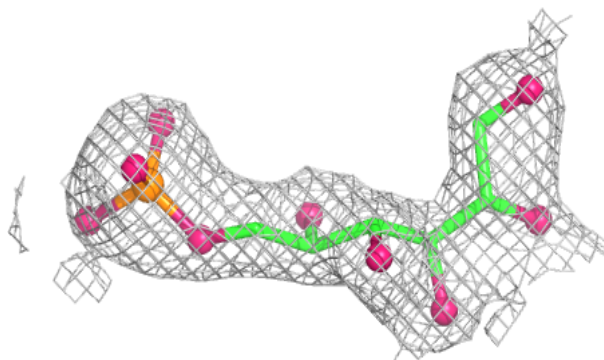
**Electron density around S6P C 503:**

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

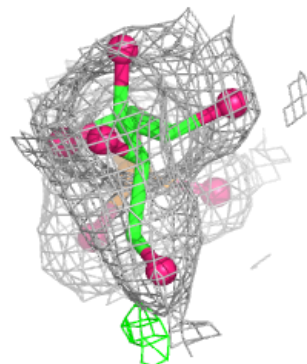
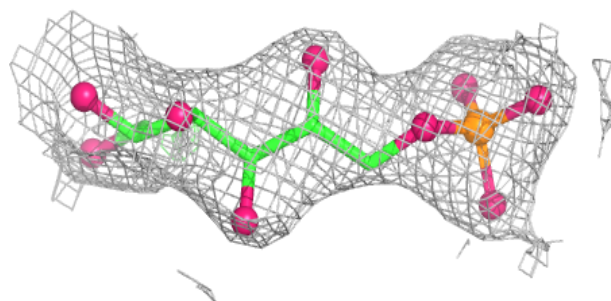
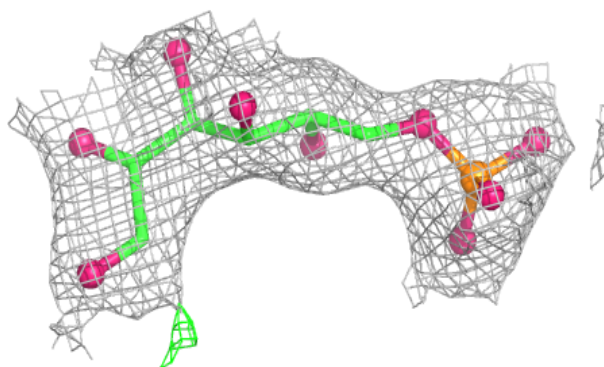


Electron density around S6P F 506:

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

**Electron density around S6P B 502:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.