



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 04:45 PM UTC

PDB ID : 8HJT / pdb_00008hjt
Title : Crystal Structure of Intracellular B30.2 Domain of VpBTN3 and VpBTN2 in Complex with HMBPP
Authors : Yang, Y.Y.; Shen, P.P.; Li, X.; Yi, S.M.; Zhang, M.T.; Huang, J.-W.; Chen, C.-C.; Guo, R.-T.
Deposited on : 2022-11-23
Resolution : 2.91 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

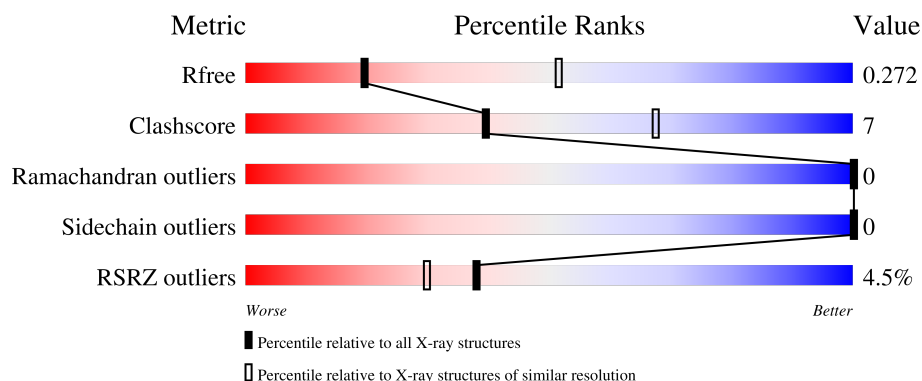
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.91 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	2995 (2.94-2.90)
Clashscore	190562	3213 (2.94-2.90)
Ramachandran outliers	187476	3128 (2.94-2.90)
Sidechain outliers	187428	3130 (2.94-2.90)
RSRZ outliers	180081	2995 (2.94-2.90)

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	233	2% 70% 14% 15%
1	B	233	12% 63% 21% 16%
2	C	198	86% 5% 9%
2	D	198	2% 73% 17% 10%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6181 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 butyrophilin subfamily 2 member A2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	197	Total	C	N	O	S	0	0	0
			1570	995	279	288	8			
1	B	195	Total	C	N	O	S	0	0	0
			1554	986	277	283	8			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	305	GLY	-	expression tag	UNP A0A6J0B3M7
A	306	ALA	-	expression tag	UNP A0A6J0B3M7
A	307	GLY	-	expression tag	UNP A0A6J0B3M7
A	308	ALA	-	expression tag	UNP A0A6J0B3M7
A	309	GLY	-	expression tag	UNP A0A6J0B3M7
A	310	ALA	-	expression tag	UNP A0A6J0B3M7
A	536	LEU	-	expression tag	UNP A0A6J0B3M7
A	537	GLU	-	expression tag	UNP A0A6J0B3M7
B	305	GLY	-	expression tag	UNP A0A6J0B3M7
B	306	ALA	-	expression tag	UNP A0A6J0B3M7
B	307	GLY	-	expression tag	UNP A0A6J0B3M7
B	308	ALA	-	expression tag	UNP A0A6J0B3M7
B	309	GLY	-	expression tag	UNP A0A6J0B3M7
B	310	ALA	-	expression tag	UNP A0A6J0B3M7
B	536	LEU	-	expression tag	UNP A0A6J0B3M7
B	537	GLU	-	expression tag	UNP A0A6J0B3M7

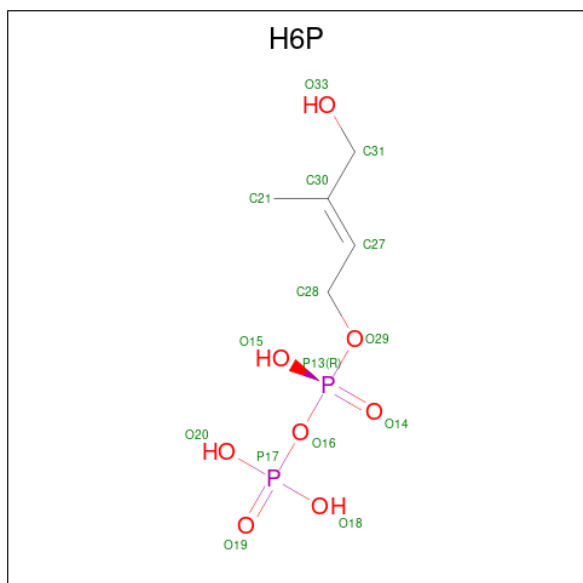
- Molecule 2 is a protein called Butyrophilin 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	180	Total	C	N	O	S	0	0	0
			1457	932	250	268	7			
2	D	178	Total	C	N	O	S	0	0	0
			1443	923	247	266	7			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	316	GLY	-	expression tag	UNP A0A345DF50
C	317	ALA	-	expression tag	UNP A0A345DF50
C	318	GLY	-	expression tag	UNP A0A345DF50
C	319	ALA	-	expression tag	UNP A0A345DF50
C	320	GLY	-	expression tag	UNP A0A345DF50
D	316	GLY	-	expression tag	UNP A0A345DF50
D	317	ALA	-	expression tag	UNP A0A345DF50
D	318	GLY	-	expression tag	UNP A0A345DF50
D	319	ALA	-	expression tag	UNP A0A345DF50
D	320	GLY	-	expression tag	UNP A0A345DF50

- Molecule 3 is (2E)-4-hydroxy-3-methylbut-2-en-1-yl trihydrogen diphosphate (CCD ID: H6P) (formula: $C_5H_{12}O_8P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	C	1	Total	C	O	P	0	0
			15	5	8	2		
3	D	1	Total	C	O	P	0	0
			15	5	8	2		

- Molecule 4 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: $C_8H_{18}N_2O_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	C	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

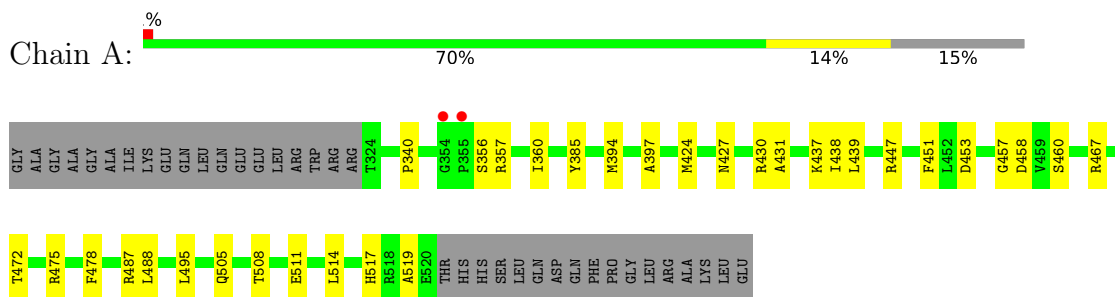
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	30	Total	O	0	0
			30	30		
5	B	12	Total	O	0	0
			12	12		
5	C	52	Total	O	0	0
			52	52		
5	D	18	Total	O	0	0
			18	18		

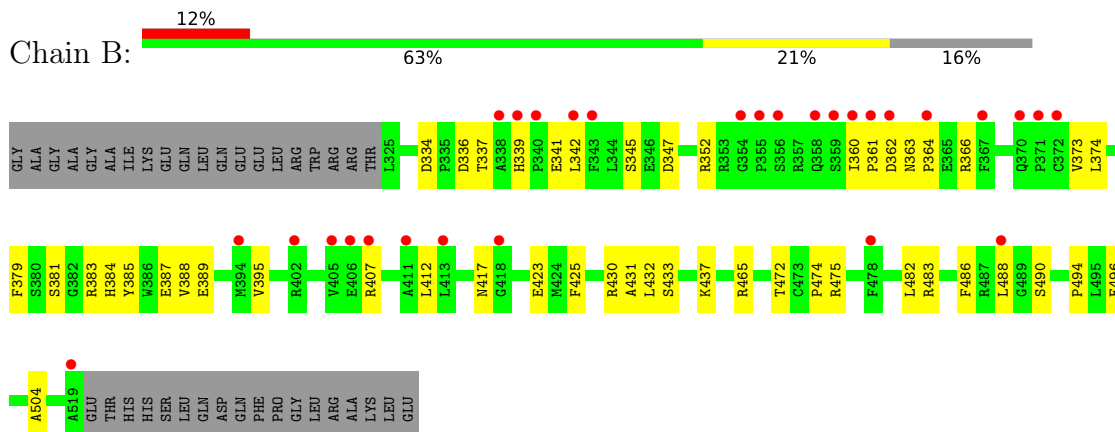
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

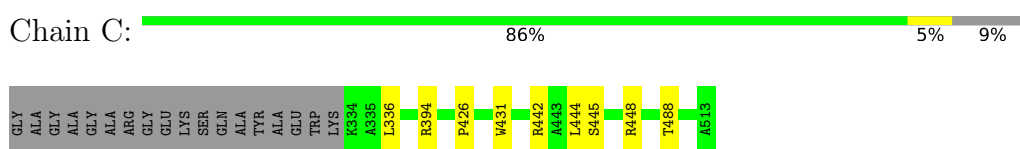
- Molecule 1: butyrophilin subfamily 2 member A2



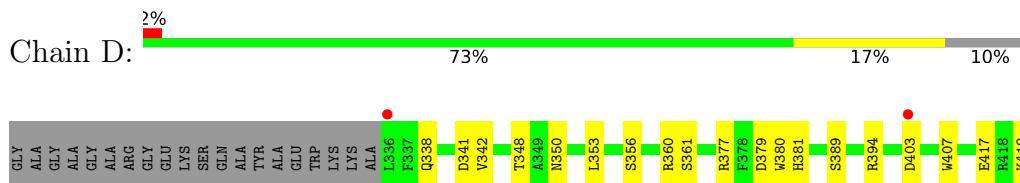
- Molecule 1: butyrophilin subfamily 2 member A2

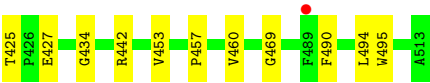


- Molecule 2: Butyrophilin 3



- Molecule 2: Butyrophilin 3





4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	78.19Å 78.19Å 299.83Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	34.66 – 2.91 34.66 – 2.91	Depositor EDS
% Data completeness (in resolution range)	95.9 (34.66-2.91) 95.8 (34.66-2.91)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.35 (at 2.90Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.222 , 0.274 0.223 , 0.272	Depositor DCC
R_{free} test set	1197 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	37.0	Xtriage
Anisotropy	0.766	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 50.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.055 for -h,-k,l	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	6181	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.52% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: H6P, EPE

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	0.11	0/1614	0.30	0/2192
1	B	0.14	0/1598	0.39	0/2170
2	C	0.11	0/1503	0.29	0/2052
2	D	0.11	0/1489	0.30	0/2034
All	All	0.12	0/6204	0.32	0/8448

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1570	0	1518	23	0
1	B	1554	0	1505	36	0
2	C	1457	0	1394	7	0
2	D	1443	0	1376	21	0
3	C	15	0	9	2	0
3	D	15	0	9	4	0
4	C	15	0	17	1	0
5	A	30	0	0	0	0
5	B	12	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	C	52	0	0	0	0
5	D	18	0	0	0	0
All	All	6181	0	5828	80	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 7.

All (80) 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:360:ILE:HG13	1:B:361:PRO:HD2	1.67	0.75
2:D:425:THR:HG22	2:D:427:GLU:H	1.53	0.71
2:C:336:LEU:O	2:C:394:ARG:NH1	2.26	0.68
1:A:385:TYR:OH	1:B:385:TYR:OH	2.12	0.68
1:B:412:LEU:O	1:B:417:ASN:ND2	2.32	0.63
1:B:336:ASP:O	1:B:366:ARG:HB3	2.00	0.61
1:B:423:GLU:OE1	1:B:433:SER:OG	2.19	0.60
1:A:397:ALA:HB3	1:A:487:ARG:HB3	1.84	0.60
1:B:363:ASN:H	1:B:366:ARG:HD2	1.69	0.58
2:D:350:ASN:ND2	2:D:381:HIS:O	2.35	0.58
1:A:447:ARG:NH2	1:B:465:ARG:O	2.30	0.57
1:B:345:SER:OG	1:B:347:ASP:OD1	2.23	0.57
2:D:379:ASP:HB3	2:D:419:LYS:HA	1.87	0.56
1:A:437:LYS:HE3	1:A:439:LEU:HD23	1.87	0.56
1:A:340:PRO:HA	1:A:360:ILE:HD11	1.88	0.56
1:B:360:ILE:HG13	1:B:361:PRO:CD	2.36	0.55
2:D:417:GLU:HB3	2:D:422:VAL:HG21	1.88	0.55
1:B:423:GLU:OE2	1:B:425:PHE:HB2	2.07	0.55
1:A:424:MET:HE3	1:A:427:ASN:HA	1.90	0.54
1:A:467:ARG:NH1	1:B:387:GLU:OE2	2.40	0.54
2:C:394:ARG:NH2	4:C:602:EPE:O2S	2.41	0.53
1:B:339:HIS:ND1	1:B:341:GLU:HG2	2.23	0.53
2:D:389:SER:HB3	2:D:495:TRP:CE2	2.44	0.53
1:B:475:ARG:NE	3:D:601:H6P:O14	2.41	0.53
1:A:511:GLU:OE1	2:D:423:LYS:NZ	2.36	0.52
1:A:431:ALA:HB3	1:A:437:LYS:HG3	1.91	0.52
1:B:352:ARG:HB2	1:B:494:PRO:HB3	1.91	0.52
1:A:505:GLN:OE1	1:B:383:ARG:NH2	2.43	0.52
2:D:342:VAL:O	2:D:360:ARG:NH1	2.43	0.52
1:A:453:ASP:HB3	1:A:458:ASP:HB3	1.92	0.51
2:C:444:LEU:HA	2:C:448:ARG:HD2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:334:ASP:OD2	1:B:337:THR:HG23	2.11	0.50
1:B:374:LEU:HD23	1:B:483:ARG:HD2	1.93	0.49
1:B:363:ASN:OD1	1:B:366:ARG:HG2	2.14	0.48
2:D:380:TRP:CZ3	2:D:421:TRP:HD1	2.32	0.48
1:A:394:MET:O	1:A:424:MET:HG2	2.13	0.48
1:A:430:ARG:HG2	1:A:438:ILE:HD13	1.95	0.48
2:D:407:TRP:CZ3	2:D:434:GLY:HA2	2.48	0.48
1:A:451:PHE:HB3	1:A:460:SER:HB2	1.96	0.47
2:D:341:ASP:OD1	2:D:360:ARG:NH2	2.33	0.47
2:D:356:SER:HB2	2:D:361:SER:HB2	1.96	0.47
1:A:475:ARG:NE	3:C:601:H6P:O15	2.44	0.47
2:D:442:ARG:NH2	3:D:601:H6P:O20	2.40	0.47
1:A:514:LEU:HB3	1:B:472:THR:HB	1.96	0.46
1:B:366:ARG:O	1:B:407:ARG:HB3	2.15	0.46
1:B:388:VAL:HG21	1:B:486:PHE:HE2	1.80	0.46
1:B:395:VAL:H	1:B:490:SER:HB2	1.80	0.46
1:B:363:ASN:HB2	1:B:364:PRO:HD2	1.97	0.46
2:C:431:TRP:CZ2	2:C:488:THR:HG21	2.51	0.46
2:D:490:PHE:CD1	2:D:494:LEU:HD11	2.51	0.45
1:A:488:LEU:HD13	1:A:495:LEU:HG	1.97	0.45
1:A:356:SER:OG	1:A:357:ARG:N	2.50	0.45
2:C:442:ARG:NH2	3:C:601:H6P:O19	2.40	0.45
2:C:445:SER:O	2:C:448:ARG:HD3	2.17	0.45
1:B:379:PHE:N	1:B:482:LEU:O	2.47	0.45
1:A:437:LYS:HA	1:A:437:LYS:HD2	1.76	0.45
1:A:508:THR:HG23	3:D:601:H6P:O16	2.17	0.44
1:B:362:ASP:HA	1:B:366:ARG:HD2	1.99	0.44
1:B:342:LEU:HD21	1:B:488:LEU:HB3	2.00	0.44
1:B:432:LEU:HD21	1:B:474:PRO:HD2	1.98	0.44
2:D:338:GLN:HG3	2:D:394:ARG:O	2.18	0.43
2:D:407:TRP:CH2	2:D:460:VAL:HG21	2.52	0.43
2:D:453:VAL:HG11	2:D:457:PRO:HD3	1.99	0.43
2:D:381:HIS:CE1	3:D:601:H6P:H27	2.54	0.43
1:B:361:PRO:O	1:B:366:ARG:HD2	2.19	0.43
1:A:517:HIS:NE2	1:A:519:ALA:HB2	2.33	0.42
1:B:431:ALA:C	1:B:433:SER:H	2.27	0.42
1:B:373:VAL:HG13	1:B:486:PHE:HB2	2.01	0.42
1:B:374:LEU:HB3	1:B:483:ARG:HD3	2.01	0.42
1:B:389:GLU:HB2	1:B:496:PHE:HB2	2.01	0.42
1:A:472:THR:HG21	1:B:504:ALA:HB2	2.01	0.42
1:B:437:LYS:HD2	1:B:437:LYS:HA	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:430:ARG:HH21	1:B:433:SER:C	2.28	0.41
1:B:381:SER:O	1:B:384:HIS:NE2	2.54	0.41
1:A:457:GLY:HA2	1:A:478:PHE:CE2	2.56	0.41
2:D:350:ASN:HB3	2:D:353:LEU:HG	2.03	0.41
2:D:469:GLY:HA2	2:D:490:PHE:CE2	2.55	0.41
2:D:403:ASP:OD2	2:D:403:ASP:N	2.53	0.40
2:C:426:PRO:HB3	2:C:431:TRP:NE1	2.35	0.40
2:D:348:THR:HA	2:D:377:ARG:HA	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	195/233 (84%)	188 (96%)	7 (4%)	0	100	100
1	B	193/233 (83%)	179 (93%)	14 (7%)	0	100	100
2	C	178/198 (90%)	173 (97%)	5 (3%)	0	100	100
2	D	176/198 (89%)	171 (97%)	5 (3%)	0	100	100
All	All	742/862 (86%)	711 (96%)	31 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	173/201 (86%)	173 (100%)	0	100	100
1	B	171/201 (85%)	171 (100%)	0	100	100
2	C	160/169 (95%)	160 (100%)	0	100	100
2	D	159/169 (94%)	159 (100%)	0	100	100
All	All	663/740 (90%)	663 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	427	ASN
2	C	363	GLN
2	C	369	GLN
2	D	347	ASN
2	D	369	GLN
2	D	458	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](#)

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	H6P	C	601	-	13,14,14	1.77	2 (15%)	15,20,20	1.21	1 (6%)
3	H6P	D	601	-	13,14,14	1.78	2 (15%)	15,20,20	1.15	1 (6%)
4	EPE	C	602	-	15,15,15	0.83	1 (6%)	19,20,20	1.63	4 (21%)

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	H6P	C	601	-	-	3/15/15/15	-
3	H6P	D	601	-	-	2/15/15/15	-
4	EPE	C	602	-	-	6/9/19/19	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	601	H6P	P13-O16	5.23	1.65	1.59
3	D	601	H6P	P13-O16	5.21	1.65	1.59
4	C	602	EPE	C10-S	2.77	1.81	1.77
3	C	601	H6P	O29-C28	-2.28	1.40	1.44
3	D	601	H6P	O29-C28	-2.23	1.40	1.44

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	602	EPE	C5-N4-C3	4.15	117.77	108.84
3	C	601	H6P	C28-C27-C30	-3.21	120.93	126.20
4	C	602	EPE	C7-N4-C3	3.13	119.59	111.24
3	D	601	H6P	C28-C27-C30	-2.96	121.35	126.20
4	C	602	EPE	C7-N4-C5	2.54	118.00	111.24
4	C	602	EPE	O1S-S-C10	2.10	109.91	106.73

There are no chirality outliers.

All (11) torsion outliers are listed below:

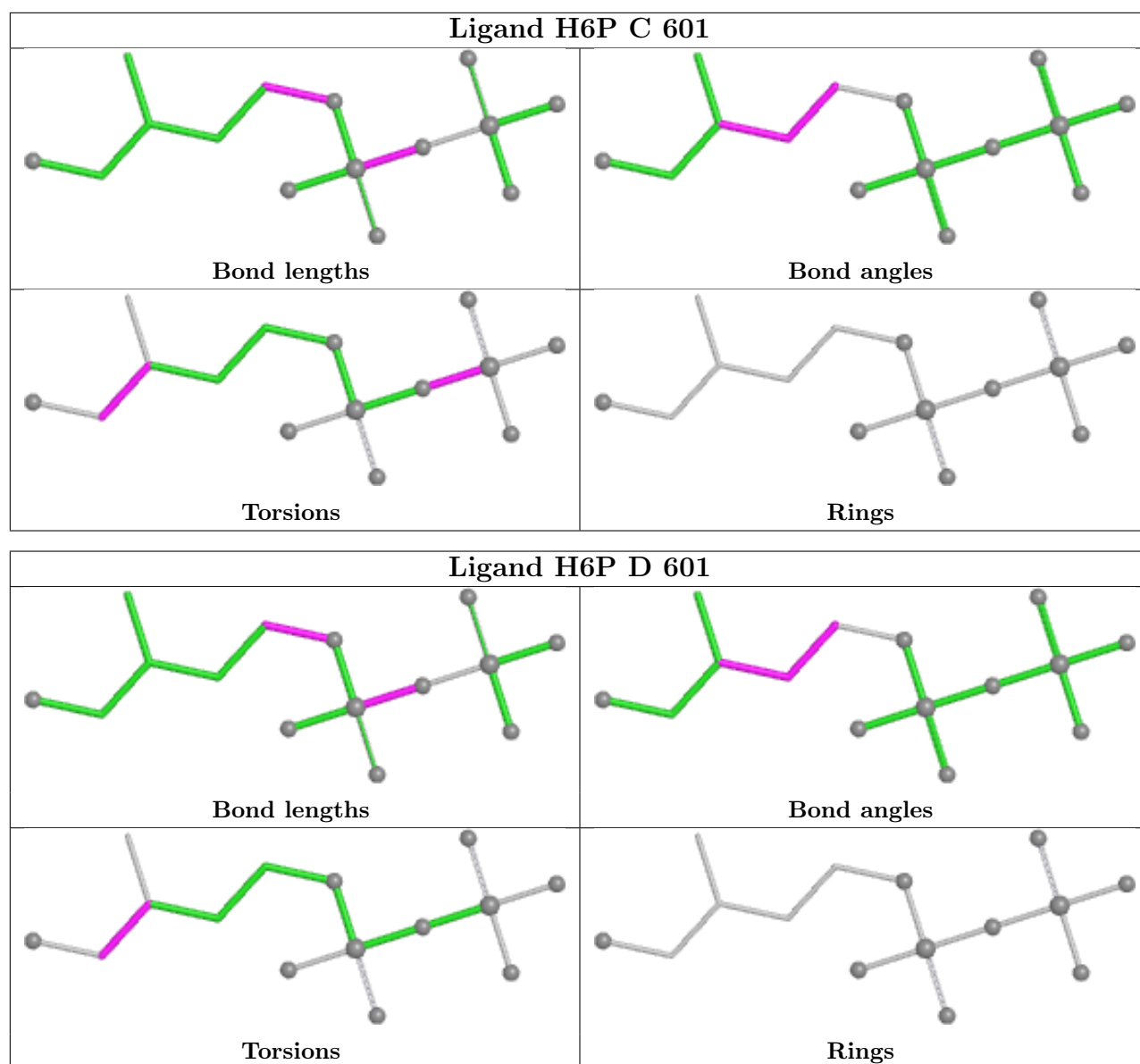
Mol	Chain	Res	Type	Atoms
3	C	601	H6P	C21-C30-C31-O33
3	D	601	H6P	C21-C30-C31-O33
3	D	601	H6P	C27-C30-C31-O33
4	C	602	EPE	C9-C10-S-O1S
4	C	602	EPE	C9-C10-S-O3S
4	C	602	EPE	C10-C9-N1-C2
4	C	602	EPE	C10-C9-N1-C6
3	C	601	H6P	C27-C30-C31-O33
4	C	602	EPE	C9-C10-S-O2S
3	C	601	H6P	P13-O16-P17-O19
4	C	602	EPE	C8-C7-N4-C3

There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	601	H6P	2	0
3	D	601	H6P	4	0
4	C	602	EPE	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.



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	197/233 (84%)	0.07	2 (1%) 79 72	17, 31, 59, 101	0
1	B	195/233 (83%)	0.87	29 (14%) 5 4	17, 50, 83, 98	0
2	C	180/198 (90%)	-0.30	0 100 100	14, 22, 35, 47	0
2	D	178/198 (89%)	0.33	3 (1%) 69 60	21, 38, 55, 68	0
All	All	750/862 (87%)	0.25	34 (4%) 38 30	14, 33, 74, 101	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	372	CYS	4.9
1	B	360	ILE	4.5
1	A	355	PRO	4.4
1	B	367	PHE	4.3
1	B	411	ALA	4.2
1	B	359	SER	4.0
1	B	340	PRO	3.8
1	B	342	LEU	3.7
1	A	354	GLY	3.5
1	B	519	ALA	3.3
1	B	356	SER	3.3
1	B	402	ARG	3.1
1	B	405	VAL	3.1
1	B	355	PRO	3.1
1	B	371	PRO	3.0
1	B	338	ALA	3.0
1	B	370	GLN	2.7
1	B	407	ARG	2.7
1	B	406	GLU	2.7
1	B	361	PRO	2.5
1	B	354	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	362	ASP	2.3
2	D	489	PHE	2.3
1	B	413	LEU	2.3
1	B	339	HIS	2.3
1	B	488	LEU	2.2
1	B	358	GLN	2.2
2	D	336	LEU	2.2
1	B	364	PRO	2.1
1	B	343	PHE	2.1
1	B	394	MET	2.1
1	B	418	GLY	2.0
1	B	478	PHE	2.0
2	D	403	ASP	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 [i](#)

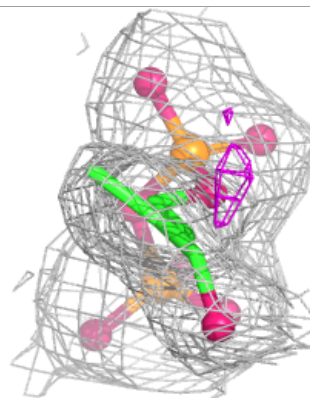
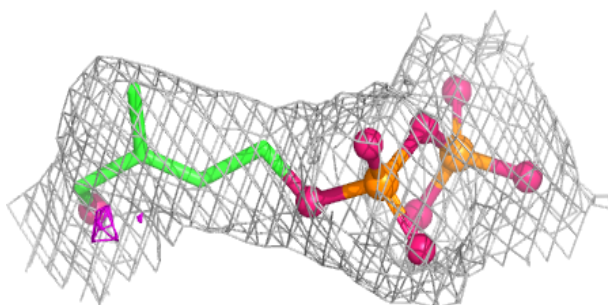
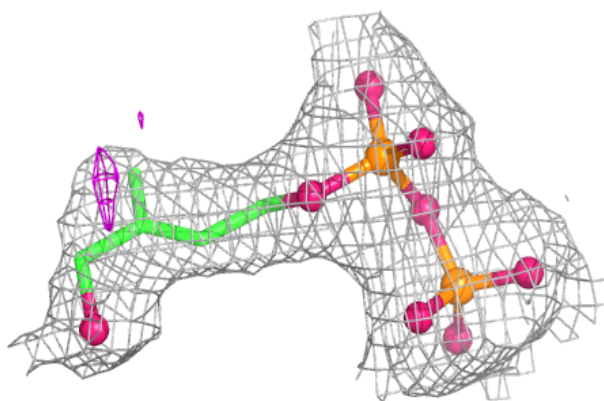
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	EPE	C	602	15/15	0.95	0.10	22,29,38,38	0
3	H6P	D	601	15/15	0.97	0.08	22,26,33,35	0
3	H6P	C	601	15/15	0.98	0.06	10,16,19,19	0

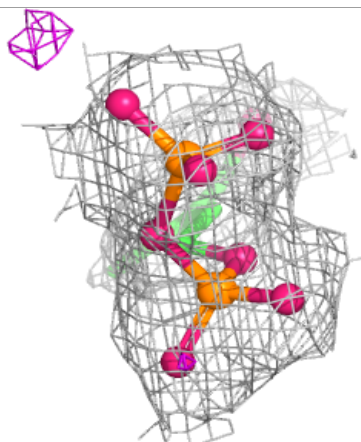
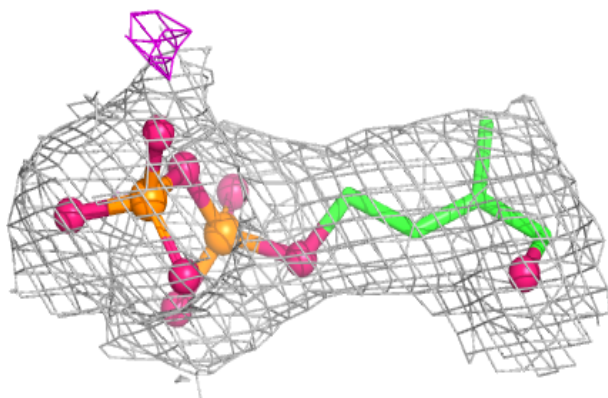
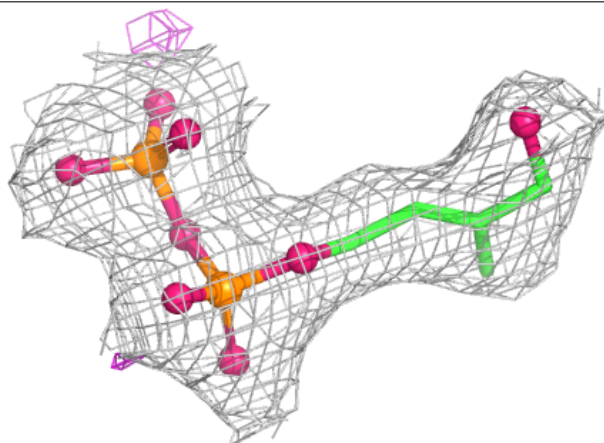
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around H6P 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 H6P 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.