



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 6, 2025 – 08:05 pm BST

PDB ID : 9R3O / pdb_00009r3o
Title : Structure of liver pyruvate kinase in complex with fluorescent probe 4a
Authors : Bogucka, A.; Nilsson, O.; Grotli, M.; Hyvonen, M.
Deposited on : 2025-05-05
Resolution : 2.04 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 Phenix2.0rc1
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.45.1

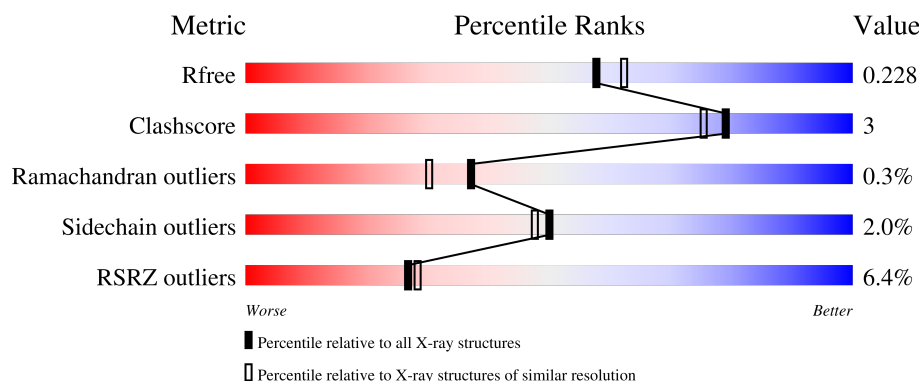
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.04 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}	164625	2096 (2.04-2.04)
Clashscore	180529	2229 (2.04-2.04)
Ramachandran outliers	177936	2217 (2.04-2.04)
Sidechain outliers	177891	2217 (2.04-2.04)
RSRZ outliers	164620	2096 (2.04-2.04)

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	447	<div> <div>10%</div> <div> <div></div> <div>87%</div> <div>7%</div> <div>• 5%</div> </div> </div>
1	B	447	<div> <div>4%</div> <div> <div></div> <div>87%</div> <div>10%</div> <div>• •</div> </div> </div>
1	C	447	<div> <div>6%</div> <div> <div></div> <div>88%</div> <div>7%</div> <div>•</div> </div> </div>
1	D	447	<div> <div>4%</div> <div> <div></div> <div>88%</div> <div>6%</div> <div>• 5%</div> </div> </div>
1	E	447	<div> <div>13%</div> <div> <div></div> <div>85%</div> <div>9%</div> <div>• 5%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	F	447	<div><div></div><div>7%</div><div>89%</div><div>8%</div><div></div></div>
1	G	447	<div><div></div><div>2%</div><div>87%</div><div>7%</div><div>• 5%</div></div>
1	H	447	<div><div></div><div>4%</div><div>87%</div><div>8%</div><div>5%</div></div>

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 28135 atoms, of which 84 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 Isoform L-type of Pyruvate kinase PKLR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	423	Total	C	N	O	S	0	6	0
			3243	2039	586	598	20			
1	B	436	Total	C	N	O	S	0	4	0
			3329	2090	604	615	20			
1	C	427	Total	C	N	O	S	0	4	0
			3257	2045	587	606	19			
1	D	425	Total	C	N	O	S	0	6	0
			3252	2042	590	601	19			
1	E	423	Total	C	N	O	S	0	5	0
			3229	2028	583	598	20			
1	F	435	Total	C	N	O	S	0	7	0
			3335	2097	600	618	20			
1	G	423	Total	C	N	O	S	0	6	0
			3241	2036	583	603	19			
1	H	425	Total	C	N	O	S	0	4	0
			3251	2040	594	598	19			

There are 832 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P30613
A	0	SER	-	expression tag	UNP P30613
A	12	ASP	SER	conflict	UNP P30613
A	?	-	GLU	deletion	UNP P30613
A	?	-	ILE	deletion	UNP P30613
A	?	-	ARG	deletion	UNP P30613
A	?	-	THR	deletion	UNP P30613
A	?	-	GLY	deletion	UNP P30613
A	?	-	ILE	deletion	UNP P30613
A	?	-	LEU	deletion	UNP P30613
A	?	-	GLN	deletion	UNP P30613
A	?	-	GLY	deletion	UNP P30613
A	?	-	GLY	deletion	UNP P30613

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	PRO	deletion	UNP P30613
A	?	-	GLU	deletion	UNP P30613
A	?	-	SER	deletion	UNP P30613
A	?	-	GLU	deletion	UNP P30613
A	?	-	VAL	deletion	UNP P30613
A	?	-	GLU	deletion	UNP P30613
A	?	-	LEU	deletion	UNP P30613
A	?	-	VAL	deletion	UNP P30613
A	?	-	LYS	deletion	UNP P30613
A	?	-	GLY	deletion	UNP P30613
A	?	-	SER	deletion	UNP P30613
A	?	-	GLN	deletion	UNP P30613
A	?	-	VAL	deletion	UNP P30613
A	?	-	LEU	deletion	UNP P30613
A	?	-	VAL	deletion	UNP P30613
A	?	-	THR	deletion	UNP P30613
A	?	-	VAL	deletion	UNP P30613
A	?	-	ASP	deletion	UNP P30613
A	?	-	PRO	deletion	UNP P30613
A	?	-	ALA	deletion	UNP P30613
A	?	-	PHE	deletion	UNP P30613
A	?	-	ARG	deletion	UNP P30613
A	?	-	THR	deletion	UNP P30613
A	?	-	ARG	deletion	UNP P30613
A	?	-	GLY	deletion	UNP P30613
A	?	-	ASN	deletion	UNP P30613
A	?	-	ALA	deletion	UNP P30613
A	?	-	ASN	deletion	UNP P30613
A	?	-	THR	deletion	UNP P30613
A	?	-	VAL	deletion	UNP P30613
A	?	-	TRP	deletion	UNP P30613
A	?	-	VAL	deletion	UNP P30613
A	?	-	ASP	deletion	UNP P30613
A	?	-	TYR	deletion	UNP P30613
A	?	-	PRO	deletion	UNP P30613
A	?	-	ASN	deletion	UNP P30613
A	?	-	ILE	deletion	UNP P30613
A	?	-	VAL	deletion	UNP P30613
A	?	-	ARG	deletion	UNP P30613
A	?	-	VAL	deletion	UNP P30613
A	?	-	VAL	deletion	UNP P30613
A	?	-	PRO	deletion	UNP P30613

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	VAL	deletion	UNP P30613
A	?	-	GLY	deletion	UNP P30613
A	?	-	GLY	deletion	UNP P30613
A	?	-	ARG	deletion	UNP P30613
A	?	-	ILE	deletion	UNP P30613
A	?	-	TYR	deletion	UNP P30613
A	?	-	ILE	deletion	UNP P30613
A	?	-	ASP	deletion	UNP P30613
A	?	-	ASP	deletion	UNP P30613
A	?	-	GLY	deletion	UNP P30613
A	?	-	LEU	deletion	UNP P30613
A	?	-	ILE	deletion	UNP P30613
A	?	-	SER	deletion	UNP P30613
A	?	-	LEU	deletion	UNP P30613
A	?	-	VAL	deletion	UNP P30613
A	?	-	VAL	deletion	UNP P30613
A	?	-	GLN	deletion	UNP P30613
A	?	-	LYS	deletion	UNP P30613
A	?	-	ILE	deletion	UNP P30613
A	?	-	GLY	deletion	UNP P30613
A	?	-	PRO	deletion	UNP P30613
A	?	-	GLU	deletion	UNP P30613
A	?	-	GLY	deletion	UNP P30613
A	?	-	LEU	deletion	UNP P30613
A	?	-	VAL	deletion	UNP P30613
A	?	-	THR	deletion	UNP P30613
A	?	-	GLN	deletion	UNP P30613
A	?	-	VAL	deletion	UNP P30613
A	?	-	GLU	deletion	UNP P30613
A	?	-	ASN	deletion	UNP P30613
A	?	-	GLY	deletion	UNP P30613
A	?	-	GLY	deletion	UNP P30613
A	?	-	VAL	deletion	UNP P30613
A	?	-	LEU	deletion	UNP P30613
A	?	-	GLY	deletion	UNP P30613
A	?	-	SER	deletion	UNP P30613
A	?	-	ARG	deletion	UNP P30613
A	?	-	LYS	deletion	UNP P30613
A	?	-	GLY	deletion	UNP P30613
A	?	-	VAL	deletion	UNP P30613
A	?	-	ASN	deletion	UNP P30613
A	?	-	LEU	deletion	UNP P30613

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	PRO	deletion	UNP P30613
A	?	-	GLY	deletion	UNP P30613
A	?	-	ALA	deletion	UNP P30613
A	?	-	GLN	deletion	UNP P30613
A	130	GLY	VAL	linker	UNP P30613
A	229	SER	ASP	linker	UNP P30613
A	230	GLY	LEU	linker	UNP P30613
B	-1	GLY	-	expression tag	UNP P30613
B	0	SER	-	expression tag	UNP P30613
B	12	ASP	SER	conflict	UNP P30613
B	?	-	GLU	deletion	UNP P30613
B	?	-	ILE	deletion	UNP P30613
B	?	-	ARG	deletion	UNP P30613
B	?	-	THR	deletion	UNP P30613
B	?	-	GLY	deletion	UNP P30613
B	?	-	ILE	deletion	UNP P30613
B	?	-	LEU	deletion	UNP P30613
B	?	-	GLN	deletion	UNP P30613
B	?	-	GLY	deletion	UNP P30613
B	?	-	GLY	deletion	UNP P30613
B	?	-	PRO	deletion	UNP P30613
B	?	-	GLU	deletion	UNP P30613
B	?	-	SER	deletion	UNP P30613
B	?	-	GLU	deletion	UNP P30613
B	?	-	VAL	deletion	UNP P30613
B	?	-	GLU	deletion	UNP P30613
B	?	-	LEU	deletion	UNP P30613
B	?	-	VAL	deletion	UNP P30613
B	?	-	LYS	deletion	UNP P30613
B	?	-	GLY	deletion	UNP P30613
B	?	-	SER	deletion	UNP P30613
B	?	-	GLN	deletion	UNP P30613
B	?	-	VAL	deletion	UNP P30613
B	?	-	LEU	deletion	UNP P30613
B	?	-	VAL	deletion	UNP P30613
B	?	-	THR	deletion	UNP P30613
B	?	-	VAL	deletion	UNP P30613
B	?	-	ASP	deletion	UNP P30613
B	?	-	PRO	deletion	UNP P30613
B	?	-	ALA	deletion	UNP P30613
B	?	-	PHE	deletion	UNP P30613
B	?	-	ARG	deletion	UNP P30613

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	THR	deletion	UNP P30613
B	?	-	ARG	deletion	UNP P30613
B	?	-	GLY	deletion	UNP P30613
B	?	-	ASN	deletion	UNP P30613
B	?	-	ALA	deletion	UNP P30613
B	?	-	ASN	deletion	UNP P30613
B	?	-	THR	deletion	UNP P30613
B	?	-	VAL	deletion	UNP P30613
B	?	-	TRP	deletion	UNP P30613
B	?	-	VAL	deletion	UNP P30613
B	?	-	ASP	deletion	UNP P30613
B	?	-	TYR	deletion	UNP P30613
B	?	-	PRO	deletion	UNP P30613
B	?	-	ASN	deletion	UNP P30613
B	?	-	ILE	deletion	UNP P30613
B	?	-	VAL	deletion	UNP P30613
B	?	-	ARG	deletion	UNP P30613
B	?	-	VAL	deletion	UNP P30613
B	?	-	VAL	deletion	UNP P30613
B	?	-	PRO	deletion	UNP P30613
B	?	-	VAL	deletion	UNP P30613
B	?	-	GLY	deletion	UNP P30613
B	?	-	GLY	deletion	UNP P30613
B	?	-	ARG	deletion	UNP P30613
B	?	-	ILE	deletion	UNP P30613
B	?	-	TYR	deletion	UNP P30613
B	?	-	ILE	deletion	UNP P30613
B	?	-	ASP	deletion	UNP P30613
B	?	-	ASP	deletion	UNP P30613
B	?	-	GLY	deletion	UNP P30613
B	?	-	LEU	deletion	UNP P30613
B	?	-	ILE	deletion	UNP P30613
B	?	-	SER	deletion	UNP P30613
B	?	-	LEU	deletion	UNP P30613
B	?	-	VAL	deletion	UNP P30613
B	?	-	VAL	deletion	UNP P30613
B	?	-	GLN	deletion	UNP P30613
B	?	-	LYS	deletion	UNP P30613
B	?	-	ILE	deletion	UNP P30613
B	?	-	GLY	deletion	UNP P30613
B	?	-	PRO	deletion	UNP P30613
B	?	-	GLU	deletion	UNP P30613

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	GLY	deletion	UNP P30613
B	?	-	LEU	deletion	UNP P30613
B	?	-	VAL	deletion	UNP P30613
B	?	-	THR	deletion	UNP P30613
B	?	-	GLN	deletion	UNP P30613
B	?	-	VAL	deletion	UNP P30613
B	?	-	GLU	deletion	UNP P30613
B	?	-	ASN	deletion	UNP P30613
B	?	-	GLY	deletion	UNP P30613
B	?	-	GLY	deletion	UNP P30613
B	?	-	VAL	deletion	UNP P30613
B	?	-	LEU	deletion	UNP P30613
B	?	-	GLY	deletion	UNP P30613
B	?	-	SER	deletion	UNP P30613
B	?	-	ARG	deletion	UNP P30613
B	?	-	LYS	deletion	UNP P30613
B	?	-	GLY	deletion	UNP P30613
B	?	-	VAL	deletion	UNP P30613
B	?	-	ASN	deletion	UNP P30613
B	?	-	LEU	deletion	UNP P30613
B	?	-	PRO	deletion	UNP P30613
B	?	-	GLY	deletion	UNP P30613
B	?	-	ALA	deletion	UNP P30613
B	?	-	GLN	deletion	UNP P30613
B	130	GLY	VAL	linker	UNP P30613
B	229	SER	ASP	linker	UNP P30613
B	230	GLY	LEU	linker	UNP P30613
C	-1	GLY	-	expression tag	UNP P30613
C	0	SER	-	expression tag	UNP P30613
C	12	ASP	SER	conflict	UNP P30613
C	?	-	GLU	deletion	UNP P30613
C	?	-	ILE	deletion	UNP P30613
C	?	-	ARG	deletion	UNP P30613
C	?	-	THR	deletion	UNP P30613
C	?	-	GLY	deletion	UNP P30613
C	?	-	ILE	deletion	UNP P30613
C	?	-	LEU	deletion	UNP P30613
C	?	-	GLN	deletion	UNP P30613
C	?	-	GLY	deletion	UNP P30613
C	?	-	GLY	deletion	UNP P30613
C	?	-	PRO	deletion	UNP P30613
C	?	-	GLU	deletion	UNP P30613

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Chain	Residue	Modelled	Actual	Comment	Reference
C	?	-	SER	deletion	UNP P30613
C	?	-	GLU	deletion	UNP P30613
C	?	-	VAL	deletion	UNP P30613
C	?	-	GLU	deletion	UNP P30613
C	?	-	LEU	deletion	UNP P30613
C	?	-	VAL	deletion	UNP P30613
C	?	-	LYS	deletion	UNP P30613
C	?	-	GLY	deletion	UNP P30613
C	?	-	SER	deletion	UNP P30613
C	?	-	GLN	deletion	UNP P30613
C	?	-	VAL	deletion	UNP P30613
C	?	-	LEU	deletion	UNP P30613
C	?	-	VAL	deletion	UNP P30613
C	?	-	THR	deletion	UNP P30613
C	?	-	VAL	deletion	UNP P30613
C	?	-	ASP	deletion	UNP P30613
C	?	-	PRO	deletion	UNP P30613
C	?	-	ALA	deletion	UNP P30613
C	?	-	PHE	deletion	UNP P30613
C	?	-	ARG	deletion	UNP P30613
C	?	-	THR	deletion	UNP P30613
C	?	-	ARG	deletion	UNP P30613
C	?	-	GLY	deletion	UNP P30613
C	?	-	ASN	deletion	UNP P30613
C	?	-	ALA	deletion	UNP P30613
C	?	-	ASN	deletion	UNP P30613
C	?	-	THR	deletion	UNP P30613
C	?	-	VAL	deletion	UNP P30613
C	?	-	TRP	deletion	UNP P30613
C	?	-	VAL	deletion	UNP P30613
C	?	-	ASP	deletion	UNP P30613
C	?	-	TYR	deletion	UNP P30613
C	?	-	PRO	deletion	UNP P30613
C	?	-	ASN	deletion	UNP P30613
C	?	-	ILE	deletion	UNP P30613
C	?	-	VAL	deletion	UNP P30613
C	?	-	ARG	deletion	UNP P30613
C	?	-	VAL	deletion	UNP P30613
C	?	-	VAL	deletion	UNP P30613
C	?	-	PRO	deletion	UNP P30613
C	?	-	VAL	deletion	UNP P30613
C	?	-	GLY	deletion	UNP P30613

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Chain	Residue	Modelled	Actual	Comment	Reference
C	?	-	GLY	deletion	UNP P30613
C	?	-	ARG	deletion	UNP P30613
C	?	-	ILE	deletion	UNP P30613
C	?	-	TYR	deletion	UNP P30613
C	?	-	ILE	deletion	UNP P30613
C	?	-	ASP	deletion	UNP P30613
C	?	-	ASP	deletion	UNP P30613
C	?	-	GLY	deletion	UNP P30613
C	?	-	LEU	deletion	UNP P30613
C	?	-	ILE	deletion	UNP P30613
C	?	-	SER	deletion	UNP P30613
C	?	-	LEU	deletion	UNP P30613
C	?	-	VAL	deletion	UNP P30613
C	?	-	VAL	deletion	UNP P30613
C	?	-	GLN	deletion	UNP P30613
C	?	-	LYS	deletion	UNP P30613
C	?	-	ILE	deletion	UNP P30613
C	?	-	GLY	deletion	UNP P30613
C	?	-	PRO	deletion	UNP P30613
C	?	-	GLU	deletion	UNP P30613
C	?	-	GLY	deletion	UNP P30613
C	?	-	LEU	deletion	UNP P30613
C	?	-	VAL	deletion	UNP P30613
C	?	-	THR	deletion	UNP P30613
C	?	-	GLN	deletion	UNP P30613
C	?	-	VAL	deletion	UNP P30613
C	?	-	GLU	deletion	UNP P30613
C	?	-	ASN	deletion	UNP P30613
C	?	-	GLY	deletion	UNP P30613
C	?	-	GLY	deletion	UNP P30613
C	?	-	VAL	deletion	UNP P30613
C	?	-	LEU	deletion	UNP P30613
C	?	-	GLY	deletion	UNP P30613
C	?	-	SER	deletion	UNP P30613
C	?	-	ARG	deletion	UNP P30613
C	?	-	LYS	deletion	UNP P30613
C	?	-	GLY	deletion	UNP P30613
C	?	-	VAL	deletion	UNP P30613
C	?	-	ASN	deletion	UNP P30613
C	?	-	LEU	deletion	UNP P30613
C	?	-	PRO	deletion	UNP P30613
C	?	-	GLY	deletion	UNP P30613

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Chain	Residue	Modelled	Actual	Comment	Reference
C	?	-	ALA	deletion	UNP P30613
C	?	-	GLN	deletion	UNP P30613
C	130	GLY	VAL	linker	UNP P30613
C	229	SER	ASP	linker	UNP P30613
C	230	GLY	LEU	linker	UNP P30613
D	-1	GLY	-	expression tag	UNP P30613
D	0	SER	-	expression tag	UNP P30613
D	12	ASP	SER	conflict	UNP P30613
D	?	-	GLU	deletion	UNP P30613
D	?	-	ILE	deletion	UNP P30613
D	?	-	ARG	deletion	UNP P30613
D	?	-	THR	deletion	UNP P30613
D	?	-	GLY	deletion	UNP P30613
D	?	-	ILE	deletion	UNP P30613
D	?	-	LEU	deletion	UNP P30613
D	?	-	GLN	deletion	UNP P30613
D	?	-	GLY	deletion	UNP P30613
D	?	-	GLY	deletion	UNP P30613
D	?	-	PRO	deletion	UNP P30613
D	?	-	GLU	deletion	UNP P30613
D	?	-	SER	deletion	UNP P30613
D	?	-	GLU	deletion	UNP P30613
D	?	-	VAL	deletion	UNP P30613
D	?	-	GLU	deletion	UNP P30613
D	?	-	LEU	deletion	UNP P30613
D	?	-	VAL	deletion	UNP P30613
D	?	-	LYS	deletion	UNP P30613
D	?	-	GLY	deletion	UNP P30613
D	?	-	SER	deletion	UNP P30613
D	?	-	GLN	deletion	UNP P30613
D	?	-	VAL	deletion	UNP P30613
D	?	-	LEU	deletion	UNP P30613
D	?	-	VAL	deletion	UNP P30613
D	?	-	THR	deletion	UNP P30613
D	?	-	VAL	deletion	UNP P30613
D	?	-	ASP	deletion	UNP P30613
D	?	-	PRO	deletion	UNP P30613
D	?	-	ALA	deletion	UNP P30613
D	?	-	PHE	deletion	UNP P30613
D	?	-	ARG	deletion	UNP P30613
D	?	-	THR	deletion	UNP P30613
D	?	-	ARG	deletion	UNP P30613

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Chain	Residue	Modelled	Actual	Comment	Reference
D	?	-	GLY	deletion	UNP P30613
D	?	-	ASN	deletion	UNP P30613
D	?	-	ALA	deletion	UNP P30613
D	?	-	ASN	deletion	UNP P30613
D	?	-	THR	deletion	UNP P30613
D	?	-	VAL	deletion	UNP P30613
D	?	-	TRP	deletion	UNP P30613
D	?	-	VAL	deletion	UNP P30613
D	?	-	ASP	deletion	UNP P30613
D	?	-	TYR	deletion	UNP P30613
D	?	-	PRO	deletion	UNP P30613
D	?	-	ASN	deletion	UNP P30613
D	?	-	ILE	deletion	UNP P30613
D	?	-	VAL	deletion	UNP P30613
D	?	-	ARG	deletion	UNP P30613
D	?	-	VAL	deletion	UNP P30613
D	?	-	VAL	deletion	UNP P30613
D	?	-	PRO	deletion	UNP P30613
D	?	-	VAL	deletion	UNP P30613
D	?	-	GLY	deletion	UNP P30613
D	?	-	GLY	deletion	UNP P30613
D	?	-	ARG	deletion	UNP P30613
D	?	-	ILE	deletion	UNP P30613
D	?	-	TYR	deletion	UNP P30613
D	?	-	ILE	deletion	UNP P30613
D	?	-	ASP	deletion	UNP P30613
D	?	-	ASP	deletion	UNP P30613
D	?	-	GLY	deletion	UNP P30613
D	?	-	LEU	deletion	UNP P30613
D	?	-	ILE	deletion	UNP P30613
D	?	-	SER	deletion	UNP P30613
D	?	-	LEU	deletion	UNP P30613
D	?	-	VAL	deletion	UNP P30613
D	?	-	VAL	deletion	UNP P30613
D	?	-	GLN	deletion	UNP P30613
D	?	-	LYS	deletion	UNP P30613
D	?	-	ILE	deletion	UNP P30613
D	?	-	GLY	deletion	UNP P30613
D	?	-	PRO	deletion	UNP P30613
D	?	-	GLU	deletion	UNP P30613
D	?	-	GLY	deletion	UNP P30613
D	?	-	LEU	deletion	UNP P30613

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Chain	Residue	Modelled	Actual	Comment	Reference
D	?	-	VAL	deletion	UNP P30613
D	?	-	THR	deletion	UNP P30613
D	?	-	GLN	deletion	UNP P30613
D	?	-	VAL	deletion	UNP P30613
D	?	-	GLU	deletion	UNP P30613
D	?	-	ASN	deletion	UNP P30613
D	?	-	GLY	deletion	UNP P30613
D	?	-	GLY	deletion	UNP P30613
D	?	-	VAL	deletion	UNP P30613
D	?	-	LEU	deletion	UNP P30613
D	?	-	GLY	deletion	UNP P30613
D	?	-	SER	deletion	UNP P30613
D	?	-	ARG	deletion	UNP P30613
D	?	-	LYS	deletion	UNP P30613
D	?	-	GLY	deletion	UNP P30613
D	?	-	VAL	deletion	UNP P30613
D	?	-	ASN	deletion	UNP P30613
D	?	-	LEU	deletion	UNP P30613
D	?	-	PRO	deletion	UNP P30613
D	?	-	GLY	deletion	UNP P30613
D	?	-	ALA	deletion	UNP P30613
D	?	-	GLN	deletion	UNP P30613
D	130	GLY	VAL	linker	UNP P30613
D	229	SER	ASP	linker	UNP P30613
D	230	GLY	LEU	linker	UNP P30613
E	-1	GLY	-	expression tag	UNP P30613
E	0	SER	-	expression tag	UNP P30613
E	12	ASP	SER	conflict	UNP P30613
E	?	-	GLU	deletion	UNP P30613
E	?	-	ILE	deletion	UNP P30613
E	?	-	ARG	deletion	UNP P30613
E	?	-	THR	deletion	UNP P30613
E	?	-	GLY	deletion	UNP P30613
E	?	-	ILE	deletion	UNP P30613
E	?	-	LEU	deletion	UNP P30613
E	?	-	GLN	deletion	UNP P30613
E	?	-	GLY	deletion	UNP P30613
E	?	-	GLY	deletion	UNP P30613
E	?	-	PRO	deletion	UNP P30613
E	?	-	GLU	deletion	UNP P30613
E	?	-	SER	deletion	UNP P30613
E	?	-	GLU	deletion	UNP P30613

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Chain	Residue	Modelled	Actual	Comment	Reference
E	?	-	VAL	deletion	UNP P30613
E	?	-	GLU	deletion	UNP P30613
E	?	-	LEU	deletion	UNP P30613
E	?	-	VAL	deletion	UNP P30613
E	?	-	LYS	deletion	UNP P30613
E	?	-	GLY	deletion	UNP P30613
E	?	-	SER	deletion	UNP P30613
E	?	-	GLN	deletion	UNP P30613
E	?	-	VAL	deletion	UNP P30613
E	?	-	LEU	deletion	UNP P30613
E	?	-	VAL	deletion	UNP P30613
E	?	-	THR	deletion	UNP P30613
E	?	-	VAL	deletion	UNP P30613
E	?	-	ASP	deletion	UNP P30613
E	?	-	PRO	deletion	UNP P30613
E	?	-	ALA	deletion	UNP P30613
E	?	-	PHE	deletion	UNP P30613
E	?	-	ARG	deletion	UNP P30613
E	?	-	THR	deletion	UNP P30613
E	?	-	ARG	deletion	UNP P30613
E	?	-	GLY	deletion	UNP P30613
E	?	-	ASN	deletion	UNP P30613
E	?	-	ALA	deletion	UNP P30613
E	?	-	ASN	deletion	UNP P30613
E	?	-	THR	deletion	UNP P30613
E	?	-	VAL	deletion	UNP P30613
E	?	-	TRP	deletion	UNP P30613
E	?	-	VAL	deletion	UNP P30613
E	?	-	ASP	deletion	UNP P30613
E	?	-	TYR	deletion	UNP P30613
E	?	-	PRO	deletion	UNP P30613
E	?	-	ASN	deletion	UNP P30613
E	?	-	ILE	deletion	UNP P30613
E	?	-	VAL	deletion	UNP P30613
E	?	-	ARG	deletion	UNP P30613
E	?	-	VAL	deletion	UNP P30613
E	?	-	VAL	deletion	UNP P30613
E	?	-	PRO	deletion	UNP P30613
E	?	-	VAL	deletion	UNP P30613
E	?	-	GLY	deletion	UNP P30613
E	?	-	GLY	deletion	UNP P30613
E	?	-	ARG	deletion	UNP P30613

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Chain	Residue	Modelled	Actual	Comment	Reference
E	?	-	ILE	deletion	UNP P30613
E	?	-	TYR	deletion	UNP P30613
E	?	-	ILE	deletion	UNP P30613
E	?	-	ASP	deletion	UNP P30613
E	?	-	ASP	deletion	UNP P30613
E	?	-	GLY	deletion	UNP P30613
E	?	-	LEU	deletion	UNP P30613
E	?	-	ILE	deletion	UNP P30613
E	?	-	SER	deletion	UNP P30613
E	?	-	LEU	deletion	UNP P30613
E	?	-	VAL	deletion	UNP P30613
E	?	-	VAL	deletion	UNP P30613
E	?	-	GLN	deletion	UNP P30613
E	?	-	LYS	deletion	UNP P30613
E	?	-	ILE	deletion	UNP P30613
E	?	-	GLY	deletion	UNP P30613
E	?	-	PRO	deletion	UNP P30613
E	?	-	GLU	deletion	UNP P30613
E	?	-	GLY	deletion	UNP P30613
E	?	-	LEU	deletion	UNP P30613
E	?	-	VAL	deletion	UNP P30613
E	?	-	THR	deletion	UNP P30613
E	?	-	GLN	deletion	UNP P30613
E	?	-	VAL	deletion	UNP P30613
E	?	-	GLU	deletion	UNP P30613
E	?	-	ASN	deletion	UNP P30613
E	?	-	GLY	deletion	UNP P30613
E	?	-	GLY	deletion	UNP P30613
E	?	-	VAL	deletion	UNP P30613
E	?	-	LEU	deletion	UNP P30613
E	?	-	GLY	deletion	UNP P30613
E	?	-	SER	deletion	UNP P30613
E	?	-	ARG	deletion	UNP P30613
E	?	-	LYS	deletion	UNP P30613
E	?	-	GLY	deletion	UNP P30613
E	?	-	VAL	deletion	UNP P30613
E	?	-	ASN	deletion	UNP P30613
E	?	-	LEU	deletion	UNP P30613
E	?	-	PRO	deletion	UNP P30613
E	?	-	GLY	deletion	UNP P30613
E	?	-	ALA	deletion	UNP P30613
E	?	-	GLN	deletion	UNP P30613

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Chain	Residue	Modelled	Actual	Comment	Reference
E	130	GLY	VAL	linker	UNP P30613
E	229	SER	ASP	linker	UNP P30613
E	230	GLY	LEU	linker	UNP P30613
F	-1	GLY	-	expression tag	UNP P30613
F	0	SER	-	expression tag	UNP P30613
F	12	ASP	SER	conflict	UNP P30613
F	?	-	GLU	deletion	UNP P30613
F	?	-	ILE	deletion	UNP P30613
F	?	-	ARG	deletion	UNP P30613
F	?	-	THR	deletion	UNP P30613
F	?	-	GLY	deletion	UNP P30613
F	?	-	ILE	deletion	UNP P30613
F	?	-	LEU	deletion	UNP P30613
F	?	-	GLN	deletion	UNP P30613
F	?	-	GLY	deletion	UNP P30613
F	?	-	GLY	deletion	UNP P30613
F	?	-	PRO	deletion	UNP P30613
F	?	-	GLU	deletion	UNP P30613
F	?	-	SER	deletion	UNP P30613
F	?	-	GLU	deletion	UNP P30613
F	?	-	VAL	deletion	UNP P30613
F	?	-	GLU	deletion	UNP P30613
F	?	-	LEU	deletion	UNP P30613
F	?	-	VAL	deletion	UNP P30613
F	?	-	LYS	deletion	UNP P30613
F	?	-	GLY	deletion	UNP P30613
F	?	-	SER	deletion	UNP P30613
F	?	-	GLN	deletion	UNP P30613
F	?	-	VAL	deletion	UNP P30613
F	?	-	LEU	deletion	UNP P30613
F	?	-	VAL	deletion	UNP P30613
F	?	-	THR	deletion	UNP P30613
F	?	-	VAL	deletion	UNP P30613
F	?	-	ASP	deletion	UNP P30613
F	?	-	PRO	deletion	UNP P30613
F	?	-	ALA	deletion	UNP P30613
F	?	-	PHE	deletion	UNP P30613
F	?	-	ARG	deletion	UNP P30613
F	?	-	THR	deletion	UNP P30613
F	?	-	ARG	deletion	UNP P30613
F	?	-	GLY	deletion	UNP P30613
F	?	-	ASN	deletion	UNP P30613

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Chain	Residue	Modelled	Actual	Comment	Reference
F	?	-	ALA	deletion	UNP P30613
F	?	-	ASN	deletion	UNP P30613
F	?	-	THR	deletion	UNP P30613
F	?	-	VAL	deletion	UNP P30613
F	?	-	TRP	deletion	UNP P30613
F	?	-	VAL	deletion	UNP P30613
F	?	-	ASP	deletion	UNP P30613
F	?	-	TYR	deletion	UNP P30613
F	?	-	PRO	deletion	UNP P30613
F	?	-	ASN	deletion	UNP P30613
F	?	-	ILE	deletion	UNP P30613
F	?	-	VAL	deletion	UNP P30613
F	?	-	ARG	deletion	UNP P30613
F	?	-	VAL	deletion	UNP P30613
F	?	-	VAL	deletion	UNP P30613
F	?	-	PRO	deletion	UNP P30613
F	?	-	VAL	deletion	UNP P30613
F	?	-	GLY	deletion	UNP P30613
F	?	-	GLY	deletion	UNP P30613
F	?	-	ARG	deletion	UNP P30613
F	?	-	ILE	deletion	UNP P30613
F	?	-	TYR	deletion	UNP P30613
F	?	-	ILE	deletion	UNP P30613
F	?	-	ASP	deletion	UNP P30613
F	?	-	ASP	deletion	UNP P30613
F	?	-	GLY	deletion	UNP P30613
F	?	-	LEU	deletion	UNP P30613
F	?	-	ILE	deletion	UNP P30613
F	?	-	SER	deletion	UNP P30613
F	?	-	LEU	deletion	UNP P30613
F	?	-	VAL	deletion	UNP P30613
F	?	-	VAL	deletion	UNP P30613
F	?	-	GLN	deletion	UNP P30613
F	?	-	LYS	deletion	UNP P30613
F	?	-	ILE	deletion	UNP P30613
F	?	-	GLY	deletion	UNP P30613
F	?	-	PRO	deletion	UNP P30613
F	?	-	GLU	deletion	UNP P30613
F	?	-	GLY	deletion	UNP P30613
F	?	-	LEU	deletion	UNP P30613
F	?	-	VAL	deletion	UNP P30613
F	?	-	THR	deletion	UNP P30613

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Chain	Residue	Modelled	Actual	Comment	Reference
F	?	-	GLN	deletion	UNP P30613
F	?	-	VAL	deletion	UNP P30613
F	?	-	GLU	deletion	UNP P30613
F	?	-	ASN	deletion	UNP P30613
F	?	-	GLY	deletion	UNP P30613
F	?	-	GLY	deletion	UNP P30613
F	?	-	VAL	deletion	UNP P30613
F	?	-	LEU	deletion	UNP P30613
F	?	-	GLY	deletion	UNP P30613
F	?	-	SER	deletion	UNP P30613
F	?	-	ARG	deletion	UNP P30613
F	?	-	LYS	deletion	UNP P30613
F	?	-	GLY	deletion	UNP P30613
F	?	-	VAL	deletion	UNP P30613
F	?	-	ASN	deletion	UNP P30613
F	?	-	LEU	deletion	UNP P30613
F	?	-	PRO	deletion	UNP P30613
F	?	-	GLY	deletion	UNP P30613
F	?	-	ALA	deletion	UNP P30613
F	?	-	GLN	deletion	UNP P30613
F	130	GLY	VAL	linker	UNP P30613
F	229	SER	ASP	linker	UNP P30613
F	230	GLY	LEU	linker	UNP P30613
G	-1	GLY	-	expression tag	UNP P30613
G	0	SER	-	expression tag	UNP P30613
G	12	ASP	SER	conflict	UNP P30613
G	?	-	GLU	deletion	UNP P30613
G	?	-	ILE	deletion	UNP P30613
G	?	-	ARG	deletion	UNP P30613
G	?	-	THR	deletion	UNP P30613
G	?	-	GLY	deletion	UNP P30613
G	?	-	ILE	deletion	UNP P30613
G	?	-	LEU	deletion	UNP P30613
G	?	-	GLN	deletion	UNP P30613
G	?	-	GLY	deletion	UNP P30613
G	?	-	GLY	deletion	UNP P30613
G	?	-	PRO	deletion	UNP P30613
G	?	-	GLU	deletion	UNP P30613
G	?	-	SER	deletion	UNP P30613
G	?	-	GLU	deletion	UNP P30613
G	?	-	VAL	deletion	UNP P30613
G	?	-	GLU	deletion	UNP P30613

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Chain	Residue	Modelled	Actual	Comment	Reference
G	?	-	LEU	deletion	UNP P30613
G	?	-	VAL	deletion	UNP P30613
G	?	-	LYS	deletion	UNP P30613
G	?	-	GLY	deletion	UNP P30613
G	?	-	SER	deletion	UNP P30613
G	?	-	GLN	deletion	UNP P30613
G	?	-	VAL	deletion	UNP P30613
G	?	-	LEU	deletion	UNP P30613
G	?	-	VAL	deletion	UNP P30613
G	?	-	THR	deletion	UNP P30613
G	?	-	VAL	deletion	UNP P30613
G	?	-	ASP	deletion	UNP P30613
G	?	-	PRO	deletion	UNP P30613
G	?	-	ALA	deletion	UNP P30613
G	?	-	PHE	deletion	UNP P30613
G	?	-	ARG	deletion	UNP P30613
G	?	-	THR	deletion	UNP P30613
G	?	-	ARG	deletion	UNP P30613
G	?	-	GLY	deletion	UNP P30613
G	?	-	ASN	deletion	UNP P30613
G	?	-	ALA	deletion	UNP P30613
G	?	-	ASN	deletion	UNP P30613
G	?	-	THR	deletion	UNP P30613
G	?	-	VAL	deletion	UNP P30613
G	?	-	TRP	deletion	UNP P30613
G	?	-	VAL	deletion	UNP P30613
G	?	-	ASP	deletion	UNP P30613
G	?	-	TYR	deletion	UNP P30613
G	?	-	PRO	deletion	UNP P30613
G	?	-	ASN	deletion	UNP P30613
G	?	-	ILE	deletion	UNP P30613
G	?	-	VAL	deletion	UNP P30613
G	?	-	ARG	deletion	UNP P30613
G	?	-	VAL	deletion	UNP P30613
G	?	-	VAL	deletion	UNP P30613
G	?	-	PRO	deletion	UNP P30613
G	?	-	VAL	deletion	UNP P30613
G	?	-	GLY	deletion	UNP P30613
G	?	-	GLY	deletion	UNP P30613
G	?	-	ARG	deletion	UNP P30613
G	?	-	ILE	deletion	UNP P30613
G	?	-	TYR	deletion	UNP P30613

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Chain	Residue	Modelled	Actual	Comment	Reference
G	?	-	ILE	deletion	UNP P30613
G	?	-	ASP	deletion	UNP P30613
G	?	-	ASP	deletion	UNP P30613
G	?	-	GLY	deletion	UNP P30613
G	?	-	LEU	deletion	UNP P30613
G	?	-	ILE	deletion	UNP P30613
G	?	-	SER	deletion	UNP P30613
G	?	-	LEU	deletion	UNP P30613
G	?	-	VAL	deletion	UNP P30613
G	?	-	VAL	deletion	UNP P30613
G	?	-	GLN	deletion	UNP P30613
G	?	-	LYS	deletion	UNP P30613
G	?	-	ILE	deletion	UNP P30613
G	?	-	GLY	deletion	UNP P30613
G	?	-	PRO	deletion	UNP P30613
G	?	-	GLU	deletion	UNP P30613
G	?	-	GLY	deletion	UNP P30613
G	?	-	LEU	deletion	UNP P30613
G	?	-	VAL	deletion	UNP P30613
G	?	-	THR	deletion	UNP P30613
G	?	-	GLN	deletion	UNP P30613
G	?	-	VAL	deletion	UNP P30613
G	?	-	GLU	deletion	UNP P30613
G	?	-	ASN	deletion	UNP P30613
G	?	-	GLY	deletion	UNP P30613
G	?	-	GLY	deletion	UNP P30613
G	?	-	VAL	deletion	UNP P30613
G	?	-	LEU	deletion	UNP P30613
G	?	-	GLY	deletion	UNP P30613
G	?	-	SER	deletion	UNP P30613
G	?	-	ARG	deletion	UNP P30613
G	?	-	LYS	deletion	UNP P30613
G	?	-	GLY	deletion	UNP P30613
G	?	-	VAL	deletion	UNP P30613
G	?	-	ASN	deletion	UNP P30613
G	?	-	LEU	deletion	UNP P30613
G	?	-	PRO	deletion	UNP P30613
G	?	-	GLY	deletion	UNP P30613
G	?	-	ALA	deletion	UNP P30613
G	?	-	GLN	deletion	UNP P30613
G	130	GLY	VAL	linker	UNP P30613
G	229	SER	ASP	linker	UNP P30613

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Chain	Residue	Modelled	Actual	Comment	Reference
G	230	GLY	LEU	linker	UNP P30613
H	-1	GLY	-	expression tag	UNP P30613
H	0	SER	-	expression tag	UNP P30613
H	12	ASP	SER	conflict	UNP P30613
H	?	-	GLU	deletion	UNP P30613
H	?	-	ILE	deletion	UNP P30613
H	?	-	ARG	deletion	UNP P30613
H	?	-	THR	deletion	UNP P30613
H	?	-	GLY	deletion	UNP P30613
H	?	-	ILE	deletion	UNP P30613
H	?	-	LEU	deletion	UNP P30613
H	?	-	GLN	deletion	UNP P30613
H	?	-	GLY	deletion	UNP P30613
H	?	-	GLY	deletion	UNP P30613
H	?	-	PRO	deletion	UNP P30613
H	?	-	GLU	deletion	UNP P30613
H	?	-	SER	deletion	UNP P30613
H	?	-	GLU	deletion	UNP P30613
H	?	-	VAL	deletion	UNP P30613
H	?	-	GLU	deletion	UNP P30613
H	?	-	LEU	deletion	UNP P30613
H	?	-	VAL	deletion	UNP P30613
H	?	-	LYS	deletion	UNP P30613
H	?	-	GLY	deletion	UNP P30613
H	?	-	SER	deletion	UNP P30613
H	?	-	GLN	deletion	UNP P30613
H	?	-	VAL	deletion	UNP P30613
H	?	-	LEU	deletion	UNP P30613
H	?	-	VAL	deletion	UNP P30613
H	?	-	THR	deletion	UNP P30613
H	?	-	VAL	deletion	UNP P30613
H	?	-	ASP	deletion	UNP P30613
H	?	-	PRO	deletion	UNP P30613
H	?	-	ALA	deletion	UNP P30613
H	?	-	PHE	deletion	UNP P30613
H	?	-	ARG	deletion	UNP P30613
H	?	-	THR	deletion	UNP P30613
H	?	-	ARG	deletion	UNP P30613
H	?	-	GLY	deletion	UNP P30613
H	?	-	ASN	deletion	UNP P30613
H	?	-	ALA	deletion	UNP P30613
H	?	-	ASN	deletion	UNP P30613

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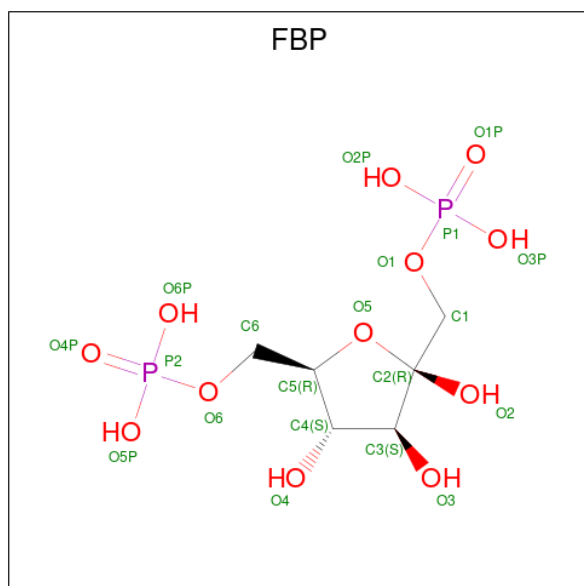
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H	?	-	VAL	deletion	UNP P30613
H	?	-	TRP	deletion	UNP P30613
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H	?	-	ASP	deletion	UNP P30613
H	?	-	TYR	deletion	UNP P30613
H	?	-	PRO	deletion	UNP P30613
H	?	-	ASN	deletion	UNP P30613
H	?	-	ILE	deletion	UNP P30613
H	?	-	VAL	deletion	UNP P30613
H	?	-	ARG	deletion	UNP P30613
H	?	-	VAL	deletion	UNP P30613
H	?	-	VAL	deletion	UNP P30613
H	?	-	PRO	deletion	UNP P30613
H	?	-	VAL	deletion	UNP P30613
H	?	-	GLY	deletion	UNP P30613
H	?	-	GLY	deletion	UNP P30613
H	?	-	ARG	deletion	UNP P30613
H	?	-	ILE	deletion	UNP P30613
H	?	-	TYR	deletion	UNP P30613
H	?	-	ILE	deletion	UNP P30613
H	?	-	ASP	deletion	UNP P30613
H	?	-	ASP	deletion	UNP P30613
H	?	-	GLY	deletion	UNP P30613
H	?	-	LEU	deletion	UNP P30613
H	?	-	ILE	deletion	UNP P30613
H	?	-	SER	deletion	UNP P30613
H	?	-	LEU	deletion	UNP P30613
H	?	-	VAL	deletion	UNP P30613
H	?	-	VAL	deletion	UNP P30613
H	?	-	GLN	deletion	UNP P30613
H	?	-	LYS	deletion	UNP P30613
H	?	-	ILE	deletion	UNP P30613
H	?	-	GLY	deletion	UNP P30613
H	?	-	PRO	deletion	UNP P30613
H	?	-	GLU	deletion	UNP P30613
H	?	-	GLY	deletion	UNP P30613
H	?	-	LEU	deletion	UNP P30613
H	?	-	VAL	deletion	UNP P30613
H	?	-	THR	deletion	UNP P30613
H	?	-	GLN	deletion	UNP P30613
H	?	-	VAL	deletion	UNP P30613

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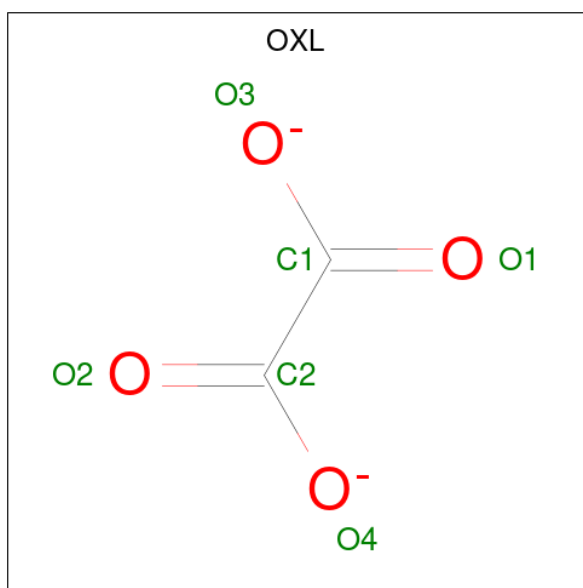
Chain	Residue	Modelled	Actual	Comment	Reference
H	?	-	GLU	deletion	UNP P30613
H	?	-	ASN	deletion	UNP P30613
H	?	-	GLY	deletion	UNP P30613
H	?	-	GLY	deletion	UNP P30613
H	?	-	VAL	deletion	UNP P30613
H	?	-	LEU	deletion	UNP P30613
H	?	-	GLY	deletion	UNP P30613
H	?	-	SER	deletion	UNP P30613
H	?	-	ARG	deletion	UNP P30613
H	?	-	LYS	deletion	UNP P30613
H	?	-	GLY	deletion	UNP P30613
H	?	-	VAL	deletion	UNP P30613
H	?	-	ASN	deletion	UNP P30613
H	?	-	LEU	deletion	UNP P30613
H	?	-	PRO	deletion	UNP P30613
H	?	-	GLY	deletion	UNP P30613
H	?	-	ALA	deletion	UNP P30613
H	?	-	GLN	deletion	UNP P30613
H	130	GLY	VAL	linker	UNP P30613
H	229	SER	ASP	linker	UNP P30613
H	230	GLY	LEU	linker	UNP P30613

- Molecule 2 is 1,6-di-O-phosphono-beta-D-fructofuranose (CCD ID: FBP) (formula: $C_6H_{14}O_{12}P_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			20	6	12	2		
2	B	1	Total	C	O	P	0	0
			20	6	12	2		
2	C	1	Total	C	O	P	0	0
			20	6	12	2		
2	D	1	Total	C	O	P	0	0
			20	6	12	2		
2	E	1	Total	C	O	P	0	0
			20	6	12	2		
2	F	1	Total	C	O	P	0	0
			20	6	12	2		
2	G	1	Total	C	O	P	0	0
			20	6	12	2		
2	H	1	Total	C	O	P	0	0
			20	6	12	2		

- Molecule 3 is OXALATE ION (CCD ID: OXL) (formula: C_2O_4).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	2	4		
3	B	1	Total	C	O	0	0
			6	2	4		
3	C	1	Total	C	O	0	0
			6	2	4		
3	D	1	Total	C	O	0	0
			6	2	4		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	E	1	Total	C	O	0	0
			6	2	4		
3	F	1	Total	C	O	0	0
			6	2	4		
3	G	1	Total	C	O	0	0
			6	2	4		
3	H	1	Total	C	O	0	0
			6	2	4		

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 5 is POTASSIUM ION (CCD ID: K) (formula: K).

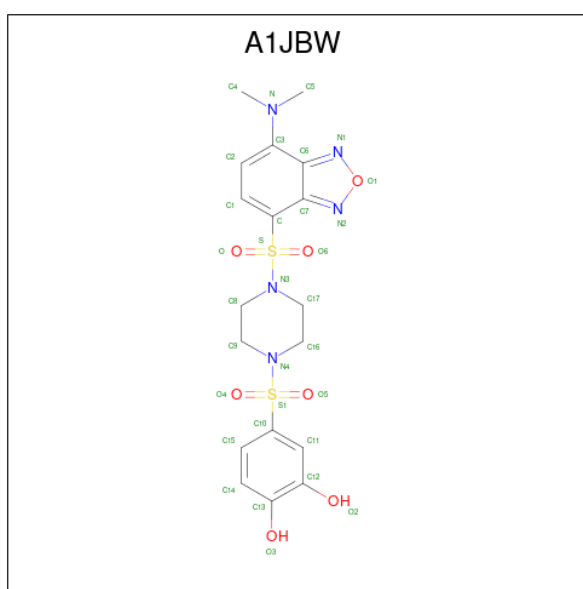
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	K	0	0
			1	1		
5	B	1	Total	K	0	0
			1	1		
5	C	1	Total	K	0	0
			1	1		
5	D	1	Total	K	0	0
			1	1		
5	E	1	Total	K	0	0
			1	1		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	F	1	Total K 1 1	0	0
5	G	1	Total K 1 1	0	0
5	H	1	Total K 1 1	0	0

- Molecule 6 is 4-[4-[[7-(dimethylamino)-2,1,3-benzoxadiazol-4-yl]sulfonyl]piperazin-1-yl]sulfonylbenzene-1,2-diol (CCD ID: A1JBW) (formula: C₁₈H₂₁N₅O₇S₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
6	C	1	Total 53	C 18	H 21	N 5	O 7	S 2	21	0
6	D	1	Total 53	C 18	H 21	N 5	O 7	S 2	21	0
6	G	1	Total 53	C 18	H 21	N 5	O 7	S 2	21	0
6	H	1	Total 53	C 18	H 21	N 5	O 7	S 2	21	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	125	Total O 125 125	0	0

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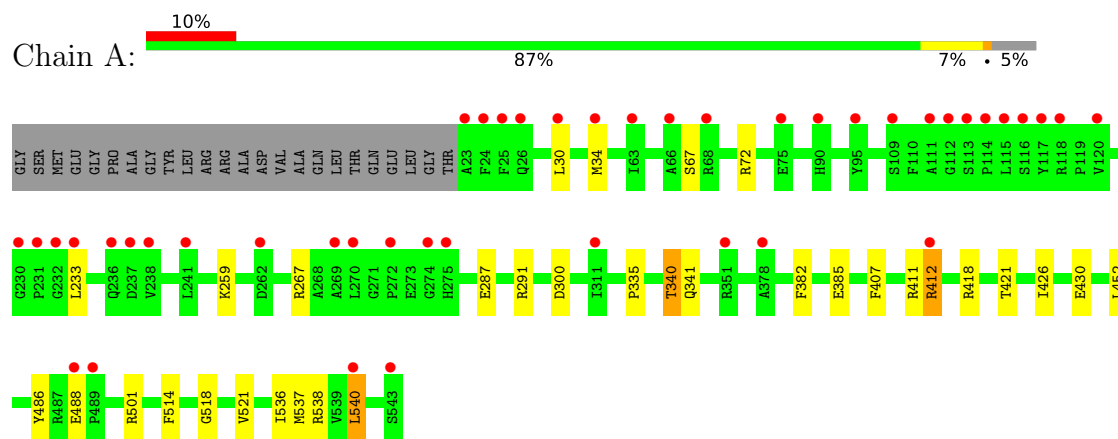
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	186	Total 186	O 186	0	0
7	C	217	Total 217	O 217	0	0
7	D	246	Total 246	O 246	0	0
7	E	149	Total 149	O 149	0	0
7	F	153	Total 153	O 153	0	0
7	G	243	Total 243	O 243	0	0
7	H	243	Total 243	O 243	0	0

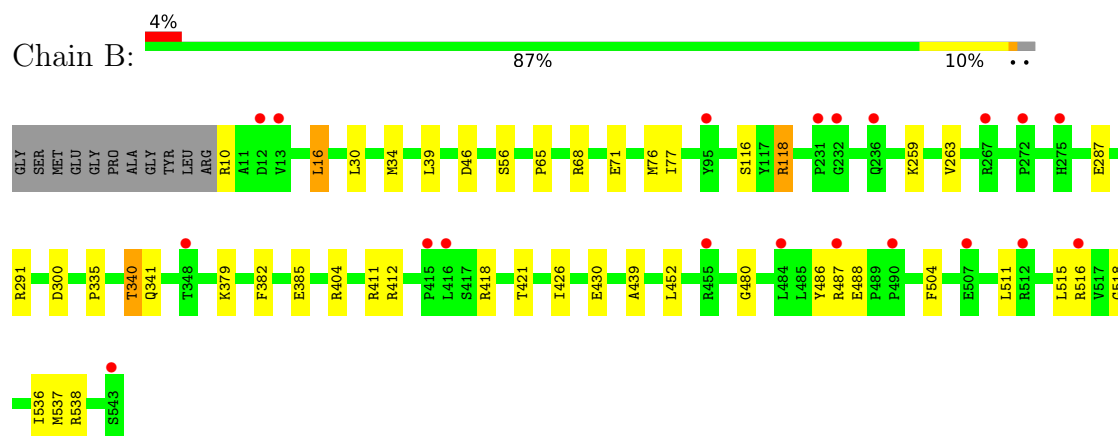
3 Residue-property plots [i](#)

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

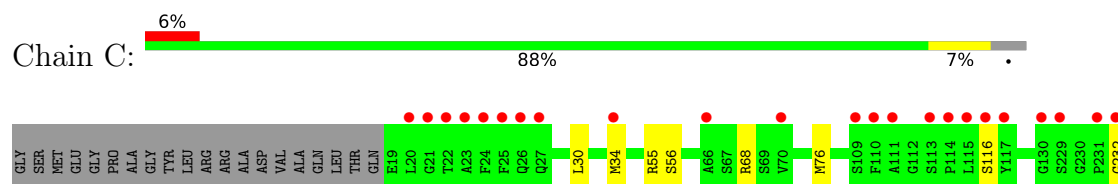
- Molecule 1: Isoform L-type of Pyruvate kinase PKLR

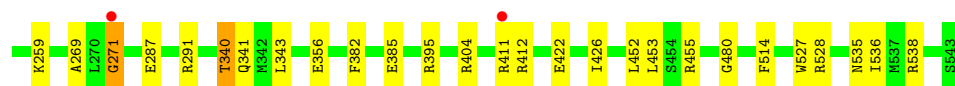


- Molecule 1: Isoform L-type of Pyruvate kinase PKLR

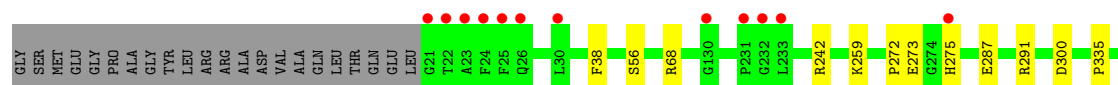
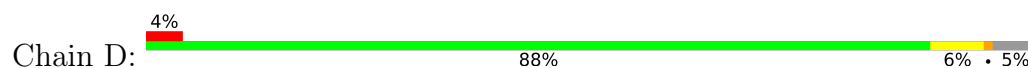


- Molecule 1: Isoform L-type of Pyruvate kinase PKLR

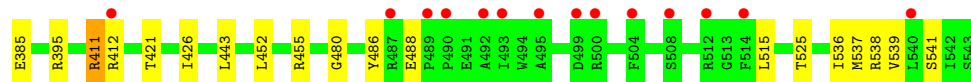
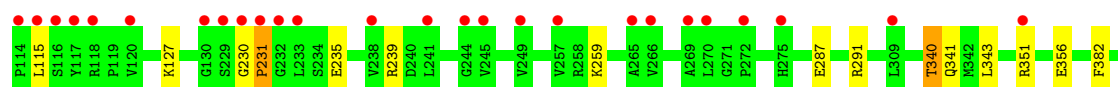
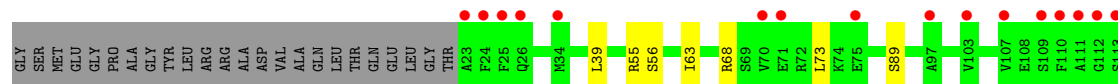
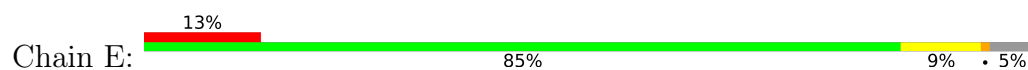




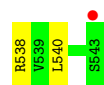
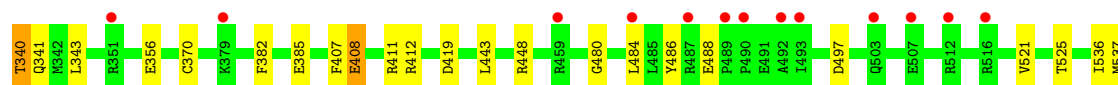
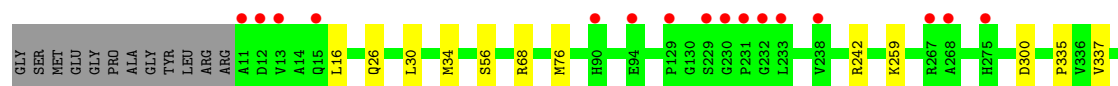
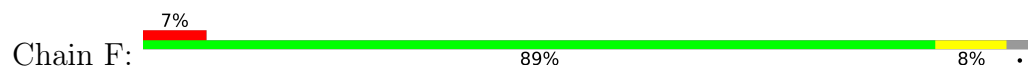
- Molecule 1: Isoform L-type of Pyruvate kinase PKLR



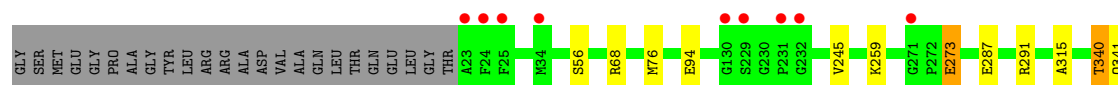
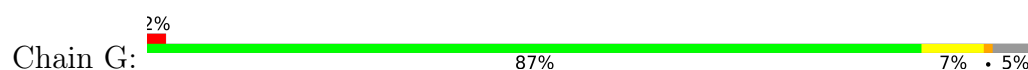
- Molecule 1: Isoform L-type of Pyruvate kinase PKLR

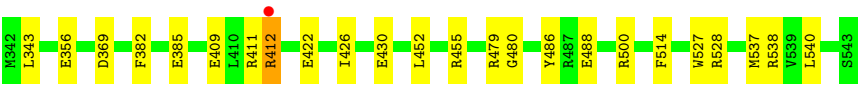


- Molecule 1: Isoform L-type of Pyruvate kinase PKLR

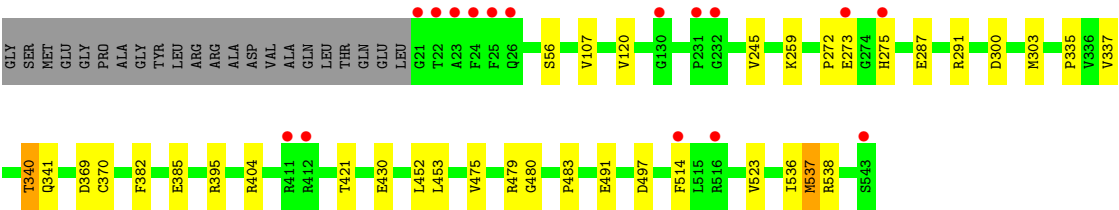
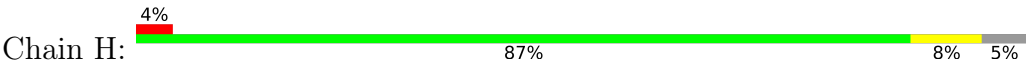


- Molecule 1: Isoform L-type of Pyruvate kinase PKLR





● Molecule 1: Isoform L-type of Pyruvate kinase PKLR



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	206.88Å 112.00Å 188.13Å 90.00° 91.90° 90.00°	Depositor
Resolution (Å)	188.03 – 2.04 188.03 – 2.04	Depositor EDS
% Data completeness (in resolution range)	60.8 (188.03-2.04) 60.8 (188.03-2.04)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.92 (at 2.05Å)	Xtriage
Refinement program	BUSTER 2.10.4	Depositor
R, R_{free}	0.206 , 0.240 0.197 , 0.228	Depositor DCC
R_{free} test set	8407 reflections (3.11%)	wwPDB-VP
Wilson B-factor (Å ²)	28.6	Xtriage
Anisotropy	0.033	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 45.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.002 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	28135	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 57.11 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.4813e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: FBP, MG, OXL, A1JBW, K

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	0.72	0/3316	1.03	1/4484 (0.0%)
1	B	0.73	0/3396	1.04	3/4592 (0.1%)
1	C	0.77	0/3324	1.06	3/4495 (0.1%)
1	D	0.77	1/3326 (0.0%)	1.05	4/4497 (0.1%)
1	E	0.70	0/3298	1.03	5/4458 (0.1%)
1	F	0.71	0/3411	1.04	3/4613 (0.1%)
1	G	0.76	0/3314	1.04	1/4481 (0.0%)
1	H	0.77	1/3316 (0.0%)	1.05	3/4483 (0.1%)
All	All	0.74	2/26701 (0.0%)	1.04	23/36103 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	374	SER	CA-C	6.84	1.55	1.52
1	H	303	MET	SD-CE	-5.55	1.65	1.79

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	231	PRO	N-CA-CB	8.28	111.95	103.25
1	E	230	GLY	CA-C-N	7.29	128.96	119.84
1	E	230	GLY	C-N-CA	7.29	128.96	119.84
1	G	514	PHE	CA-CB-CG	7.17	120.97	113.80
1	H	514	PHE	CA-CB-CG	6.21	120.01	113.80
1	E	411	ARG	CA-C-N	5.56	127.73	120.28
1	E	411	ARG	C-N-CA	5.56	127.73	120.28
1	F	408	GLU	CB-CG-CD	-5.51	103.23	112.60
1	C	514	PHE	CA-CB-CG	5.44	119.24	113.80
1	F	497	ASP	CA-C-N	5.33	127.28	120.56
1	F	497	ASP	C-N-CA	5.33	127.28	120.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	453	LEU	CA-C-N	5.29	127.37	120.28
1	C	453	LEU	C-N-CA	5.29	127.37	120.28
1	D	453	LEU	CA-C-N	5.27	127.87	120.28
1	D	453	LEU	C-N-CA	5.27	127.87	120.28
1	A	514	PHE	CA-CB-CG	5.19	118.99	113.80
1	B	46	ASP	CA-CB-CG	5.13	117.73	112.60
1	D	525	THR	CA-C-N	5.12	127.03	122.47
1	D	525	THR	C-N-CA	5.12	127.03	122.47
1	B	504	PHE	CA-C-N	5.10	125.64	119.98
1	B	504	PHE	C-N-CA	5.10	125.64	119.98
1	H	453	LEU	CA-C-N	5.05	127.05	120.28
1	H	453	LEU	C-N-CA	5.05	127.05	120.28

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	3243	0	3307	20	0
1	B	3329	0	3394	23	0
1	C	3257	0	3308	18	0
1	D	3252	0	3310	16	0
1	E	3229	0	3283	19	0
1	F	3335	0	3404	17	0
1	G	3241	0	3293	20	0
1	H	3251	0	3306	22	0
2	A	20	0	10	1	0
2	B	20	0	10	0	0
2	C	20	0	10	0	0
2	D	20	0	10	0	0
2	E	20	0	10	0	0
2	F	20	0	10	0	0
2	G	20	0	10	0	0
2	H	20	0	10	0	0
3	A	6	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	6	0	0	0	0
3	C	6	0	0	0	0
3	D	6	0	0	0	0
3	E	6	0	0	0	0
3	F	6	0	0	0	0
3	G	6	0	0	0	0
3	H	6	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
4	G	1	0	0	0	0
4	H	1	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
5	E	1	0	0	0	0
5	F	1	0	0	0	0
5	G	1	0	0	0	0
5	H	1	0	0	0	0
6	C	32	21	0	0	0
6	D	32	21	0	2	0
6	G	32	21	0	2	0
6	H	32	21	0	0	0
7	A	125	0	0	0	0
7	B	186	0	0	2	0
7	C	217	0	0	1	0
7	D	246	0	0	1	0
7	E	149	0	0	0	0
7	F	153	0	0	1	0
7	G	243	0	0	0	0
7	H	243	0	0	1	0
All	All	28051	84	26685	138	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 3.

All (138) 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:C:422[A]:GLU:HG3	1:C:452:LEU:HD13	1.60	0.84
1:G:422[A]:GLU:HG3	1:G:452:LEU:HD13	1.61	0.81
1:A:418[A]:ARG:HG3	1:B:16:LEU:HD11	1.64	0.80
1:E:411:ARG:HG2	1:E:426:ILE:HD11	1.67	0.75
1:B:411:ARG:HG2	1:B:426:ILE:HD11	1.68	0.74
1:B:487:ARG:HG2	7:B:877:HOH:O	1.93	0.69
1:F:407:PHE:CE2	1:F:411:ARG:NH1	2.61	0.69
1:G:56:SER:HB2	1:G:480:GLY:HA2	1.75	0.68
1:G:537:MET:HE3	1:H:537:MET:HG2	1.77	0.66
1:H:245:VAL:HG11	1:H:273:GLU:HG2	1.77	0.66
1:C:411:ARG:HG3	1:C:426:ILE:HD11	1.77	0.66
1:G:538:ARG:HG2	1:H:536:ILE:HG12	1.78	0.65
1:H:56:SER:HB2	1:H:480:GLY:HA2	1.79	0.65
1:B:56:SER:HB2	1:B:480:GLY:HA2	1.80	0.64
1:F:56:SER:HB2	1:F:480:GLY:HA2	1.80	0.63
1:C:56:SER:HB2	1:C:480:GLY:HA2	1.81	0.62
1:D:56:SER:HB2	1:D:480:GLY:HA2	1.82	0.61
1:E:443:LEU:HD13	1:E:525:THR:HG22	1.82	0.61
1:C:340:THR:HG22	1:C:341:GLN:HG3	1.84	0.60
1:E:39:LEU:HD13	6:G:605:A1JBW:C5	2.31	0.60
1:G:340:THR:HG22	1:G:341:GLN:HG3	1.84	0.60
1:C:538:ARG:HG2	1:D:536:ILE:HG12	1.83	0.60
1:E:56:SER:HB2	1:E:480:GLY:HA2	1.83	0.60
1:A:340:THR:HG22	1:A:341:GLN:HG3	1.84	0.60
1:D:340:THR:HG22	1:D:341:GLN:HG3	1.83	0.58
1:B:340:THR:HG22	1:B:341:GLN:HG3	1.85	0.58
1:B:486:TYR:CZ	1:B:488:GLU:HB2	2.40	0.56
1:E:340:THR:HG22	1:E:341:GLN:HG3	1.86	0.56
1:H:245:VAL:CG1	1:H:273:GLU:HG2	2.34	0.56
1:H:340:THR:HG22	1:H:341:GLN:HG3	1.88	0.54
1:H:523:VAL:HB	1:H:538[B]:ARG:HG2	1.90	0.54
1:C:232:GLY:HA3	7:C:874:HOH:O	2.08	0.53
1:F:340:THR:HG22	1:F:341:GLN:HG3	1.90	0.53
1:A:536:ILE:HG12	1:B:538:ARG:HG2	1.91	0.53
1:B:65:PRO:HG2	1:B:379:LYS:HE3	1.90	0.52
1:F:484:LEU:HD21	7:F:771:HOH:O	2.08	0.52
1:F:382:PHE:HB3	1:F:385:GLU:HB2	1.91	0.52
1:E:536:ILE:HG12	1:F:538:ARG:HG2	1.93	0.51
1:E:538:ARG:HG2	1:F:536:ILE:HG12	1.91	0.51
1:H:56:SER:HB2	1:H:480:GLY:CA	2.41	0.51
1:D:272:PRO:HA	1:D:275[A]:HIS:CE1	2.45	0.51
1:D:521:VAL:HG12	1:D:540:LEU:HB3	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:382:PHE:HB3	1:B:385:GLU:HB2	1.93	0.50
1:G:56:SER:HB2	1:G:480:GLY:CA	2.41	0.50
1:A:412:ARG:NH1	1:B:404:ARG:HH11	2.10	0.50
1:H:382:PHE:HB3	1:H:385:GLU:HB2	1.94	0.50
1:F:56:SER:HB2	1:F:480:GLY:CA	2.42	0.50
1:G:245:VAL:CG1	1:G:273:GLU:HG2	2.42	0.50
1:B:56:SER:HB2	1:B:480:GLY:CA	2.42	0.49
1:F:486:TYR:CZ	1:F:488:GLU:HB2	2.47	0.49
1:H:491:GLU:HB3	7:H:826:HOH:O	2.10	0.49
1:E:89:SER:HA	1:E:127:LYS:HG3	1.94	0.49
1:A:538:ARG:HG2	1:B:536:ILE:HG12	1.94	0.49
1:H:491:GLU:HB2	1:H:497:ASP:HB2	1.95	0.49
1:H:272:PRO:HA	1:H:275[A]:HIS:CE1	2.48	0.48
1:C:287:GLU:HG2	1:C:291:ARG:HD2	1.94	0.48
1:A:382:PHE:HB3	1:A:385:GLU:HB2	1.95	0.48
1:G:412:ARG:CZ	1:H:404:ARG:HD3	2.43	0.48
1:E:235:GLU:O	1:E:239:ARG:HD3	2.14	0.48
1:E:382:PHE:HB3	1:E:385:GLU:HB2	1.96	0.48
1:D:38:PHE:CE1	6:D:605:A1JBW:O6	2.67	0.48
1:C:56:SER:HB2	1:C:480:GLY:CA	2.44	0.47
1:C:382:PHE:HB3	1:C:385:GLU:HB2	1.97	0.47
1:E:486:TYR:CZ	1:E:488:GLU:HB2	2.51	0.46
1:D:56:SER:HB2	1:D:480:GLY:CA	2.45	0.46
1:D:535:ASN:OD1	1:D:536:ILE:HG13	2.15	0.46
1:A:430:GLU:OE2	1:B:430:GLU:OE1	2.34	0.46
1:E:56:SER:HB2	1:E:480:GLY:CA	2.45	0.46
1:A:287:GLU:HG2	1:A:291:ARG:HD3	1.98	0.45
1:B:439:ALA:HB3	1:B:515:LEU:HD21	1.99	0.45
1:A:407:PHE:CE2	1:A:411:ARG:HD3	2.51	0.45
1:A:411:ARG:HG3	1:A:426:ILE:HD11	1.97	0.45
1:D:287:GLU:HG2	1:D:291:ARG:HD3	1.99	0.45
1:B:39:LEU:HD13	6:D:605:A1JBW:C4	2.46	0.45
1:C:404:ARG:HH11	1:D:412:ARG:NH1	2.15	0.44
1:A:418[B]:ARG:NH2	1:B:518:GLY:O	2.51	0.44
1:G:486:TYR:CZ	1:G:488:GLU:HB2	2.53	0.44
1:A:67:SER:HA	1:A:72:ARG:HG2	1.99	0.44
1:B:116:SER:HB2	7:B:763:HOH:O	2.17	0.44
1:D:300:ASP:O	1:D:335:PRO:HD2	2.18	0.44
1:H:300:ASP:O	1:H:335:PRO:HD2	2.18	0.44
1:B:300:ASP:O	1:B:335:PRO:HD2	2.18	0.43
1:F:30:LEU:O	1:F:34:MET:HG2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:287:GLU:HG2	1:G:291:ARG:HD3	2.00	0.43
1:F:443:LEU:HD22	1:F:525:THR:HG22	2.00	0.43
1:G:382:PHE:HB3	1:G:385:GLU:HB2	1.99	0.43
1:G:430[B]:GLU:OE2	1:H:430:GLU:OE1	2.37	0.43
1:B:287:GLU:HG2	1:B:291:ARG:HD3	2.00	0.43
1:C:527:TRP:CD2	1:C:528:ARG:HG2	2.53	0.43
1:C:452:LEU:O	1:C:455:ARG:HG2	2.19	0.43
1:D:419:ASP:OD2	1:D:448:ARG:NH2	2.52	0.43
1:A:518:GLY:O	1:B:418:ARG:NH2	2.52	0.43
1:C:30:LEU:O	1:C:34:MET:HG2	2.19	0.43
1:G:411:ARG:HG3	1:G:426:ILE:HD11	2.01	0.42
1:G:527:TRP:CD2	1:G:528:ARG:HG2	2.54	0.42
1:A:300:ASP:O	1:A:335:PRO:HD2	2.20	0.42
1:D:382:PHE:HB3	1:D:385:GLU:HB2	1.99	0.42
1:C:535:ASN:OD1	1:C:536:ILE:HG13	2.19	0.42
1:E:452:LEU:O	1:E:455:ARG:HG2	2.19	0.42
1:F:419:ASP:OD2	1:F:448:ARG:NH2	2.51	0.42
1:C:527:TRP:CE2	1:C:528:ARG:HG2	2.55	0.42
1:F:408:GLU:HG2	1:F:411:ARG:NH2	2.34	0.42
1:E:287:GLU:HG2	1:E:291:ARG:HD3	2.01	0.42
1:G:343:LEU:HD23	1:G:356:GLU:HB3	2.01	0.42
1:H:107:VAL:HG21	1:H:120:VAL:HB	2.01	0.42
1:A:267:ARG:HA	1:A:267:ARG:HD3	1.94	0.42
1:D:421:THR:HG22	1:D:452:LEU:HD12	2.02	0.42
1:H:421:THR:HG22	1:H:452:LEU:HD12	2.02	0.42
1:B:77:ILE:CG2	1:B:118:ARG:HG3	2.50	0.41
1:D:273:GLU:HB2	7:D:716:HOH:O	2.20	0.41
1:E:421:THR:HG22	1:E:452:LEU:HD12	2.01	0.41
1:H:475:VAL:CG2	1:H:483:PRO:HB3	2.50	0.41
1:G:452:LEU:O	1:G:455:ARG:HG2	2.20	0.41
1:E:343:LEU:HD23	1:E:356:GLU:HB3	2.02	0.41
1:E:351:ARG:HH21	1:G:315:ALA:HB2	1.85	0.41
1:G:409:GLU:OE1	6:G:605:A1JBW:O1	2.38	0.41
1:A:486:TYR:CZ	1:A:488[B]:GLU:HB2	2.56	0.41
1:E:55:ARG:HB2	1:E:395:ARG:HG3	2.03	0.41
1:F:521:VAL:HG12	1:F:540[B]:LEU:HB3	2.02	0.41
1:G:430[A]:GLU:OE1	1:H:430:GLU:OE1	2.39	0.41
1:A:501:ARG:NH1	2:A:601:FBP:O2P	2.44	0.41
1:B:30:LEU:O	1:B:34:MET:HG2	2.21	0.41
1:C:343:LEU:HD23	1:C:356:GLU:HB3	2.03	0.41
1:D:369:ASP:HA	1:D:479:ARG:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:337:VAL:HG22	1:F:370:CYS:HB2	2.01	0.41
1:A:421:THR:HG22	1:A:452:LEU:HD12	2.02	0.41
1:C:269:ALA:C	1:C:271:GLY:H	2.28	0.41
1:F:343:LEU:HD23	1:F:356:GLU:HB3	2.02	0.41
1:H:287:GLU:HG2	1:H:291:ARG:HD3	2.02	0.41
1:H:337:VAL:HG22	1:H:370:CYS:HB2	2.03	0.41
1:E:63:ILE:HD12	1:E:73:LEU:HD21	2.02	0.41
1:A:30:LEU:O	1:A:34:MET:HG2	2.21	0.40
1:G:369:ASP:HA	1:G:479:ARG:HB2	2.04	0.40
1:H:369:ASP:HA	1:H:479:ARG:HB2	2.03	0.40
1:C:55:ARG:HB2	1:C:395:ARG:HG3	2.03	0.40
1:F:300:ASP:O	1:F:335:PRO:HD2	2.21	0.40
1:A:521:VAL:HG23	1:A:540:LEU:HB3	2.02	0.40
1:B:421:THR:HG22	1:B:452:LEU:HD12	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	427/447 (96%)	422 (99%)	4 (1%)	1 (0%)	44	38
1	B	438/447 (98%)	433 (99%)	4 (1%)	1 (0%)	44	38
1	C	429/447 (96%)	419 (98%)	8 (2%)	2 (0%)	25	17
1	D	429/447 (96%)	423 (99%)	5 (1%)	1 (0%)	44	38
1	E	426/447 (95%)	420 (99%)	4 (1%)	2 (0%)	25	17
1	F	440/447 (98%)	434 (99%)	5 (1%)	1 (0%)	44	38
1	G	427/447 (96%)	418 (98%)	8 (2%)	1 (0%)	44	38
1	H	427/447 (96%)	421 (99%)	5 (1%)	1 (0%)	44	38
All	All	3443/3576 (96%)	3390 (98%)	43 (1%)	10 (0%)	37	30

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	231	PRO
1	C	271	GLY
1	A	340	THR
1	B	340	THR
1	C	340	THR
1	D	340	THR
1	E	340	THR
1	F	340	THR
1	G	340	THR
1	H	340	THR

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	341/352 (97%)	335 (98%)	6 (2%)	54	52
1	B	349/352 (99%)	335 (96%)	14 (4%)	27	21
1	C	342/352 (97%)	336 (98%)	6 (2%)	54	52
1	D	342/352 (97%)	335 (98%)	7 (2%)	50	47
1	E	339/352 (96%)	329 (97%)	10 (3%)	37	32
1	F	351/352 (100%)	341 (97%)	10 (3%)	38	34
1	G	341/352 (97%)	332 (97%)	9 (3%)	41	36
1	H	340/352 (97%)	337 (99%)	3 (1%)	75	77
All	All	2745/2816 (98%)	2680 (98%)	65 (2%)	50	40

All (65) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	233	LEU
1	A	259	LYS
1	A	412	ARG
1	A	537[A]	MET

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Mol	Chain	Res	Type
1	A	537[B]	MET
1	A	540	LEU
1	B	10	ARG
1	B	16	LEU
1	B	68	ARG
1	B	71	GLU
1	B	76[A]	MET
1	B	76[B]	MET
1	B	118	ARG
1	B	259	LYS
1	B	263	VAL
1	B	412	ARG
1	B	511	LEU
1	B	516	ARG
1	B	537[A]	MET
1	B	537[B]	MET
1	C	68	ARG
1	C	76[A]	MET
1	C	76[B]	MET
1	C	116	SER
1	C	259	LYS
1	C	412	ARG
1	D	68	ARG
1	D	242[A]	ARG
1	D	242[B]	ARG
1	D	259	LYS
1	D	412	ARG
1	D	521	VAL
1	D	537	MET
1	E	68	ARG
1	E	115	LEU
1	E	259	LYS
1	E	412	ARG
1	E	515	LEU
1	E	537[A]	MET
1	E	537[B]	MET
1	E	539	VAL
1	E	541[A]	SER
1	E	541[B]	SER
1	F	16	LEU
1	F	26	GLN
1	F	68	ARG

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Mol	Chain	Res	Type
1	F	76[A]	MET
1	F	76[B]	MET
1	F	242	ARG
1	F	259	LYS
1	F	412	ARG
1	F	537[A]	MET
1	F	537[B]	MET
1	G	68	ARG
1	G	76[A]	MET
1	G	76[B]	MET
1	G	94	GLU
1	G	259	LYS
1	G	273	GLU
1	G	412	ARG
1	G	500	ARG
1	G	540	LEU
1	H	259	LYS
1	H	395	ARG
1	H	537	MET

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

Mol	Chain	Res	Type
1	B	390	GLN
1	D	26	GLN
1	D	90	HIS
1	D	535	ASN
1	F	390	GLN
1	F	405	GLN
1	G	470	GLN
1	H	390	GLN
1	H	405	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 36 ligands modelled in this entry, 16 are monoatomic - leaving 20 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	OXL	C	603	4	5,5,5	1.88	2 (40%)	6,6,6	1.16	1 (16%)
3	OXL	G	602	4	5,5,5	2.11	2 (40%)	6,6,6	0.78	0
3	OXL	F	602	4	5,5,5	1.86	2 (40%)	6,6,6	1.35	1 (16%)
2	FBP	G	601	-	18,20,20	0.53	0	23,32,32	0.70	0
3	OXL	B	602	4	5,5,5	2.10	2 (40%)	6,6,6	1.02	0
6	A1JBW	C	601	-	33,35,35	0.62	1 (3%)	45,54,54	0.70	1 (2%)
6	A1JBW	H	605	-	33,35,35	0.72	1 (3%)	45,54,54	1.16	6 (13%)
3	OXL	E	602	4	5,5,5	1.92	2 (40%)	6,6,6	1.28	1 (16%)
2	FBP	A	601	-	18,20,20	0.57	0	23,32,32	0.70	1 (4%)
3	OXL	D	602	4	5,5,5	2.28	2 (40%)	6,6,6	1.16	0
2	FBP	E	601	-	18,20,20	0.47	0	23,32,32	0.77	1 (4%)
2	FBP	H	601	-	18,20,20	0.57	0	23,32,32	0.76	1 (4%)
3	OXL	A	602	4	5,5,5	1.74	1 (20%)	6,6,6	1.60	2 (33%)
2	FBP	B	601	-	18,20,20	0.43	0	23,32,32	0.83	1 (4%)
2	FBP	D	601	-	18,20,20	0.49	0	23,32,32	1.02	2 (8%)
2	FBP	F	601	-	18,20,20	0.35	0	23,32,32	0.67	0
3	OXL	H	602	4	5,5,5	1.64	2 (40%)	6,6,6	1.30	1 (16%)
6	A1JBW	D	605	-	33,35,35	0.73	1 (3%)	45,54,54	1.08	3 (6%)
6	A1JBW	G	605	-	33,35,35	0.69	1 (3%)	45,54,54	0.98	6 (13%)
2	FBP	C	602	-	18,20,20	0.61	0	23,32,32	1.12	3 (13%)

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	OXL	C	603	4	-	0/4/4/4	-
3	OXL	G	602	4	-	0/4/4/4	-
3	OXL	F	602	4	-	0/4/4/4	-
2	FBP	G	601	-	-	2/13/32/32	0/1/1/1
3	OXL	B	602	4	-	0/4/4/4	-
6	A1JBW	C	601	-	-	17/28/38/38	0/4/4/4
6	A1JBW	H	605	-	-	13/28/38/38	0/4/4/4
3	OXL	E	602	4	-	0/4/4/4	-
2	FBP	A	601	-	-	2/13/32/32	0/1/1/1
3	OXL	D	602	4	-	0/4/4/4	-
2	FBP	E	601	-	-	2/13/32/32	0/1/1/1
2	FBP	H	601	-	-	2/13/32/32	0/1/1/1
3	OXL	A	602	4	-	0/4/4/4	-
2	FBP	B	601	-	-	2/13/32/32	0/1/1/1
2	FBP	D	601	-	-	2/13/32/32	0/1/1/1
2	FBP	F	601	-	-	2/13/32/32	0/1/1/1
3	OXL	H	602	4	-	0/4/4/4	-
6	A1JBW	D	605	-	-	8/28/38/38	1/4/4/4
6	A1JBW	G	605	-	-	15/28/38/38	1/4/4/4
2	FBP	C	602	-	-	2/13/32/32	0/1/1/1

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	602	OXL	O2-C2	4.04	1.33	1.22
3	B	602	OXL	O2-C2	3.93	1.33	1.22
3	D	602	OXL	O2-C2	3.90	1.33	1.22
3	C	603	OXL	O2-C2	3.52	1.32	1.22
3	F	602	OXL	O2-C2	3.33	1.31	1.22
3	A	602	OXL	O2-C2	3.31	1.31	1.22
3	E	602	OXL	O2-C2	3.13	1.31	1.22
3	D	602	OXL	O4-C2	-2.96	1.21	1.30
6	G	605	A1JBW	C-C7	-2.92	1.40	1.42
3	E	602	OXL	O4-C2	-2.75	1.22	1.30
6	D	605	A1JBW	C-C7	-2.73	1.40	1.42
3	F	602	OXL	O4-C2	-2.41	1.23	1.30
3	H	602	OXL	O2-C2	2.38	1.29	1.22
3	C	603	OXL	O4-C2	-2.31	1.23	1.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	601	A1JBW	C-C7	-2.31	1.41	1.42
3	G	602	OXL	O4-C2	-2.28	1.23	1.30
3	H	602	OXL	O4-C2	-2.26	1.24	1.30
6	H	605	A1JBW	C-C7	-2.21	1.41	1.42
3	B	602	OXL	O4-C2	-2.20	1.24	1.30

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	601	FBP	O6-P2-O4P	3.51	116.32	106.47
6	H	605	A1JBW	C16-C17-N3	3.19	111.35	108.91
6	H	605	A1JBW	C17-C16-N4	3.15	111.32	108.91
6	D	605	A1JBW	C16-C17-N3	3.06	111.25	108.91
3	A	602	OXL	O4-C2-C1	2.99	122.04	113.16
6	D	605	A1JBW	C9-C8-N3	2.99	111.20	108.91
2	C	602	FBP	O6-P2-O4P	2.77	114.23	106.47
6	H	605	A1JBW	C8-C9-N4	2.72	111.00	108.91
3	H	602	OXL	O4-C2-C1	2.66	121.05	113.16
6	D	605	A1JBW	C17-C16-N4	2.64	110.93	108.91
6	H	605	A1JBW	C5-N-C3	2.63	121.93	114.12
3	F	602	OXL	O4-C2-C1	2.52	120.64	113.16
6	H	605	A1JBW	C16-N4-C9	2.51	114.94	112.17
2	C	602	FBP	P1-O1-C1	2.49	125.15	118.30
6	G	605	A1JBW	C9-C8-N3	2.46	110.79	108.91
6	G	605	A1JBW	C16-C17-N3	2.45	110.78	108.91
6	G	605	A1JBW	C8-C9-N4	2.44	110.78	108.91
2	D	601	FBP	P1-O1-C1	2.34	124.75	118.30
2	E	601	FBP	P1-O1-C1	2.31	124.65	118.30
2	H	601	FBP	O6-P2-O4P	2.28	112.86	106.47
3	E	602	OXL	O4-C2-C1	2.25	119.85	113.16
2	C	602	FBP	O3-C3-C4	2.25	121.09	113.32
2	B	601	FBP	O6-P2-O4P	2.20	112.64	106.47
6	G	605	A1JBW	C7-C6-N1	-2.18	104.83	110.11
6	C	601	A1JBW	C7-C6-N1	-2.17	104.85	110.11
6	G	605	A1JBW	C16-N4-C9	2.17	114.57	112.17
3	C	603	OXL	O4-C2-C1	2.14	119.52	113.16
6	H	605	A1JBW	C7-C6-N1	-2.08	105.09	110.11
3	A	602	OXL	O2-C2-C1	-2.07	114.13	120.78
6	G	605	A1JBW	C17-N3-C8	2.05	114.43	112.17
2	A	601	FBP	P1-O1-C1	2.03	123.88	118.30

There are no chirality outliers.

All (69) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	FBP	C4-C5-C6-O6
2	B	601	FBP	C4-C5-C6-O6
2	C	602	FBP	C4-C5-C6-O6
2	D	601	FBP	C4-C5-C6-O6
2	E	601	FBP	C4-C5-C6-O6
2	F	601	FBP	C4-C5-C6-O6
2	H	601	FBP	C4-C5-C6-O6
6	C	601	A1JBW	C7-C-S-O6
6	C	601	A1JBW	C7-C-S-O
6	D	605	A1JBW	C7-C-S-O6
6	D	605	A1JBW	C7-C-S-O
6	G	605	A1JBW	C7-C-S-O6
6	G	605	A1JBW	C7-C-S-O
6	H	605	A1JBW	C7-C-S-O6
6	H	605	A1JBW	C7-C-S-O
6	C	601	A1JBW	C9-N4-S1-O4
6	C	601	A1JBW	C17-N3-S-O
6	C	601	A1JBW	C9-N4-S1-C10
6	C	601	A1JBW	C9-N4-S1-O5
6	D	605	A1JBW	C9-N4-S1-O4
6	H	605	A1JBW	C8-N3-S-O6
6	C	601	A1JBW	C16-N4-S1-O5
6	G	605	A1JBW	C8-N3-S-O6
6	G	605	A1JBW	C8-N3-S-O
6	G	605	A1JBW	C17-N3-S-O6
6	C	601	A1JBW	C17-N3-S-C
6	D	605	A1JBW	C9-N4-S1-C10
6	G	605	A1JBW	C8-N3-S-C
6	G	605	A1JBW	C17-N3-S-O
6	H	605	A1JBW	C8-N3-S-C
6	C	601	A1JBW	C16-N4-S1-O4
6	G	605	A1JBW	C17-N3-S-C
2	G	601	FBP	C4-C5-C6-O6
6	C	601	A1JBW	C16-N4-S1-C10
6	H	605	A1JBW	C16-N4-S1-O5
6	C	601	A1JBW	C2-C3-N-C4
2	C	602	FBP	O5-C5-C6-O6
2	H	601	FBP	O5-C5-C6-O6
6	H	605	A1JBW	C9-N4-S1-O5
2	A	601	FBP	O5-C5-C6-O6
2	D	601	FBP	O5-C5-C6-O6
2	E	601	FBP	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
2	F	601	FBP	O5-C5-C6-O6
6	H	605	A1JBW	C9-N4-S1-O4
2	B	601	FBP	O5-C5-C6-O6
6	D	605	A1JBW	C9-N4-S1-O5
6	H	605	A1JBW	C16-N4-S1-C10
6	D	605	A1JBW	C6-C3-N-C4
6	C	601	A1JBW	C17-N3-S-O6
6	C	601	A1JBW	C6-C3-N-C4
6	H	605	A1JBW	C8-N3-S-O
6	G	605	A1JBW	C6-C3-N-C5
6	G	605	A1JBW	C2-C3-N-C5
6	H	605	A1JBW	C2-C3-N-C5
6	D	605	A1JBW	C2-C3-N-C4
2	G	601	FBP	O5-C5-C6-O6
6	G	605	A1JBW	C9-N4-S1-O4
6	G	605	A1JBW	C1-C-S-O
6	G	605	A1JBW	C16-N4-S1-O4
6	G	605	A1JBW	C9-N4-S1-O5
6	H	605	A1JBW	C9-N4-S1-C10
6	C	601	A1JBW	C1-C-S-O6
6	D	605	A1JBW	C17-N3-S-O6
6	G	605	A1JBW	C1-C-S-O6
6	C	601	A1JBW	C8-N3-S-O
6	C	601	A1JBW	C8-N3-S-O6
6	H	605	A1JBW	C6-C3-N-C5
6	C	601	A1JBW	C1-C-S-O
6	H	605	A1JBW	C1-C-S-O6

All (2) ring outliers are listed below:

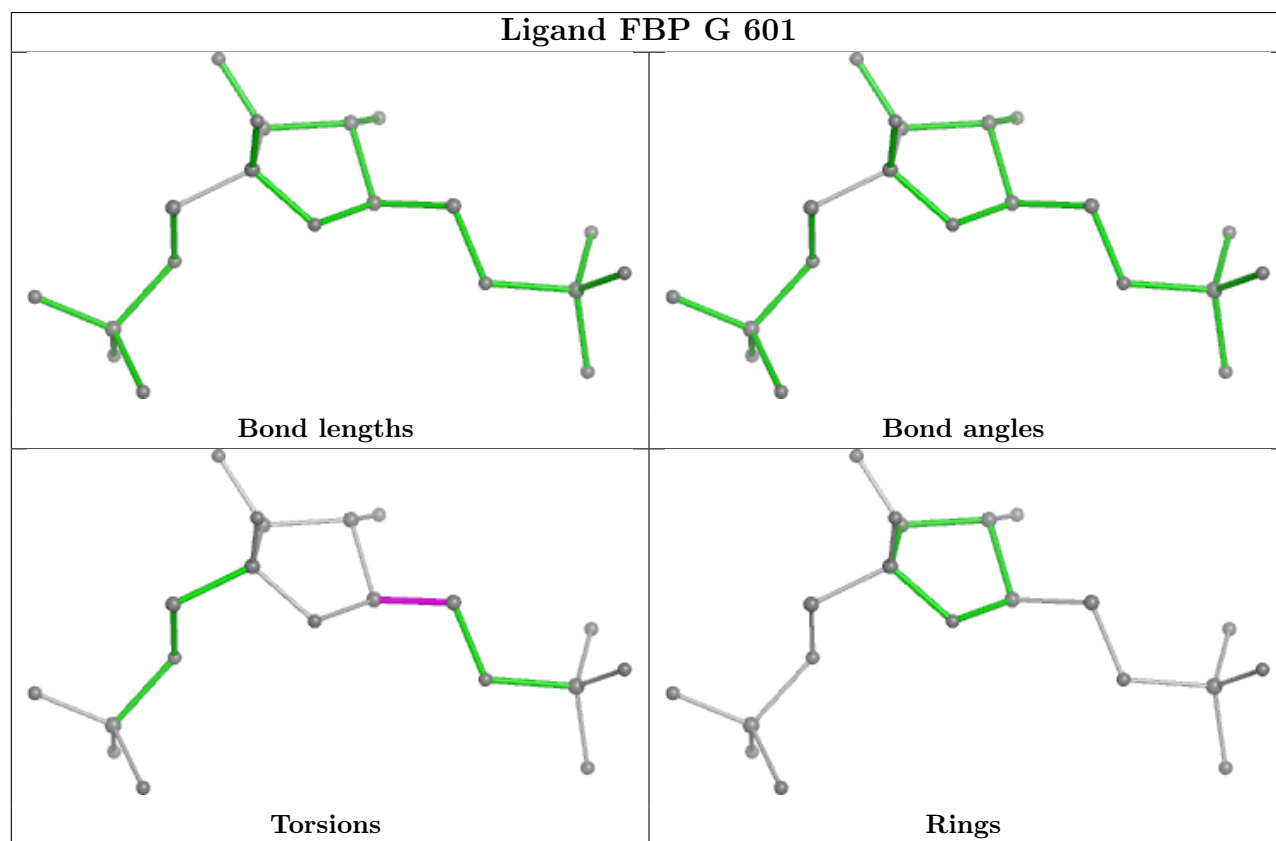
Mol	Chain	Res	Type	Atoms
6	D	605	A1JBW	C16-C17-C8-C9-N3-N4
6	G	605	A1JBW	C16-C17-C8-C9-N3-N4

3 monomers are involved in 5 short contacts:

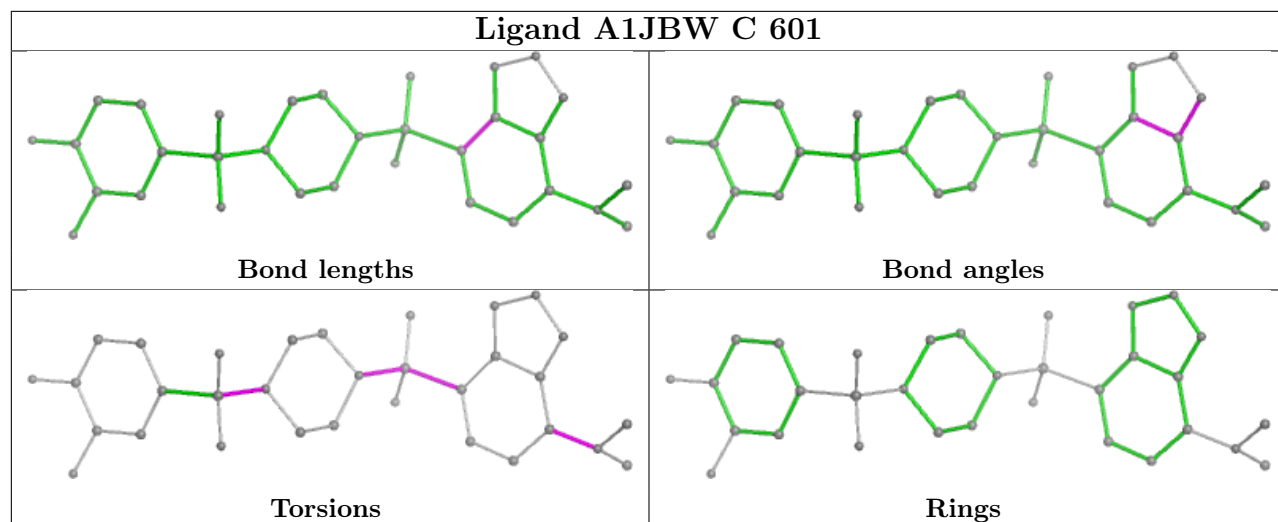
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	FBP	1	0
6	D	605	A1JBW	2	0
6	G	605	A1JBW	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

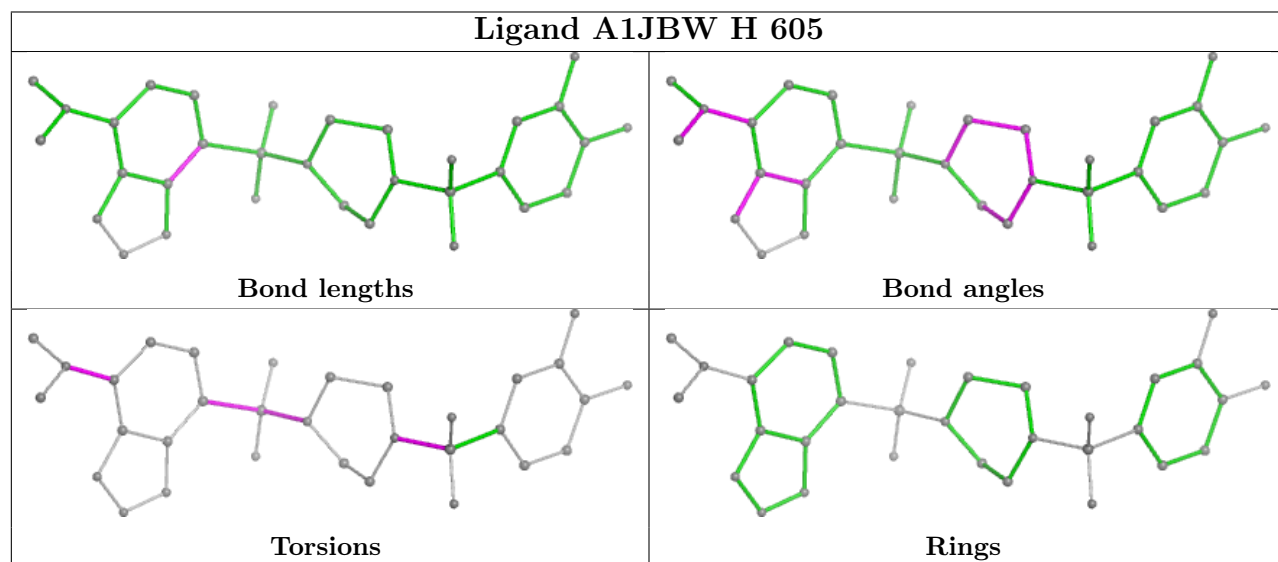
bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 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.

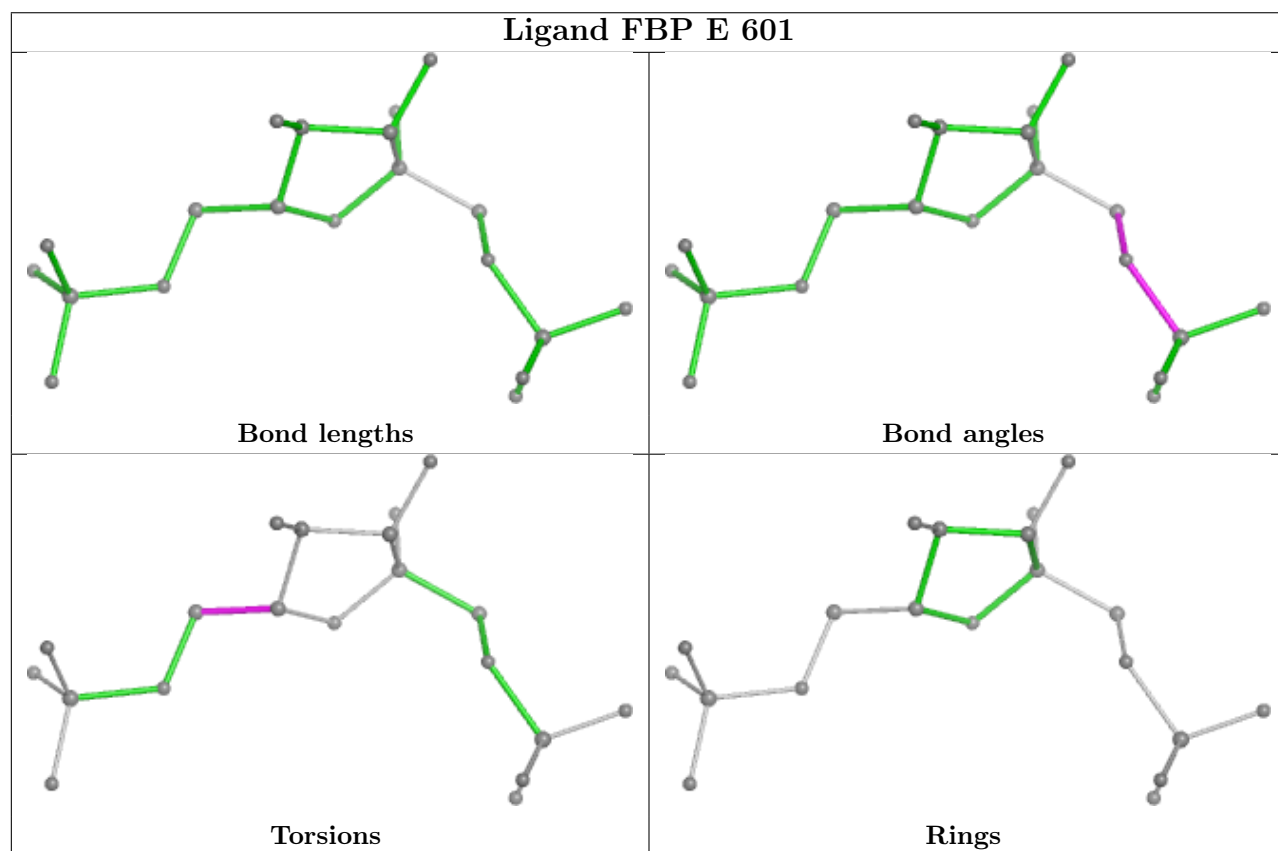
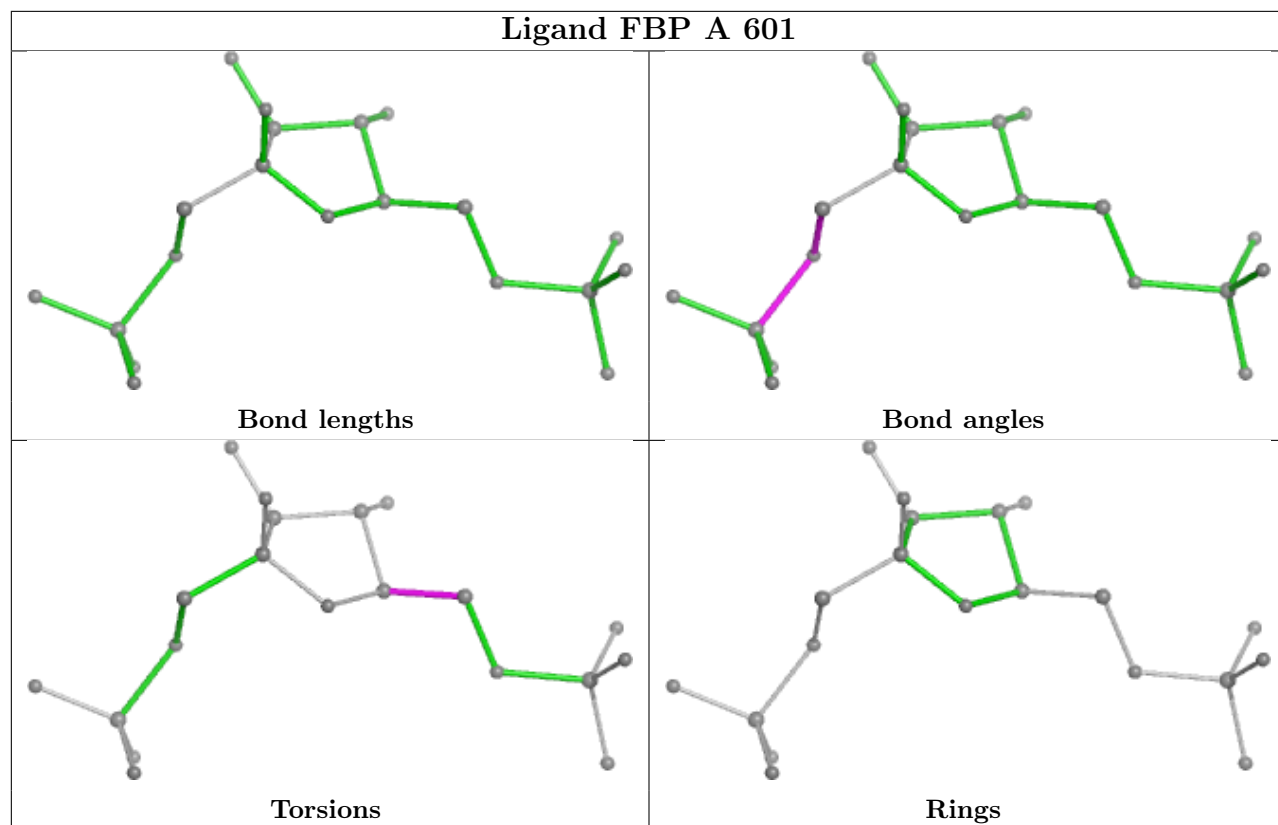


Ligand A1JBW C 601

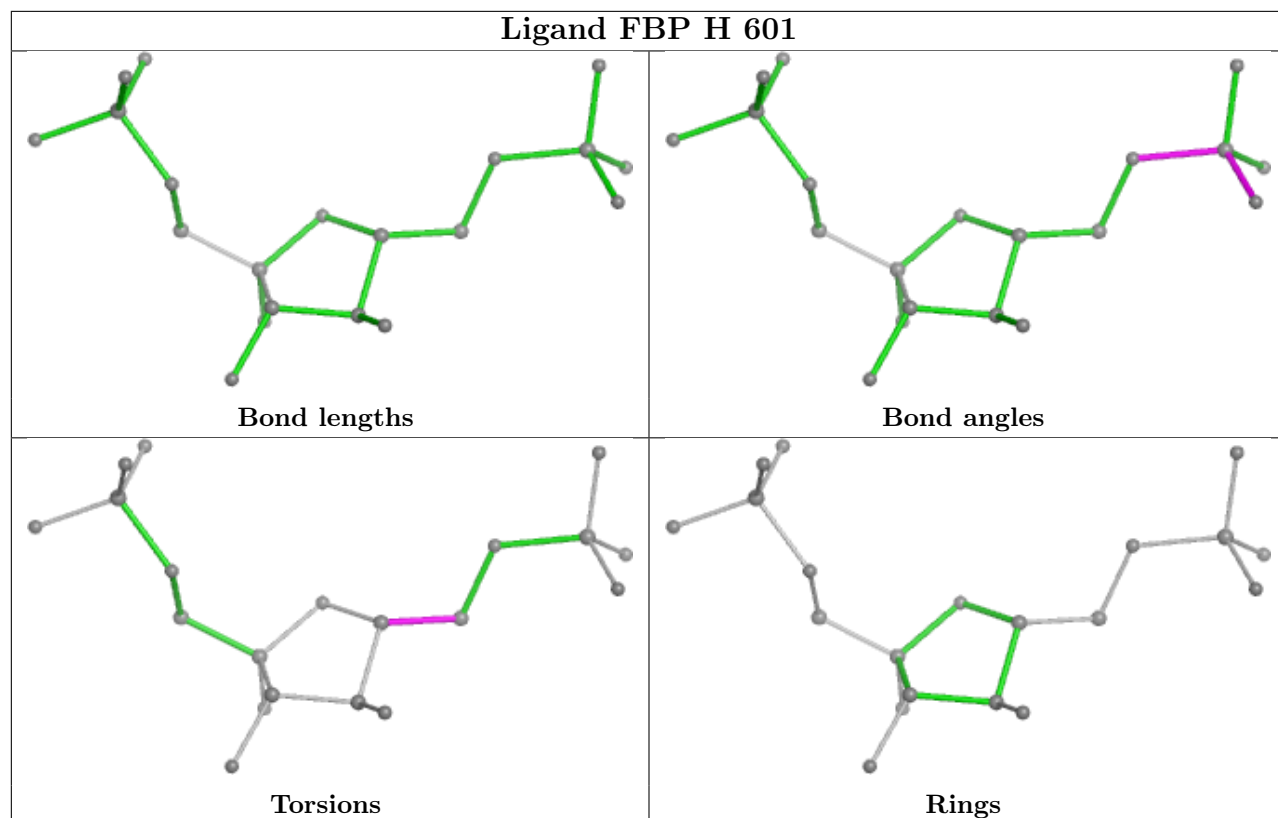


Ligand A1JBW H 605

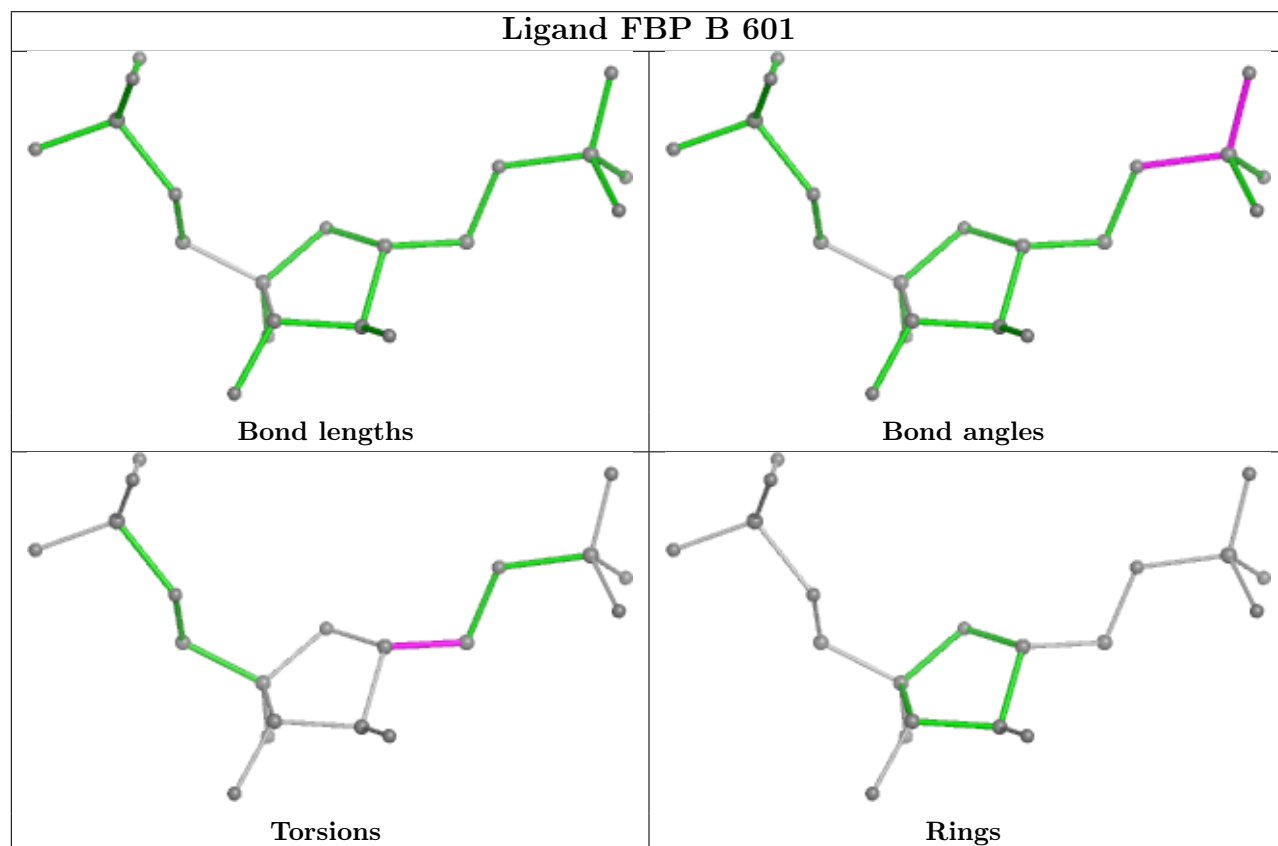


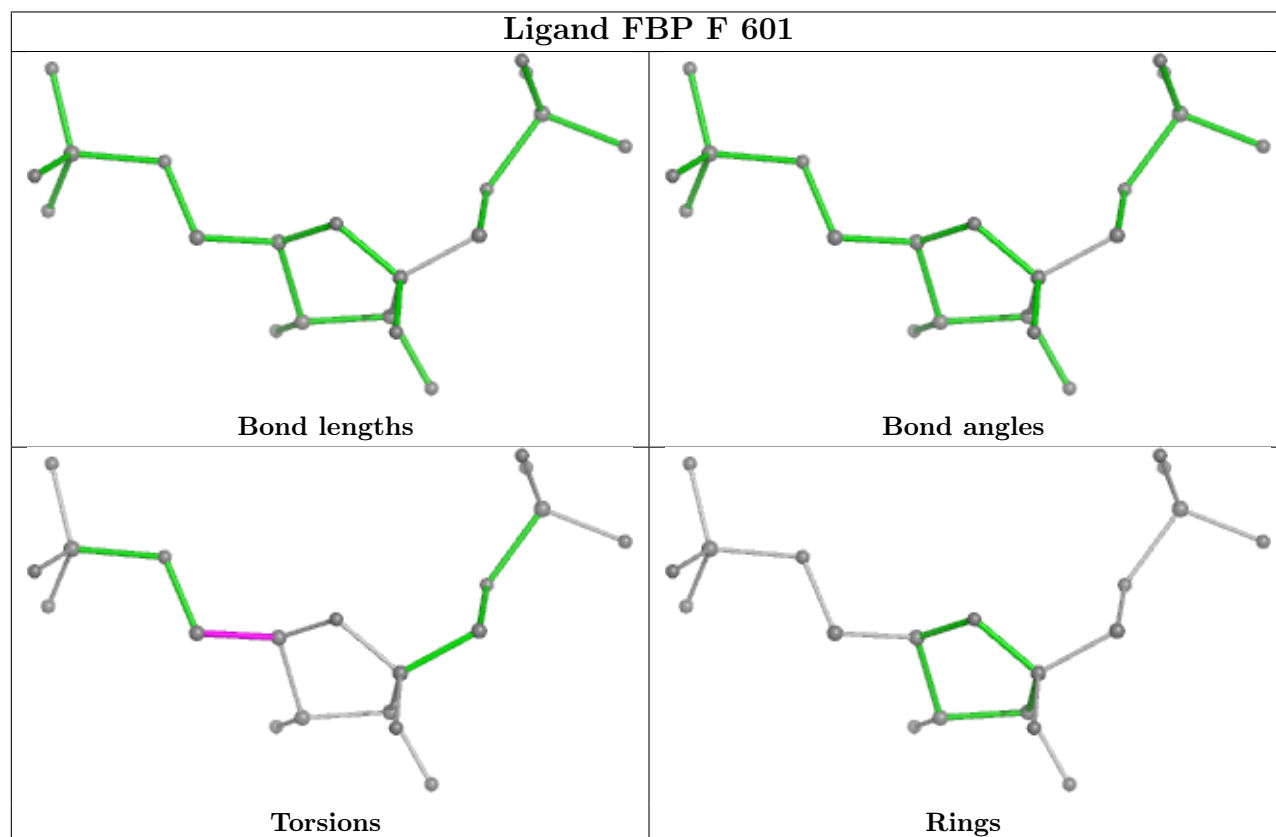
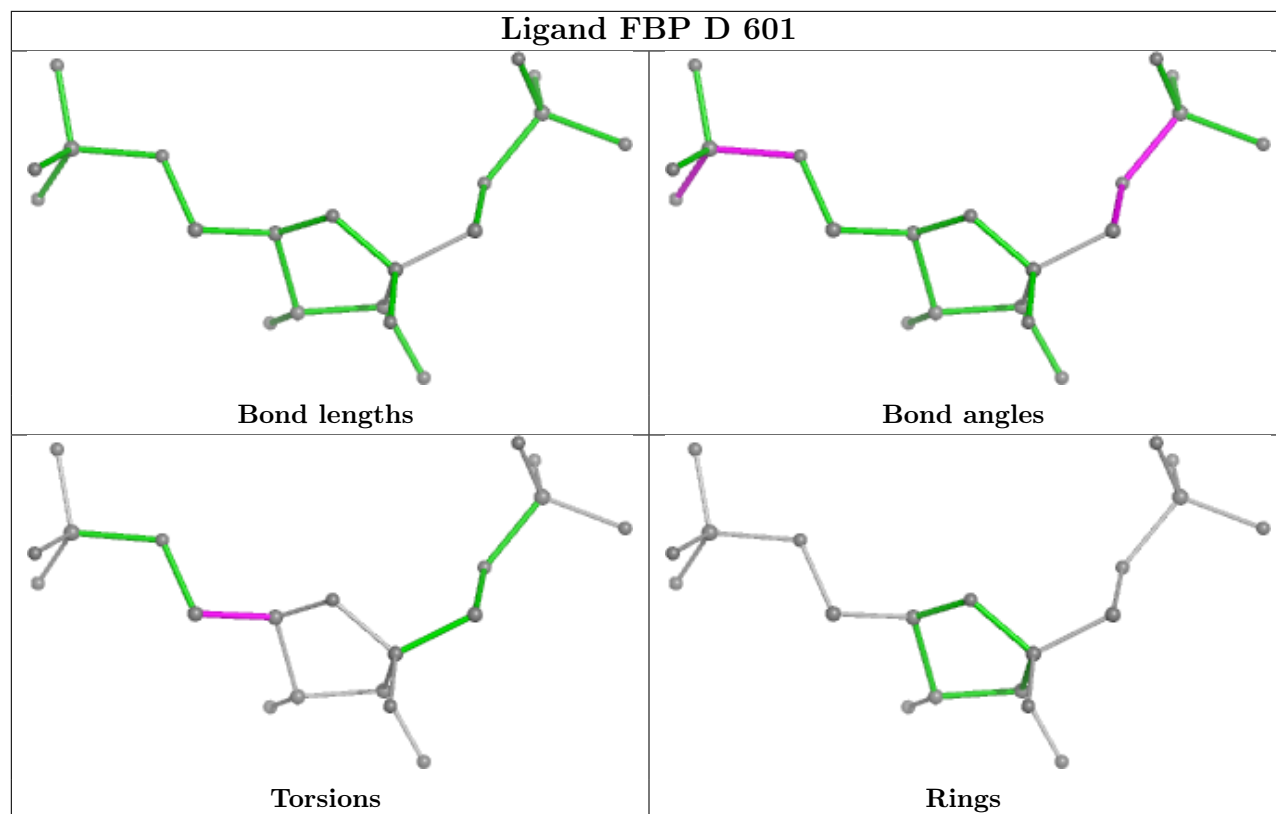


Ligand FBP H 601

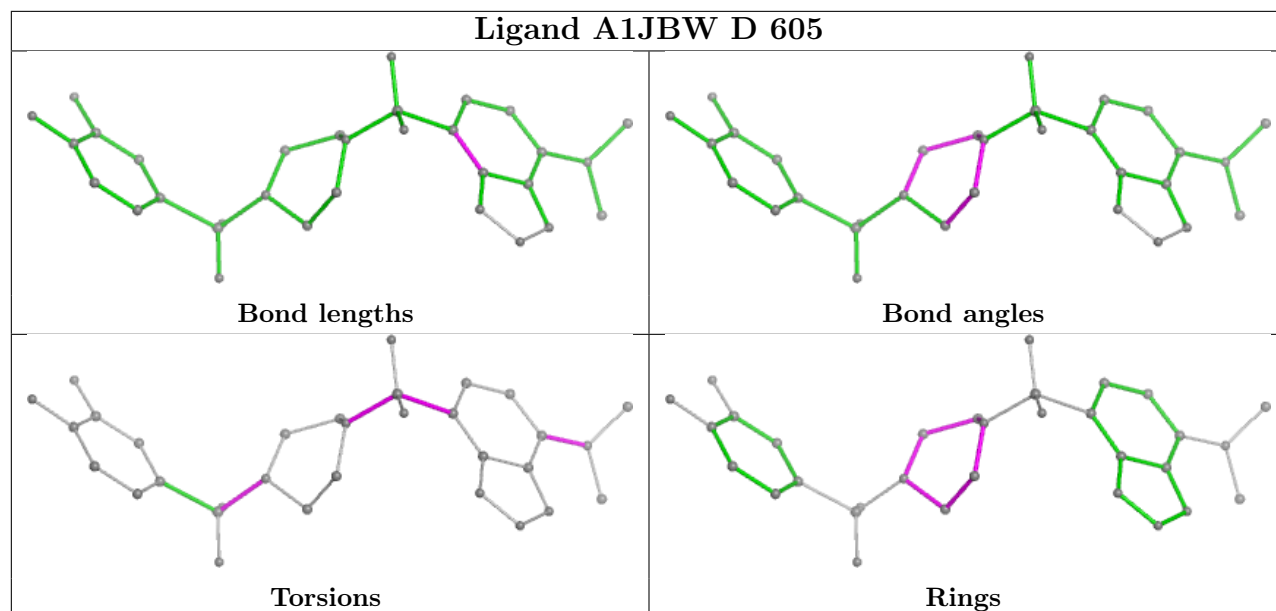


Ligand FBP B 601

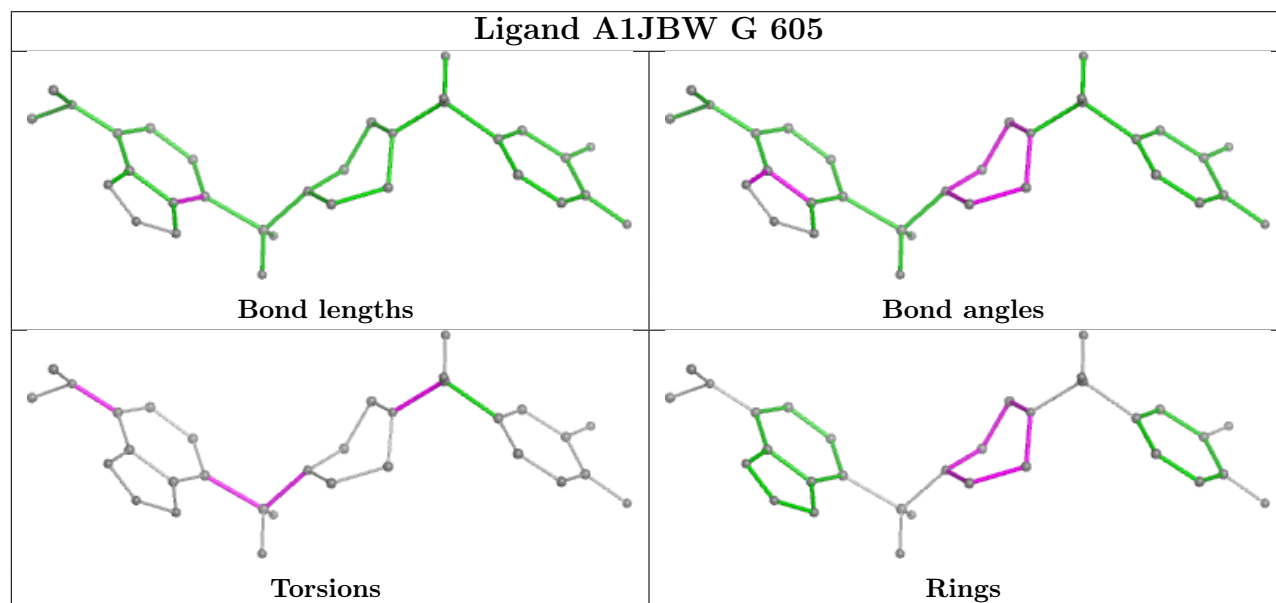


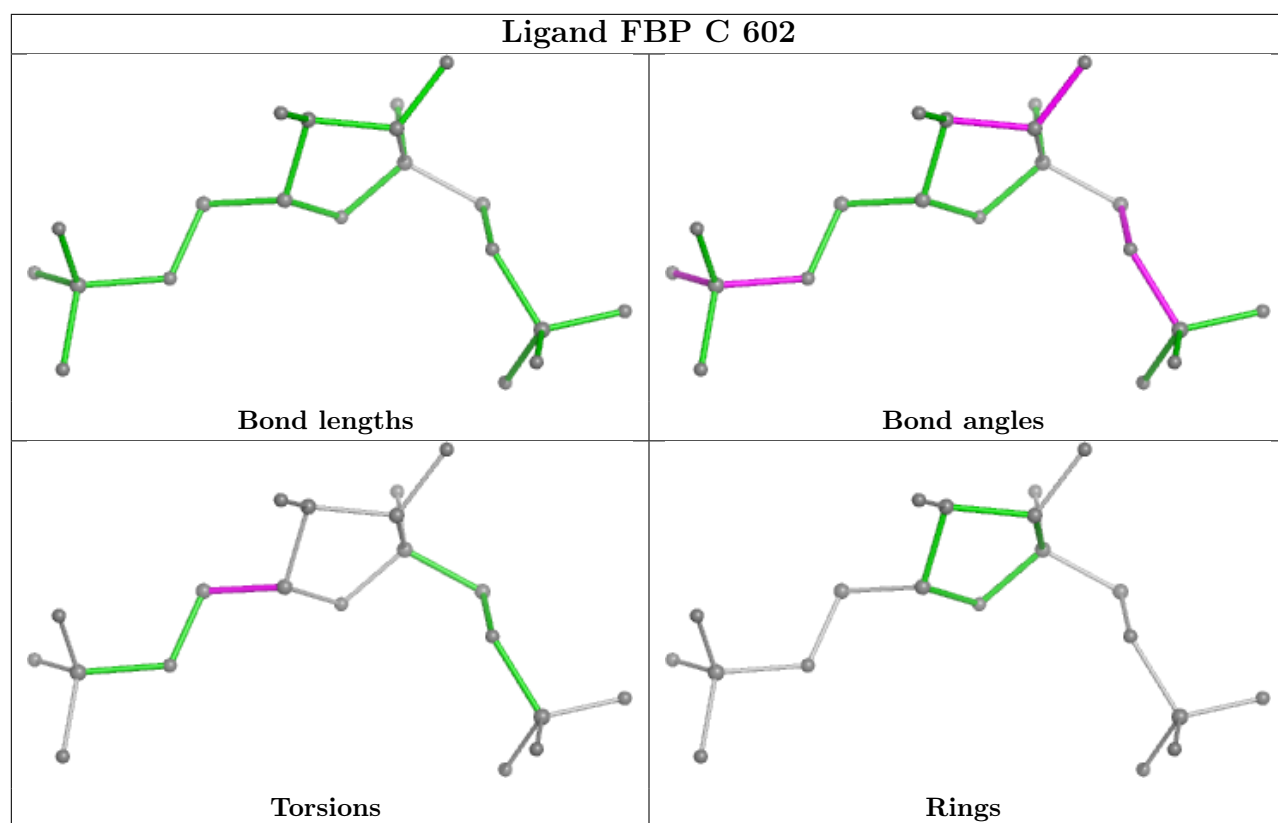


Ligand A1JBW D 605



Ligand A1JBW G 605





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	423/447 (94%)	0.78	44 (10%)	13 13	20, 41, 71, 92	6 (1%)
1	B	436/447 (97%)	0.37	20 (4%)	38 40	17, 34, 59, 77	4 (0%)
1	C	427/447 (95%)	0.23	25 (5%)	29 31	15, 31, 58, 99	4 (0%)
1	D	425/447 (95%)	-0.06	16 (3%)	44 46	12, 25, 50, 97	6 (1%)
1	E	423/447 (94%)	0.82	56 (13%)	8 8	19, 40, 72, 83	5 (1%)
1	F	435/447 (97%)	0.49	30 (6%)	24 26	20, 36, 63, 86	7 (1%)
1	G	423/447 (94%)	-0.06	10 (2%)	59 61	14, 27, 46, 68	7 (1%)
1	H	425/447 (95%)	-0.08	16 (3%)	44 46	13, 26, 49, 79	4 (0%)
All	All	3417/3576 (95%)	0.31	217 (6%)	27 28	12, 33, 62, 99	43 (1%)

All (217) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	25	PHE	7.5
1	E	114	PRO	7.5
1	D	25	PHE	7.1
1	G	25	PHE	6.5
1	E	115	LEU	6.5
1	E	23	ALA	5.8
1	H	21	GLY	5.7
1	A	231	PRO	5.5
1	D	22	THR	5.5
1	E	112	GLY	5.1
1	C	20	LEU	5.1
1	C	21	GLY	4.9
1	E	117	TYR	4.9
1	A	24	PHE	4.9
1	C	22	THR	4.9
1	H	25	PHE	4.8

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Mol	Chain	Res	Type	RSRZ
1	A	543	SER	4.8
1	E	116	SER	4.8
1	D	21	GLY	4.7
1	E	111	ALA	4.7
1	G	271	GLY	4.6
1	C	229	SER	4.6
1	A	112	GLY	4.6
1	E	25	PHE	4.5
1	F	231	PRO	4.4
1	C	25	PHE	4.4
1	A	238	VAL	4.4
1	A	115	LEU	4.3
1	F	267[A]	ARG	4.3
1	D	24	PHE	4.2
1	E	229	SER	4.2
1	E	490	PRO	4.2
1	A	23	ALA	4.2
1	B	231	PRO	4.2
1	C	231	PRO	4.2
1	E	232	GLY	4.1
1	C	232	GLY	4.0
1	B	267[A]	ARG	4.0
1	E	230	GLY	4.0
1	G	23	ALA	4.0
1	C	271	GLY	3.9
1	B	12	ASP	3.9
1	C	130	GLY	3.9
1	E	113	SER	3.8
1	G	229	SER	3.8
1	C	111	ALA	3.8
1	H	22	THR	3.8
1	C	24	PHE	3.7
1	F	129	PRO	3.7
1	C	117	TYR	3.7
1	A	95	TYR	3.7
1	C	115	LEU	3.6
1	F	12	ASP	3.6
1	D	23	ALA	3.6
1	H	24	PHE	3.6
1	A	233	LEU	3.5
1	E	231	PRO	3.5
1	F	516	ARG	3.5

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Mol	Chain	Res	Type	RSRZ
1	H	411	ARG	3.5
1	A	117	TYR	3.4
1	A	63	ILE	3.4
1	H	543	SER	3.4
1	A	230	GLY	3.4
1	A	118	ARG	3.4
1	D	275[A]	HIS	3.4
1	E	489	PRO	3.4
1	A	114	PRO	3.3
1	E	495	ALA	3.3
1	C	110	PHE	3.3
1	A	116	SER	3.3
1	E	24	PHE	3.3
1	C	114	PRO	3.3
1	F	487	ARG	3.3
1	A	111	ALA	3.3
1	C	23	ALA	3.3
1	E	269	ALA	3.3
1	G	24	PHE	3.3
1	A	351	ARG	3.3
1	A	34	MET	3.2
1	E	118	ARG	3.2
1	F	490	PRO	3.2
1	B	13	VAL	3.1
1	E	233	LEU	3.1
1	H	23	ALA	3.1
1	H	275[A]	HIS	3.1
1	F	233	LEU	3.1
1	E	351	ARG	3.1
1	D	232	GLY	3.0
1	F	230	GLY	3.0
1	F	492	ALA	3.0
1	E	26	GLN	3.0
1	A	232	GLY	3.0
1	H	232	GLY	3.0
1	A	113	SER	3.0
1	E	110	PHE	3.0
1	H	412	ARG	3.0
1	C	34	MET	3.0
1	E	109	SER	3.0
1	B	507	GLU	2.9
1	G	412	ARG	2.9

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Mol	Chain	Res	Type	RSRZ
1	H	231	PRO	2.9
1	E	540	LEU	2.9
1	F	351	ARG	2.9
1	F	459	ARG	2.9
1	F	512	ARG	2.9
1	A	237	ASP	2.8
1	A	488[A]	GLU	2.8
1	B	416	LEU	2.8
1	D	30	LEU	2.8
1	E	275	HIS	2.8
1	E	504	PHE	2.8
1	D	130	GLY	2.8
1	G	231	PRO	2.8
1	E	487	ARG	2.8
1	E	492	ALA	2.8
1	E	493	ILE	2.8
1	G	130	GLY	2.8
1	G	34	MET	2.7
1	H	516	ARG	2.7
1	E	245	VAL	2.7
1	C	26	GLN	2.7
1	C	411	ARG	2.7
1	B	543	SER	2.7
1	F	232	GLY	2.7
1	F	489	PRO	2.6
1	F	268	ALA	2.6
1	A	236	GLN	2.6
1	F	275	HIS	2.6
1	A	241	LEU	2.6
1	H	130	GLY	2.5
1	B	490	PRO	2.5
1	F	229	SER	2.5
1	E	265	ALA	2.5
1	C	70	VAL	2.5
1	E	103	VAL	2.5
1	F	493	ILE	2.4
1	E	130	GLY	2.4
1	A	540	LEU	2.4
1	E	238	VAL	2.4
1	D	231	PRO	2.4
1	D	543	SER	2.4
1	B	512	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	412	ARG	2.4
1	E	75	GLU	2.4
1	B	348	THR	2.4
1	E	257	VAL	2.4
1	A	412	ARG	2.4
1	D	459	ARG	2.4
1	E	244	GLY	2.4
1	F	15	GLN	2.4
1	A	270	LEU	2.4
1	E	270	LEU	2.4
1	D	26	GLN	2.4
1	E	241	LEU	2.3
1	A	120	VAL	2.3
1	B	455	ARG	2.3
1	C	116	SER	2.3
1	F	238	VAL	2.3
1	B	236	GLN	2.3
1	H	26	GLN	2.3
1	D	233	LEU	2.3
1	B	275	HIS	2.3
1	F	13	VAL	2.3
1	B	487	ARG	2.3
1	E	512	ARG	2.3
1	A	378	ALA	2.3
1	F	503	GLN	2.3
1	E	70	VAL	2.3
1	F	11	ALA	2.3
1	D	489	PRO	2.2
1	E	71	GLU	2.2
1	B	232	GLY	2.2
1	F	543	SER	2.2
1	E	500	ARG	2.2
1	A	311	ILE	2.2
1	C	27	GLN	2.2
1	A	75	GLU	2.2
1	A	30	LEU	2.2
1	A	109	SER	2.2
1	E	97	ALA	2.2
1	F	379	LYS	2.2
1	F	507	GLU	2.1
1	C	113	SER	2.1
1	E	412	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	272	PRO	2.1
1	A	26	GLN	2.1
1	E	120	VAL	2.1
1	B	484	LEU	2.1
1	E	514	PHE	2.1
1	H	514	PHE	2.1
1	A	262	ASP	2.1
1	E	508	SER	2.1
1	F	94	GLU	2.1
1	E	107	VAL	2.1
1	F	484	LEU	2.1
1	C	109	SER	2.1
1	E	34	MET	2.1
1	B	95	TYR	2.1
1	H	273	GLU	2.1
1	E	249	VAL	2.1
1	E	266	VAL	2.1
1	E	499	ASP	2.1
1	A	90	HIS	2.1
1	A	275	HIS	2.1
1	A	66	ALA	2.0
1	A	274	GLY	2.0
1	C	66	ALA	2.0
1	A	68	ARG	2.0
1	B	516	ARG	2.0
1	E	309	LEU	2.0
1	G	232	GLY	2.0
1	A	269	ALA	2.0
1	A	272	PRO	2.0
1	A	489	PRO	2.0
1	B	415	PRO	2.0
1	E	272	PRO	2.0
1	F	90	HIS	2.0

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 oligosaccharides in this entry.

6.4 Ligands ⓘ

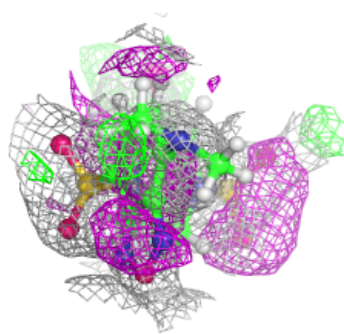
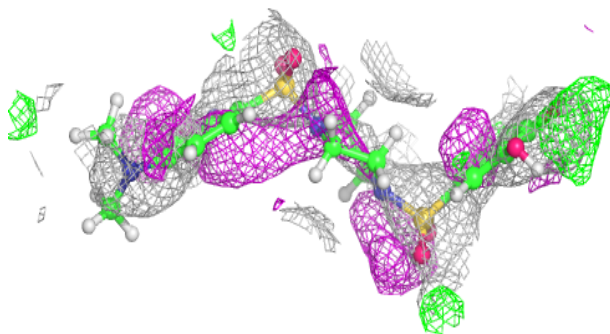
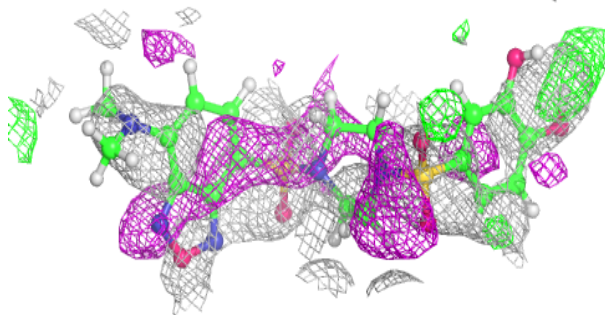
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	A1JBW	H	605	32/32	0.76	0.27	90,92,92,92	21
6	A1JBW	G	605	32/32	0.78	0.25	89,92,93,93	21
6	A1JBW	D	605	32/32	0.78	0.24	74,77,79,81	21
3	OXL	A	602	6/6	0.86	0.12	48,49,50,50	0
3	OXL	E	602	6/6	0.86	0.14	56,56,57,57	0
6	A1JBW	C	601	32/32	0.86	0.18	63,68,68,68	21
3	OXL	B	602	6/6	0.89	0.10	36,37,38,39	0
3	OXL	C	603	6/6	0.91	0.09	45,46,46,46	0
3	OXL	F	602	6/6	0.91	0.12	61,61,62,62	0
4	MG	F	603	1/1	0.93	0.14	35,35,35,35	0
2	FBP	E	601	20/20	0.94	0.08	33,34,37,38	0
5	K	B	604	1/1	0.94	0.07	53,53,53,53	0
3	OXL	G	602	6/6	0.94	0.07	30,31,31,31	0
3	OXL	D	602	6/6	0.95	0.11	28,29,30,31	0
2	FBP	A	601	20/20	0.95	0.07	33,34,35,36	0
3	OXL	H	602	6/6	0.95	0.08	32,33,34,34	0
2	FBP	B	601	20/20	0.96	0.06	27,30,32,32	0
2	FBP	F	601	20/20	0.96	0.07	29,34,37,37	0
4	MG	A	603	1/1	0.96	0.13	37,37,37,37	0
4	MG	B	603	1/1	0.97	0.11	30,30,30,30	0
5	K	A	604	1/1	0.97	0.06	54,54,54,54	0
4	MG	E	603	1/1	0.97	0.12	34,34,34,34	0
5	K	E	604	1/1	0.97	0.06	56,56,56,56	0
5	K	F	604	1/1	0.98	0.05	57,57,57,57	0
5	K	G	604	1/1	0.98	0.07	35,35,35,35	0
5	K	H	604	1/1	0.98	0.03	33,33,33,33	0
2	FBP	C	602	20/20	0.98	0.04	18,19,24,25	0
2	FBP	D	601	20/20	0.98	0.05	19,20,24,24	0
5	K	C	605	1/1	0.98	0.05	41,41,41,41	0
2	FBP	H	601	20/20	0.98	0.05	18,20,23,24	0
2	FBP	G	601	20/20	0.99	0.04	18,19,21,21	0
4	MG	C	604	1/1	0.99	0.05	26,26,26,26	0
4	MG	H	603	1/1	0.99	0.05	16,16,16,16	0
5	K	D	604	1/1	0.99	0.02	30,30,30,30	0
4	MG	G	603	1/1	1.00	0.06	15,15,15,15	0
4	MG	D	603	1/1	1.00	0.05	19,19,19,19	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.

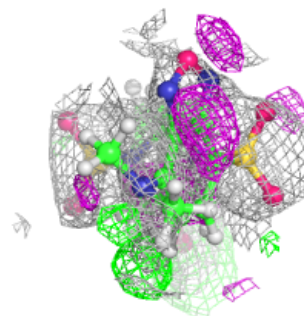
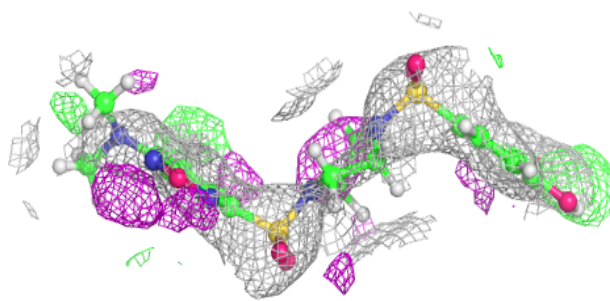
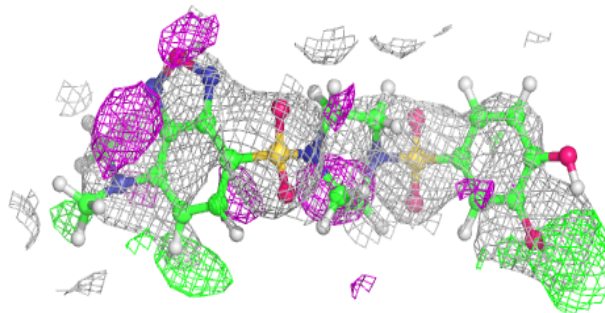
Electron density around A1JBW H 605:

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

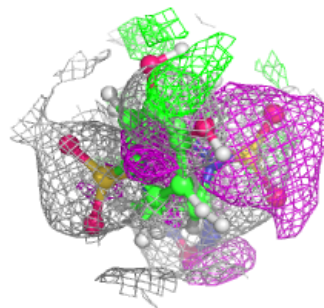
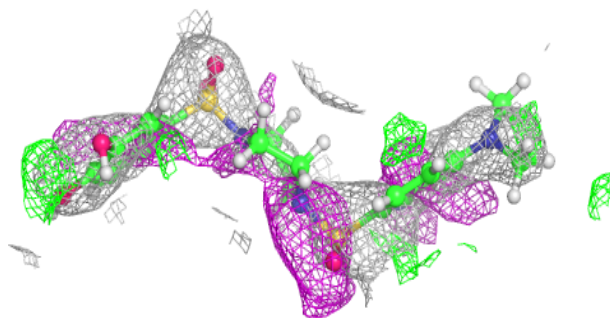
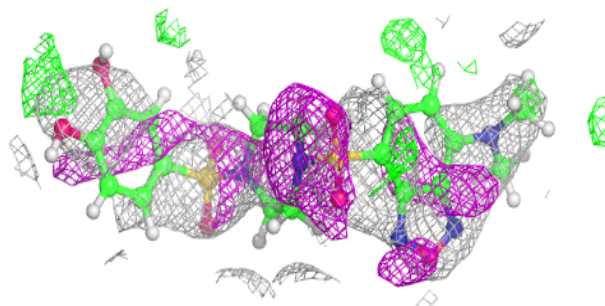


Electron density around A1JBW G 605:

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

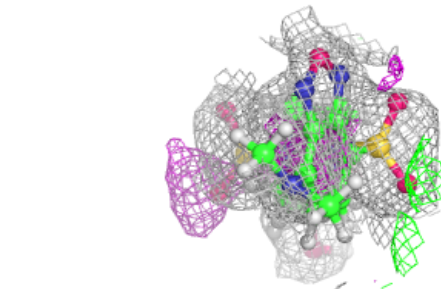
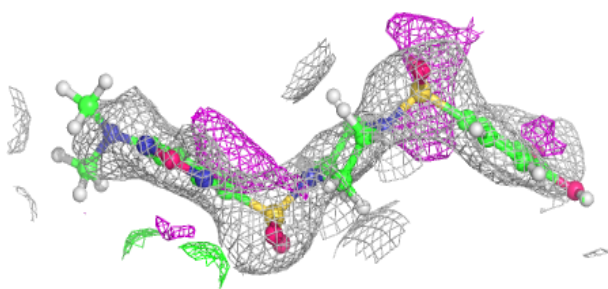
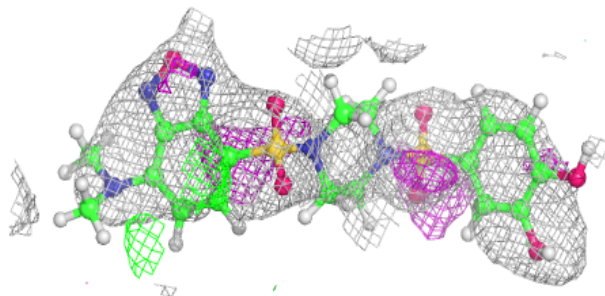
**Electron density around A1JBW D 605:**

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

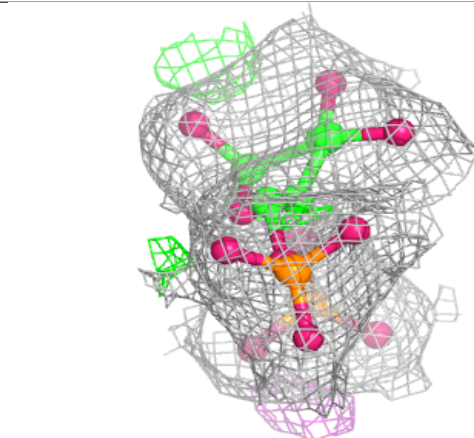
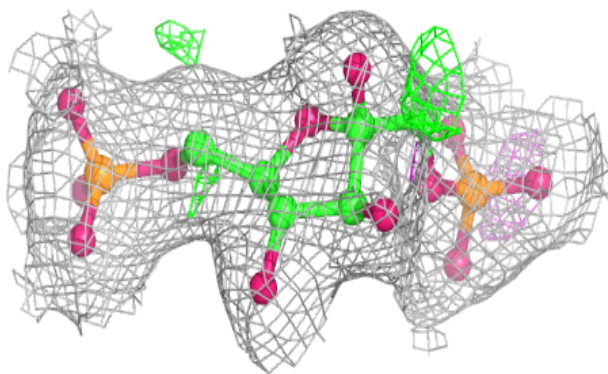
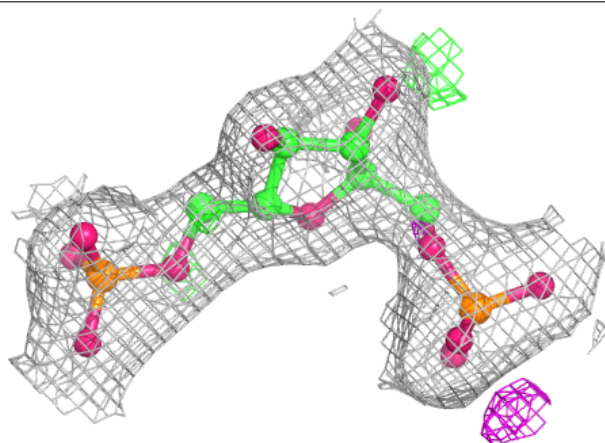


Electron density around A1JBW C 601:

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

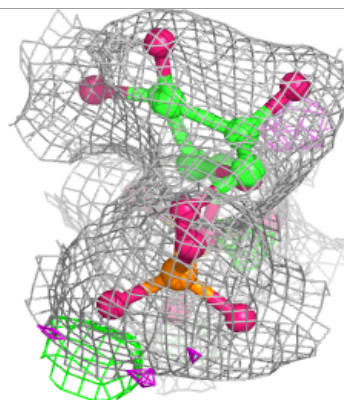
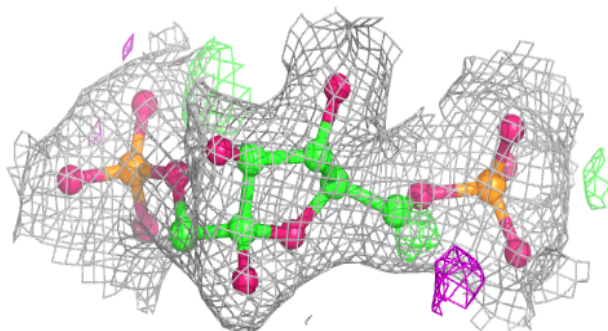
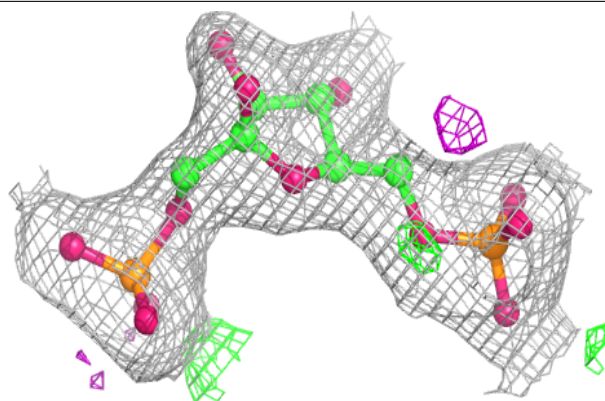
**Electron density around FBP E 601:**

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

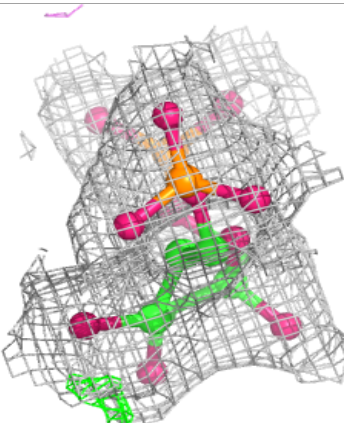
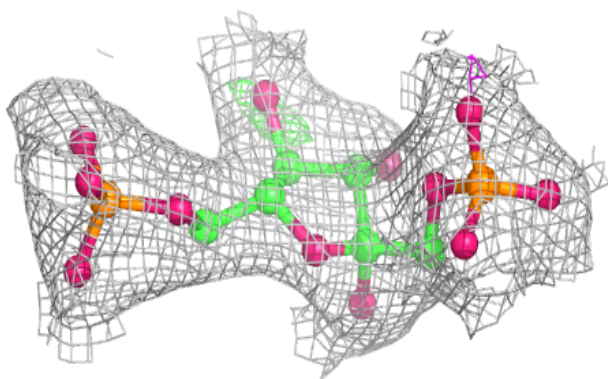
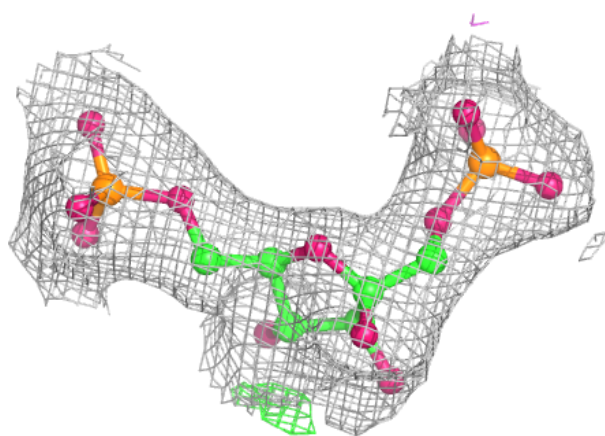


Electron density around FBP A 601:

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

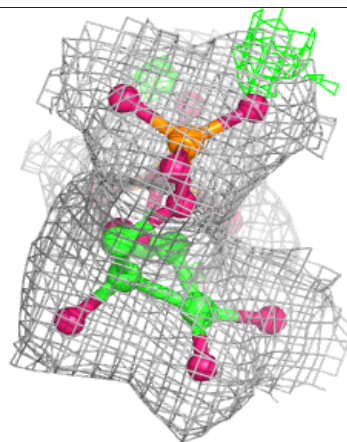
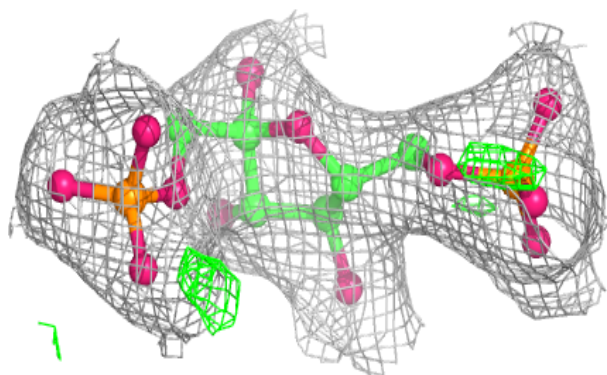
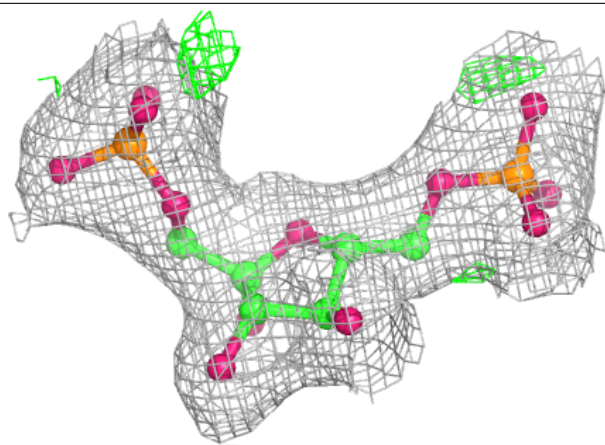
**Electron density around FBP B 601:**

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

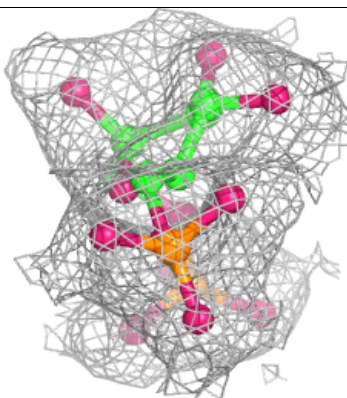
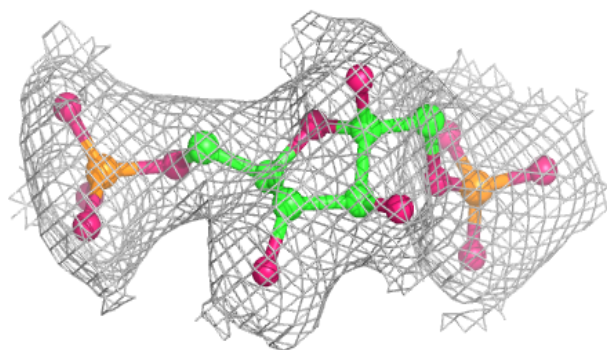
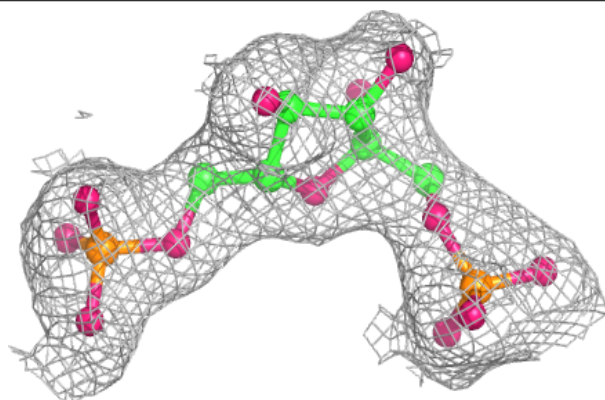


Electron density around FBP F 601:

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

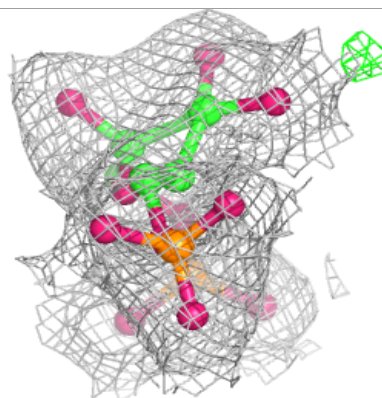
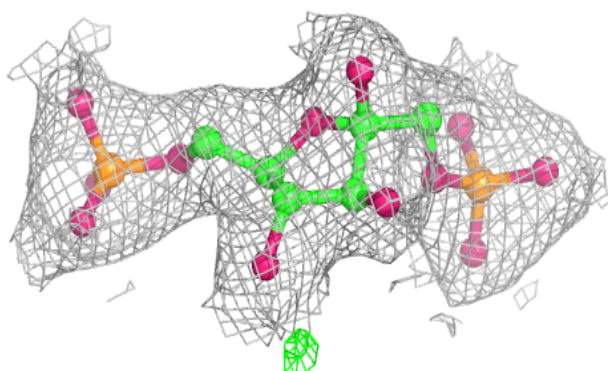
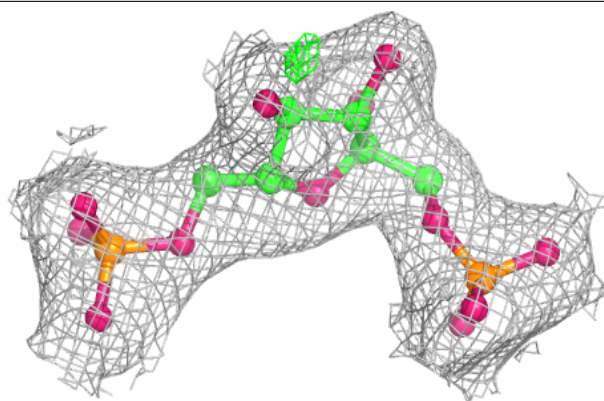
**Electron density around FBP C 602:**

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

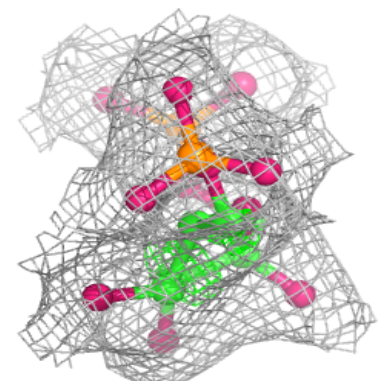
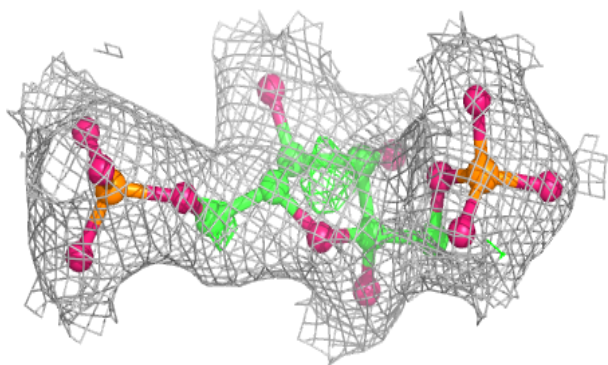
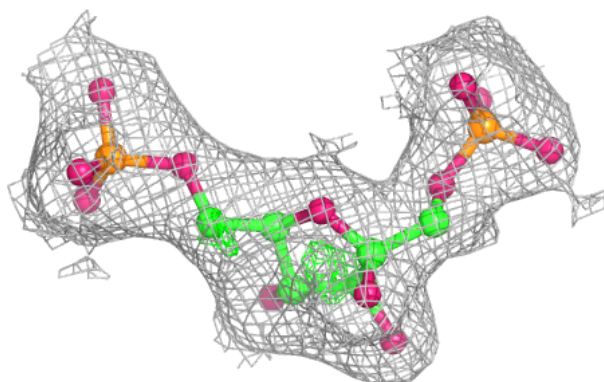


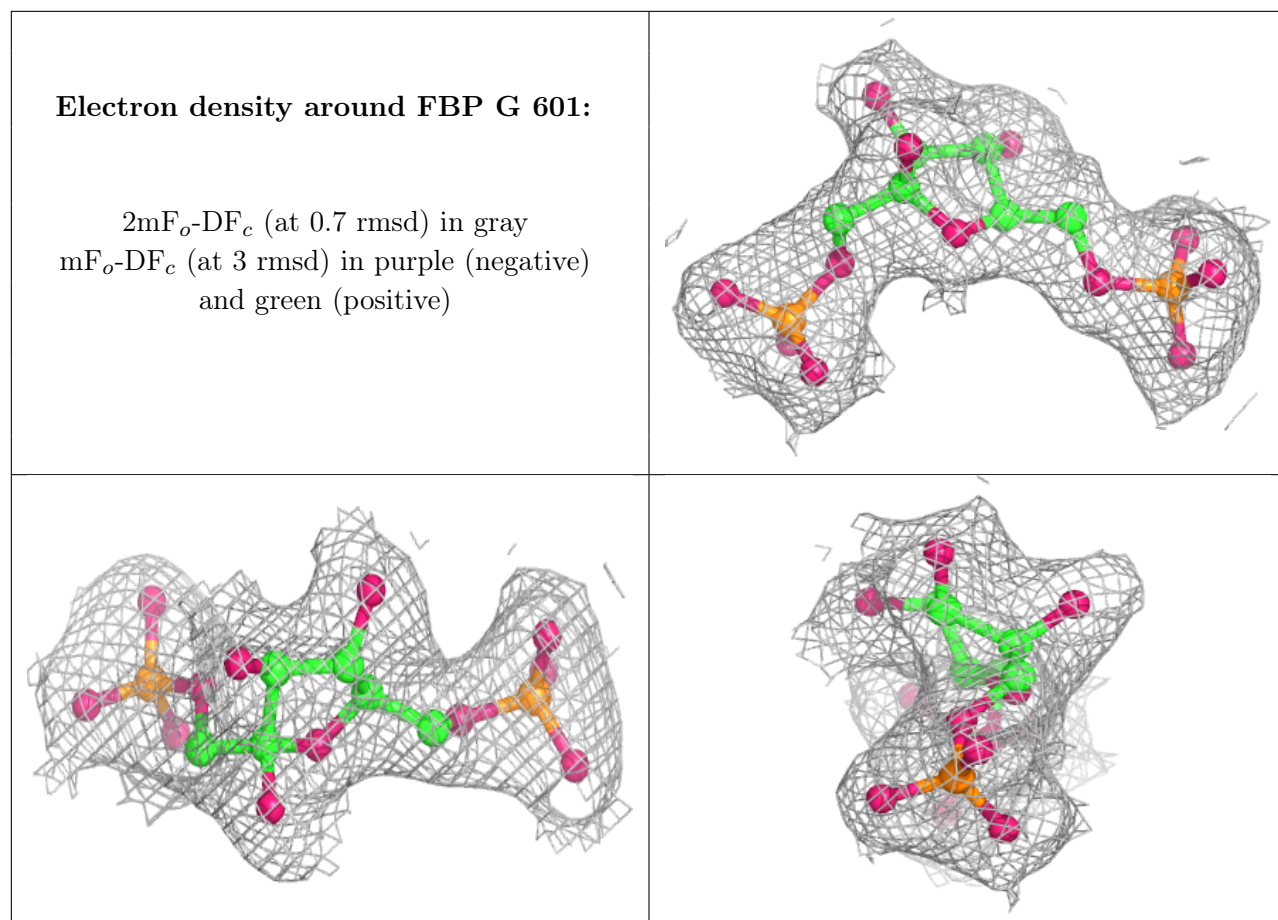
Electron density around FBP D 601:

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

**Electron density around FBP H 601:**

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





6.5 Other polymers ⓘ

There are no such residues in this entry.