



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:44 AM UTC

PDB ID : 1N95 / pdb_00001n95
Title : Aryl Tetrahydrophyridine Inhibitors of Farnesyltransferase: Glycine, Phenylalanine and Histidine Derivatives
Authors : Gwaltney II, S.L.; O'Conner, S.J.; Nelson, L.T.; Sullivan, G.M.; Imade, H.; Wang, W.; Hasvold, L.; Li, Q.; Cohen, J.; Gu, W.Z.
Deposited on : 2002-11-22
Resolution : 2.30 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

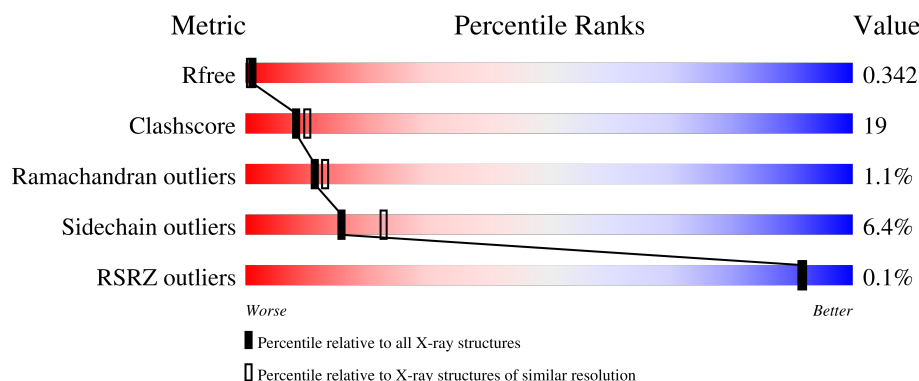
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	315	
2	B	402	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	HFP	B	501	X	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5873 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 Protein farnesyltransferase alpha subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	312	Total	C	N	O	S	0	0	0
			2660	1695	465	495	5			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	156	THR	ILE	conflict	UNP Q04631

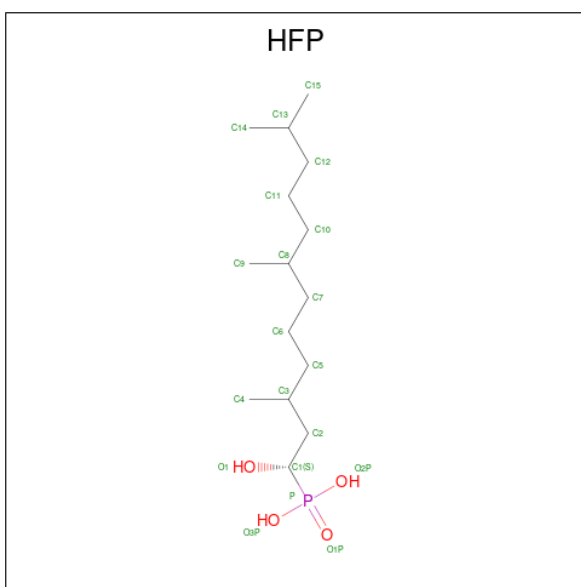
- Molecule 2 is a protein called Protein farnesyltransferase beta subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	401	Total	C	N	O	S	0	0	0
			3154	2016	543	572	23			

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

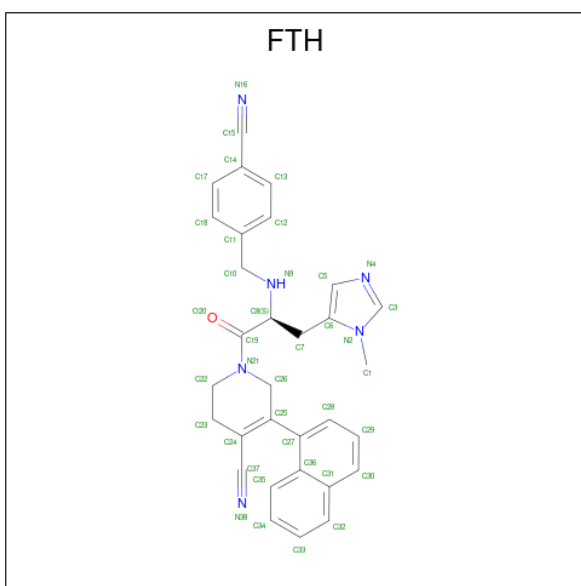
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Zn	0	0
			1	1		

- Molecule 4 is ALPHA-HYDROXYFARNESYLPHOSPHONIC ACID (CCD ID: HFP) (formula: C₁₅H₃₃O₄P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	O	P	0	0
			20	15	4	1		

- Molecule 5 is 1-[2-(4-CYANO-BENZYLAMINO)-3-(3-METHYL-3H-IMIDAZOL-4-YL)-PROPIONYL]-5-NAPHTHALEN-1-YL-1,2,3,6-TETRAHYDRO-PYRIDINE-4-CARBONITRILE (CCD ID: FTH) (formula: $C_{31}H_{28}N_6O$).

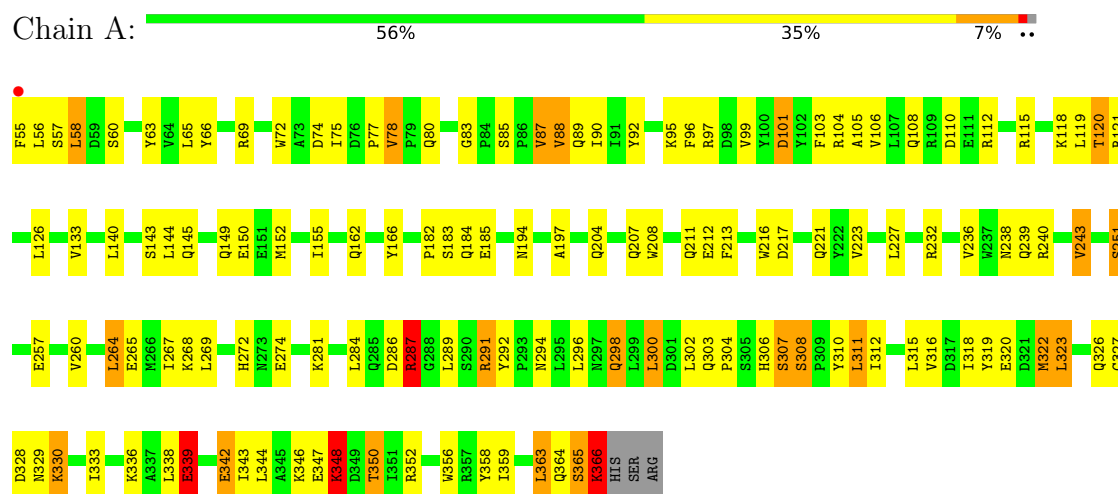


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	N	O	0	0
			38	31	6	1		

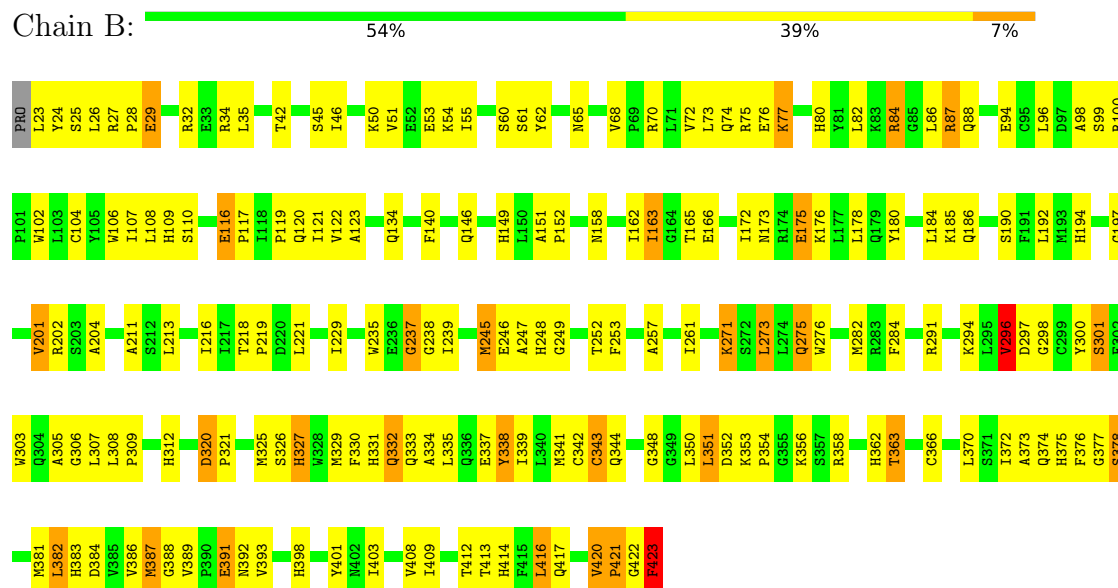
3 Residue-property plots [i](#)

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: Protein farnesyltransferase alpha subunit



• Molecule 2: Protein farnesyltransferase beta subunit



4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	171.13Å 171.13Å 69.40Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	43.59 – 2.30 43.59 – 2.30	Depositor EDS
% Data completeness (in resolution range)	(Not available) (43.59-2.30) 83.5 (43.59-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.33 (at 2.29Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.337 , 0.358 0.321 , 0.342	Depositor DCC
R_{free} test set	5035 reflections (10.08%)	wwPDB-VP
Wilson B-factor (Å ²)	29.5	Xtriage
Anisotropy	0.241	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 24.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.030 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5873	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.12% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, HFP, FTH

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	0.71	2/2725 (0.1%)	1.20	33/3700 (0.9%)
2	B	0.69	2/3239 (0.1%)	1.19	37/4397 (0.8%)
All	All	0.70	4/5964 (0.1%)	1.19	70/8097 (0.9%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	366	LYS	CA-CB	6.85	1.67	1.53
2	B	423	PHE	C-O	6.18	1.35	1.23
1	A	365	SER	C-N	6.00	1.41	1.33
2	B	423	PHE	C-OXT	5.62	1.34	1.23

All (70) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	366	LYS	CA-C-O	18.91	152.94	120.80
2	B	423	PHE	CA-C-O	16.04	169.13	121.00
1	A	217	ASP	N-CA-C	9.06	121.99	111.11
2	B	163	ILE	N-CA-C	-8.50	102.43	110.42
1	A	185	GLU	N-CA-C	8.40	121.27	111.02
1	A	287	ARG	NE-CZ-NH1	-8.38	113.11	121.50
1	A	348	LYS	N-CA-C	8.22	121.17	111.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	116	GLU	CA-C-N	7.81	128.42	120.14
2	B	116	GLU	C-N-CA	7.81	128.42	120.14
1	A	101	ASP	N-CA-C	-7.60	102.99	111.28
2	B	391	GLU	N-CA-C	-7.55	103.80	113.16
2	B	301	SER	N-CA-C	-7.32	103.62	112.54
2	B	342	CYS	N-CA-C	7.26	122.41	112.90
2	B	312	HIS	N-CA-C	-7.11	102.06	111.24
2	B	249	GLY	N-CA-C	7.05	121.19	112.73
2	B	366	CYS	N-CA-C	-6.94	103.79	111.36
2	B	296	VAL	CB-CA-C	-6.82	103.81	111.45
2	B	110	SER	N-CA-C	-6.53	104.09	111.14
1	A	318	ILE	N-CA-C	-6.50	104.31	110.42
1	A	216	TRP	N-CA-C	6.48	120.39	112.23
2	B	201	VAL	N-CA-C	6.43	120.04	111.17
1	A	183	SER	N-CA-C	6.35	120.13	112.38
1	A	267	ILE	N-CA-C	-6.33	104.68	110.82
1	A	322	MET	N-CA-C	-6.32	105.54	113.18
1	A	307	SER	N-CA-C	6.25	120.08	110.20
2	B	363	THR	N-CA-C	-6.24	104.40	111.14
1	A	350	THR	N-CA-C	6.15	120.39	113.01
1	A	83	GLY	CA-C-N	6.07	127.43	119.84
1	A	83	GLY	C-N-CA	6.07	127.43	119.84
2	B	375	HIS	N-CA-C	6.06	118.28	108.34
2	B	237	GLY	N-CA-C	-5.99	107.56	114.69
1	A	78	VAL	CA-C-N	5.96	126.16	120.31
1	A	78	VAL	C-N-CA	5.96	126.16	120.31
1	A	292	TYR	CA-C-N	5.94	125.15	118.97
1	A	292	TYR	C-N-CA	5.94	125.15	118.97
1	A	58	LEU	N-CA-C	-5.89	105.35	112.54
2	B	273	LEU	N-CA-C	-5.82	104.94	111.28
2	B	372	ILE	N-CA-C	-5.80	104.86	110.42
2	B	192	LEU	N-CA-C	-5.79	101.94	110.52
2	B	343	CYS	N-CA-C	5.69	119.21	112.72
1	A	291	ARG	N-CA-C	-5.68	106.20	113.02
2	B	109	HIS	N-CA-C	-5.67	106.91	113.88
1	A	194	ASN	N-CA-C	-5.63	106.24	113.23
2	B	35	LEU	N-CA-C	5.57	118.41	110.10
1	A	274	GLU	N-CA-C	5.57	118.28	111.82
2	B	420	VAL	N-CA-C	-5.57	102.89	108.96
2	B	370	LEU	N-CA-C	-5.56	105.12	111.07
2	B	25	SER	N-CA-C	5.54	117.40	111.36
2	B	172	ILE	N-CA-C	5.53	115.53	108.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	100	ARG	CA-C-N	-5.53	113.92	119.56
2	B	100	ARG	C-N-CA	-5.53	113.92	119.56
2	B	94	GLU	N-CA-C	-5.52	105.42	111.82
1	A	339	GLU	N-CA-C	-5.51	105.35	111.36
1	A	110	ASP	N-CA-C	-5.51	104.30	111.74
2	B	87	ARG	CB-CG-CD	5.49	123.92	111.30
1	A	311	LEU	N-CA-C	-5.48	105.22	111.14
1	A	264	LEU	N-CA-C	-5.46	105.48	111.82
1	A	150	GLU	N-CA-C	-5.44	105.43	111.36
1	A	243	VAL	N-CA-C	5.40	115.54	110.30
2	B	320	ASP	CA-C-N	5.27	126.43	119.84
2	B	320	ASP	C-N-CA	5.27	126.43	119.84
1	A	308	SER	N-CA-C	-5.24	103.41	108.07
1	A	120	THR	N-CA-C	-5.24	105.75	111.82
2	B	65	ASN	N-CA-C	5.20	119.62	113.28
2	B	351	LEU	N-CA-C	5.11	116.57	108.96
2	B	298	GLY	N-CA-C	5.11	120.06	113.27
2	B	62	TYR	N-CA-C	5.08	116.51	110.97
2	B	327	HIS	N-CA-C	5.08	116.71	109.14
1	A	85	SER	CA-C-N	5.02	125.00	120.03
1	A	85	SER	C-N-CA	5.02	125.00	120.03

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	338	TYR	Sidechain

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	2660	0	2585	87	3
2	B	3154	0	3085	133	2
3	B	1	0	0	0	0
4	B	20	0	28	10	0
5	B	38	0	28	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5873	0	5726	223	3

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 19.

All (223) 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)
2:B:77:LYS:HE3	2:B:77:LYS:HA	1.53	0.90
2:B:271:LYS:HA	2:B:271:LYS:HE3	1.54	0.87
2:B:84:ARG:HH22	2:B:88:GLN:HG2	1.40	0.83
2:B:218:THR:HB	2:B:219:PRO:HD2	1.62	0.81
2:B:185:LYS:HE3	2:B:221:LEU:O	1.82	0.79
2:B:106:TRP:CH2	5:B:1001:FTH:HC13	2.20	0.76
1:A:312:ILE:O	1:A:316:VAL:HG23	1.86	0.75
2:B:178:LEU:HD12	2:B:421:PRO:HB2	1.68	0.74
2:B:116:GLU:HB3	2:B:117:PRO:HD2	1.70	0.73
1:A:287:ARG:HD3	1:A:291:ARG:HD3	1.71	0.72
2:B:84:ARG:NH2	2:B:88:GLN:HG2	2.05	0.71
2:B:178:LEU:HG	2:B:216:ILE:HB	1.72	0.71
1:A:322:MET:HE3	1:A:333:ILE:HD13	1.73	0.70
2:B:245:MET:HE2	2:B:246:GLU:H	1.57	0.69
2:B:338:TYR:CE2	2:B:343:CYS:SG	2.86	0.69
1:A:319:TYR:HD2	1:A:322:MET:HE2	1.57	0.68
2:B:151:ALA:HB3	2:B:152:PRO:HD3	1.75	0.68
1:A:327:CYS:O	1:A:330:LYS:HB3	1.93	0.67
2:B:73:LEU:O	2:B:75:ARG:N	2.28	0.66
2:B:253:PHE:HA	2:B:307:LEU:HD21	1.78	0.66
2:B:325:MET:HE3	2:B:381:MET:SD	2.36	0.66
2:B:82:LEU:HD21	2:B:363:THR:HG21	1.78	0.66
1:A:365:SER:HB2	1:A:366:LYS:HD3	1.77	0.66
1:A:268:LYS:HE2	1:A:302:LEU:HD11	1.79	0.65
1:A:344:LEU:HD23	1:A:348:LYS:HB3	1.78	0.65
1:A:343:ILE:HG22	1:A:348:LYS:HB2	1.78	0.64
1:A:303:GLN:O	1:A:307:SER:HB2	1.98	0.63
1:A:312:ILE:HD12	1:A:348:LYS:HG2	1.79	0.63
1:A:302:LEU:HD22	1:A:306:HIS:CD2	2.33	0.63
2:B:72:VAL:HG22	2:B:389:VAL:HG21	1.80	0.63
2:B:335:LEU:O	2:B:339:ILE:HG13	1.99	0.63
2:B:96:LEU:HD11	5:B:1001:FTH:C14	2.29	0.63
2:B:301:SER:O	2:B:305:ALA:HB3	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:337:GLU:HB3	2:B:341:MET:HE3	1.81	0.62
1:A:223:VAL:HG11	1:A:240:ARG:HB2	1.81	0.62
2:B:327:HIS:HB3	2:B:332:GLN:HE22	1.64	0.62
2:B:73:LEU:HD12	2:B:344:GLN:OE1	1.99	0.62
2:B:353:LYS:HB2	2:B:354:PRO:HD2	1.81	0.61
1:A:80:GLN:HB2	1:A:104:ARG:CZ	2.31	0.61
2:B:51:VAL:HA	2:B:54:LYS:HE2	1.83	0.59
2:B:308:LEU:HD13	2:B:330:PHE:HB3	1.84	0.59
1:A:359:ILE:O	1:A:363:LEU:HB2	2.02	0.59
2:B:239:ILE:HB	2:B:252:THR:HA	1.85	0.59
2:B:96:LEU:HD11	5:B:1001:FTH:C15	2.32	0.59
2:B:73:LEU:H	2:B:392:ASN:ND2	2.00	0.58
2:B:352:ASP:HB3	2:B:356:LYS:HG3	1.86	0.58
1:A:87:VAL:O	1:A:88:VAL:C	2.43	0.58
1:A:347:GLU:HG2	1:A:348:LYS:HE3	1.85	0.58
2:B:180:TYR:CZ	2:B:184:LEU:HD11	2.38	0.58
4:B:501:HFP:H52	5:B:1001:FTH:H231	1.85	0.58
1:A:208:TRP:NE1	1:A:212:GLU:HG3	2.20	0.57
2:B:104:CYS:O	2:B:108:LEU:HB2	2.05	0.57
2:B:308:LEU:CD1	2:B:330:PHE:HB3	2.35	0.57
2:B:282:MET:CG	2:B:296:VAL:HG13	2.34	0.57
4:B:501:HFP:C5	5:B:1001:FTH:H231	2.35	0.57
2:B:98:ALA:HA	2:B:146:GLN:HE22	1.69	0.56
1:A:342:GLU:OE1	1:A:346:LYS:HE3	2.06	0.56
2:B:245:MET:CE	2:B:245:MET:HA	2.35	0.56
1:A:366:LYS:HD3	1:A:366:LYS:N	2.21	0.56
1:A:55:PHE:HB2	1:A:118:LYS:HD3	1.87	0.56
1:A:104:ARG:O	1:A:108:GLN:HB2	2.05	0.55
1:A:90:ILE:HB	1:A:92:TYR:CE2	2.42	0.55
1:A:149:GLN:HE22	1:A:184:GLN:HE22	1.54	0.55
2:B:282:MET:HG3	2:B:296:VAL:HG13	1.89	0.55
1:A:286:ASP:O	1:A:287:ARG:HB2	2.06	0.55
1:A:338:LEU:HD11	1:A:364:GLN:HE22	1.72	0.55
2:B:72:VAL:HG22	2:B:389:VAL:CG2	2.37	0.55
2:B:75:ARG:NH2	2:B:391:GLU:O	2.40	0.54
2:B:257:ALA:O	2:B:261:ILE:HG13	2.07	0.54
2:B:386:VAL:HG21	2:B:393:VAL:HB	1.89	0.54
1:A:294:ASN:O	1:A:298:GLN:HG2	2.06	0.54
2:B:374:GLN:O	2:B:384:ASP:HA	2.08	0.54
2:B:398:HIS:CD2	2:B:408:VAL:HG11	2.42	0.54
2:B:326:SER:O	2:B:383:HIS:HB3	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:356:TRP:HA	1:A:356:TRP:CE3	2.44	0.53
2:B:362:HIS:CE1	5:B:1001:FTH:N4	2.77	0.53
2:B:202:ARG:HD3	5:B:1001:FTH:N38	2.23	0.53
2:B:84:ARG:HH22	2:B:88:GLN:CG	2.17	0.53
1:A:75:ILE:HD11	1:A:115:ARG:CZ	2.39	0.53
2:B:86:LEU:HB2	2:B:107:ILE:HG21	1.90	0.53
2:B:381:MET:O	2:B:382:LEU:HD22	2.09	0.53
1:A:287:ARG:HD3	1:A:287:ARG:O	2.09	0.52
4:B:501:HFP:H112	5:B:1001:FTH:C28	2.39	0.52
2:B:50:LYS:O	2:B:54:LYS:HG3	2.09	0.52
2:B:398:HIS:CD2	2:B:408:VAL:HG21	2.44	0.52
1:A:96:PHE:HA	1:A:126:LEU:HD13	1.93	0.51
2:B:186:GLN:HB2	2:B:190:SER:O	2.10	0.51
1:A:223:VAL:HG13	1:A:236:VAL:HG12	1.93	0.51
2:B:46:ILE:HG22	2:B:50:LYS:HE3	1.93	0.51
1:A:72:TRP:CE3	1:A:75:ILE:HD12	2.45	0.51
2:B:76:GLU:O	2:B:80:HIS:ND1	2.44	0.51
2:B:158:ASN:O	2:B:162:ILE:HG13	2.12	0.50
2:B:414:HIS:O	2:B:417:GLN:HG2	2.11	0.50
2:B:348:GLY:O	2:B:358:ARG:HD2	2.11	0.50
1:A:302:LEU:HD22	1:A:306:HIS:HD2	1.74	0.50
1:A:103:PHE:CZ	1:A:133:VAL:HG22	2.46	0.50
1:A:296:LEU:O	1:A:300:LEU:HB2	2.11	0.50
2:B:275:GLN:HE21	2:B:276:TRP:N	2.10	0.50
1:A:78:VAL:HG23	1:A:105:ALA:HB2	1.94	0.50
1:A:328:ASP:O	1:A:329:ASN:HB2	2.12	0.50
2:B:344:GLN:HA	2:B:350:LEU:HD13	1.93	0.50
2:B:297:ASP:HB3	2:B:300:TYR:HD1	1.76	0.49
2:B:412:THR:O	2:B:416:LEU:HB2	2.12	0.49
2:B:23:LEU:O	2:B:27:ARG:HG3	2.12	0.49
2:B:389:VAL:HG12	2:B:391:GLU:HB2	1.94	0.48
2:B:173:ASN:CG	2:B:176:LYS:HB2	2.39	0.48
2:B:350:LEU:HB2	2:B:363:THR:HA	1.95	0.48
1:A:182:PRO:HG3	1:A:213:PHE:CD2	2.49	0.48
2:B:245:MET:HE2	2:B:245:MET:HA	1.94	0.48
1:A:227:LEU:HG	1:A:236:VAL:CG1	2.44	0.48
1:A:89:GLN:OE1	2:B:87:ARG:NH2	2.47	0.48
2:B:73:LEU:H	2:B:392:ASN:HD21	1.62	0.48
2:B:23:LEU:HD12	2:B:26:LEU:CD1	2.44	0.48
2:B:24:TYR:HB2	2:B:333:GLN:CD	2.39	0.47
1:A:238:ASN:HA	2:B:235:TRP:CZ2	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:23:LEU:HD13	2:B:341:MET:HE2	1.96	0.47
2:B:326:SER:HB2	2:B:383:HIS:CD2	2.49	0.47
2:B:121:ILE:N	2:B:121:ILE:HD12	2.30	0.47
1:A:311:LEU:O	1:A:315:LEU:HG	2.14	0.47
1:A:312:ILE:HG22	1:A:344:LEU:HD11	1.96	0.47
2:B:216:ILE:HG22	2:B:421:PRO:CD	2.44	0.47
2:B:308:LEU:HD22	2:B:329:MET:HB2	1.97	0.47
2:B:51:VAL:O	2:B:55:ILE:HG12	2.15	0.47
2:B:119:PRO:O	2:B:122:VAL:HG12	2.15	0.46
2:B:376:PHE:CZ	2:B:378:SER:HB2	2.50	0.46
2:B:175:GLU:CD	2:B:175:GLU:H	2.22	0.46
2:B:134:GLN:HB2	2:B:140:PHE:CE2	2.51	0.46
1:A:92:TYR:HB2	1:A:97:ARG:HG3	1.98	0.46
2:B:55:ILE:HD13	2:B:354:PRO:HG3	1.98	0.46
1:A:80:GLN:HB2	1:A:104:ARG:NH2	2.31	0.45
2:B:108:LEU:O	2:B:162:ILE:HG21	2.17	0.45
1:A:143:SER:C	1:A:145:GLN:H	2.25	0.45
1:A:312:ILE:CD1	1:A:348:LYS:HG2	2.45	0.45
2:B:378:SER:HB3	2:B:381:MET:HG3	1.99	0.45
2:B:423:PHE:N	2:B:423:PHE:CD2	2.84	0.45
1:A:308:SER:C	1:A:310:TYR:H	2.25	0.45
1:A:264:LEU:HD23	1:A:264:LEU:HA	1.86	0.45
1:A:300:LEU:HD12	1:A:300:LEU:HA	1.81	0.45
2:B:306:GLY:O	2:B:309:PRO:HD2	2.17	0.45
2:B:218:THR:HB	2:B:219:PRO:CD	2.42	0.44
2:B:282:MET:HG2	2:B:296:VAL:HG13	1.99	0.44
2:B:213:LEU:HD23	2:B:412:THR:HG22	2.00	0.44
1:A:166:TYR:HE1	5:B:1001:FTH:H232	1.82	0.44
1:A:204:GLN:HA	2:B:245:MET:SD	2.58	0.44
1:A:239:GLN:O	1:A:243:VAL:HG23	2.18	0.44
2:B:420:VAL:O	2:B:422:GLY:N	2.50	0.44
1:A:58:LEU:O	1:A:95:LYS:NZ	2.49	0.44
1:A:112:ARG:O	1:A:144:LEU:HD21	2.18	0.44
2:B:248:HIS:CE1	4:B:501:HFP:H62	2.53	0.44
2:B:194:HIS:CD2	2:B:197:GLY:HA3	2.53	0.44
2:B:331:HIS:CD2	2:B:334:ALA:H	2.36	0.44
1:A:72:TRP:CZ3	1:A:75:ILE:HD12	2.53	0.43
1:A:77:PRO:HB2	1:A:101:ASP:HB3	2.00	0.43
2:B:388:GLY:O	2:B:389:VAL:C	2.61	0.43
1:A:316:VAL:O	1:A:320:GLU:HG3	2.17	0.43
1:A:319:TYR:CE1	1:A:336:LYS:HG3	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:237:GLY:O	2:B:273:LEU:HA	2.19	0.43
2:B:303:TRP:CH2	4:B:501:HFP:H121	2.53	0.43
4:B:501:HFP:H112	5:B:1001:FTH:HC28	2.00	0.43
1:A:339:GLU:O	1:A:343:ILE:HG13	2.18	0.43
2:B:46:ILE:O	2:B:50:LYS:HG3	2.18	0.43
2:B:398:HIS:HD2	2:B:408:VAL:HG11	1.83	0.43
2:B:376:PHE:CG	2:B:377:GLY:N	2.86	0.43
2:B:122:VAL:HG13	2:B:123:ALA:N	2.33	0.43
2:B:149:HIS:HB3	2:B:152:PRO:HD2	1.99	0.43
2:B:99:SER:O	2:B:102:TRP:HB2	2.19	0.43
2:B:163:ILE:HG22	2:B:165:THR:HG23	2.00	0.43
1:A:260:VAL:HG21	1:A:284:LEU:HD21	2.00	0.43
4:B:501:HFP:H52	5:B:1001:FTH:C23	2.49	0.43
1:A:99:VAL:HG13	1:A:119:LEU:CD1	2.49	0.43
2:B:34:ARG:HH22	2:B:53:GLU:CD	2.27	0.43
1:A:155:ILE:HD12	1:A:155:ILE:HA	1.88	0.42
1:A:207:GLN:NE2	2:B:245:MET:HE3	2.34	0.42
1:A:227:LEU:HD23	1:A:227:LEU:HA	1.91	0.42
2:B:121:ILE:HD12	2:B:121:ILE:H	1.83	0.42
1:A:312:ILE:HB	1:A:344:LEU:HD21	2.02	0.42
1:A:358:TYR:CD2	1:A:358:TYR:C	2.96	0.42
2:B:204:ALA:HB1	2:B:229:ILE:HD11	2.01	0.42
2:B:409:ILE:O	2:B:413:THR:HG23	2.19	0.42
2:B:403:ILE:HG13	2:B:408:VAL:HG23	2.00	0.42
1:A:232:ARG:NH1	2:B:42:THR:HG23	2.34	0.42
2:B:331:HIS:HD2	2:B:334:ALA:H	1.66	0.42
2:B:408:VAL:O	2:B:412:THR:HG23	2.20	0.42
2:B:29:GLU:O	2:B:32:ARG:HD2	2.20	0.42
2:B:238:GLY:HA3	2:B:247:ALA:HB1	2.01	0.42
4:B:501:HFP:H21	5:B:1001:FTH:H231	2.01	0.42
2:B:60:SER:O	2:B:61:SER:C	2.63	0.42
2:B:173:ASN:OD1	2:B:175:GLU:HG2	2.19	0.42
2:B:333:GLN:HG3	2:B:387:MET:CE	2.49	0.42
2:B:291:ARG:HB2	2:B:294:LYS:CG	2.50	0.42
1:A:112:ARG:HA	1:A:140:LEU:HD21	2.02	0.42
1:A:152:MET:HE3	1:A:152:MET:HB3	1.96	0.42
2:B:218:THR:CB	2:B:219:PRO:HD2	2.44	0.42
2:B:284:PHE:CD2	2:B:284:PHE:C	2.97	0.41
1:A:99:VAL:HG13	1:A:119:LEU:HD11	2.02	0.41
1:A:103:PHE:HE1	1:A:120:THR:HG22	1.85	0.41
2:B:335:LEU:HD23	2:B:373:ALA:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:57:SER:O	1:A:63:TYR:HD1	2.04	0.41
1:A:272:HIS:CD2	1:A:308:SER:HB3	2.56	0.41
1:A:287:ARG:CD	1:A:291:ARG:HD3	2.45	0.41
2:B:294:LYS:HD2	2:B:294:LYS:HA	1.94	0.41
4:B:501:HFP:H112	5:B:1001:FTH:C29	2.50	0.41
2:B:320:ASP:HA	2:B:321:PRO:HD3	1.70	0.41
1:A:143:SER:C	1:A:145:GLN:N	2.79	0.41
1:A:302:LEU:HB3	1:A:306:HIS:HB2	2.02	0.41
4:B:501:HFP:H61	5:B:1001:FTH:H231	2.02	0.41
1:A:338:LEU:HD21	1:A:363:LEU:HB3	2.01	0.41
2:B:165:THR:O	2:B:166:GLU:C	2.61	0.41
1:A:58:LEU:HD22	1:A:95:LYS:HE3	2.02	0.41
2:B:122:VAL:CG1	2:B:123:ALA:N	2.84	0.41
2:B:211:ALA:HA	2:B:216:ILE:CG1	2.51	0.41
2:B:213:LEU:HG	2:B:401:TYR:CE2	2.56	0.41
1:A:65:LEU:O	1:A:69:ARG:HG3	2.21	0.41
1:A:207:GLN:O	1:A:211:GLN:HB2	2.21	0.40
1:A:66:TYR:CZ	1:A:119:LEU:HD13	2.55	0.40
1:A:72:TRP:CZ2	1:A:115:ARG:HD2	2.57	0.40
1:A:328:ASP:O	1:A:329:ASN:CB	2.68	0.40
1:A:363:LEU:HD12	1:A:363:LEU:HA	1.90	0.40
2:B:403:ILE:HG13	2:B:408:VAL:CG2	2.52	0.40
1:A:323:LEU:HD13	1:A:333:ILE:HG21	2.02	0.40
2:B:27:ARG:HA	2:B:28:PRO:HD3	1.87	0.40
2:B:34:ARG:HD2	2:B:284:PHE:CE1	2.56	0.40
2:B:352:ASP:OD1	2:B:352:ASP:C	2.65	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:60:SER:OG	1:A:257:GLU:OE1[6_555]	2.08	0.12
1:A:251:SER:CB	2:B:120:GLN:OE1[2_655]	2.17	0.03
1:A:74:ASP:O	2:B:84:ARG:NH2[4_665]	2.19	0.01

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	310/315 (98%)	278 (90%)	27 (9%)	5 (2%)	7	7
2	B	399/402 (99%)	370 (93%)	26 (6%)	3 (1%)	16	20
All	All	709/717 (99%)	648 (91%)	53 (8%)	8 (1%)	11	13

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	287	ARG
2	B	74	GLN
1	A	326	GLN
2	B	378	SER
1	A	197	ALA
2	B	421	PRO
1	A	88	VAL
1	A	304	PRO

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	291/294 (99%)	269 (92%)	22 (8%)	12	16
2	B	338/339 (100%)	320 (95%)	18 (5%)	20	30
All	All	629/633 (99%)	589 (94%)	40 (6%)	16	23

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	56	LEU
1	A	87	VAL
1	A	106	VAL
1	A	121	ARG
1	A	162	GLN
1	A	221	GLN
1	A	251	SER
1	A	265	GLU
1	A	269	LEU
1	A	281	LYS
1	A	289	LEU
1	A	298	GLN
1	A	300	LEU
1	A	323	LEU
1	A	330	LYS
1	A	339	GLU
1	A	342	GLU
1	A	348	LYS
1	A	350	THR
1	A	352	ARG
1	A	363	LEU
1	A	366	LYS
2	B	29	GLU
2	B	45	SER
2	B	68	VAL
2	B	70	ARG
2	B	77	LYS
2	B	84	ARG
2	B	175	GLU
2	B	201	VAL
2	B	245	MET
2	B	271	LYS
2	B	275	GLN
2	B	296	VAL
2	B	332	GLN
2	B	351	LEU
2	B	382	LEU
2	B	387	MET
2	B	416	LEU
2	B	423	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	81	ASN
1	A	108	GLN
1	A	149	GLN
1	A	204	GLN
1	A	221	GLN
1	A	285	GLN
1	A	294	ASN
1	A	306	HIS
1	A	325	ASN
1	A	364	GLN
2	B	48	GLN
2	B	146	GLN
2	B	215	ASN
2	B	327	HIS
2	B	331	HIS
2	B	332	GLN
2	B	392	ASN
2	B	402	ASN
2	B	410	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
5	FTH	B	1001	3	39,42,42	1.97	15 (38%)	47,58,58	1.98	6 (12%)
4	HFP	B	501	-	16,19,19	1.76	4 (25%)	20,25,25	2.51	4 (20%)

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
5	FTH	B	1001	3	-	11/23/38/38	0/5/5/5
4	HFP	B	501	-	2/2/5/5	10/22/22/22	-

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	501	HFP	C2-C3	-4.81	1.35	1.53
5	B	1001	FTH	C22-N21	-3.68	1.40	1.47
5	B	1001	FTH	C26-N21	3.46	1.51	1.46
4	B	501	HFP	C7-C8	-3.35	1.36	1.52
5	B	1001	FTH	C5-N4	-3.23	1.32	1.37
5	B	1001	FTH	C37-C24	3.14	1.46	1.43
5	B	1001	FTH	C28-C27	3.03	1.44	1.38
5	B	1001	FTH	C13-C12	2.96	1.43	1.38
5	B	1001	FTH	C33-C32	2.83	1.42	1.36
5	B	1001	FTH	C7-C6	2.82	1.55	1.49
5	B	1001	FTH	C5-C6	2.66	1.40	1.36
5	B	1001	FTH	C8-C19	2.53	1.58	1.53
5	B	1001	FTH	C18-C17	2.49	1.42	1.38
5	B	1001	FTH	C18-C11	2.33	1.43	1.38
5	B	1001	FTH	C29-C28	2.25	1.42	1.38
5	B	1001	FTH	C34-C35	2.22	1.41	1.36
4	B	501	HFP	C12-C13	-2.12	1.38	1.51
4	B	501	HFP	P-O1P	-2.01	1.46	1.49
5	B	1001	FTH	C6-N2	-2.00	1.34	1.38

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	501	HFP	C3-C2-C1	8.20	123.53	115.21
5	B	1001	FTH	C22-C23-C24	7.32	118.40	109.12
5	B	1001	FTH	C25-C26-N21	6.43	115.27	109.60
4	B	501	HFP	C4-C3-C2	3.60	121.84	110.84
5	B	1001	FTH	C27-C25-C24	-3.59	119.70	123.72
5	B	1001	FTH	C23-C22-N21	3.53	116.43	110.67
5	B	1001	FTH	C26-N21-C22	3.45	122.15	114.59
5	B	1001	FTH	C24-C37-N38	-3.28	171.88	177.08
4	B	501	HFP	C2-C3-C5	3.14	122.14	111.86
4	B	501	HFP	C9-C8-C7	2.76	121.11	111.27

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	B	501	HFP	C8
4	B	501	HFP	C3

All (21) torsion outliers are listed below:

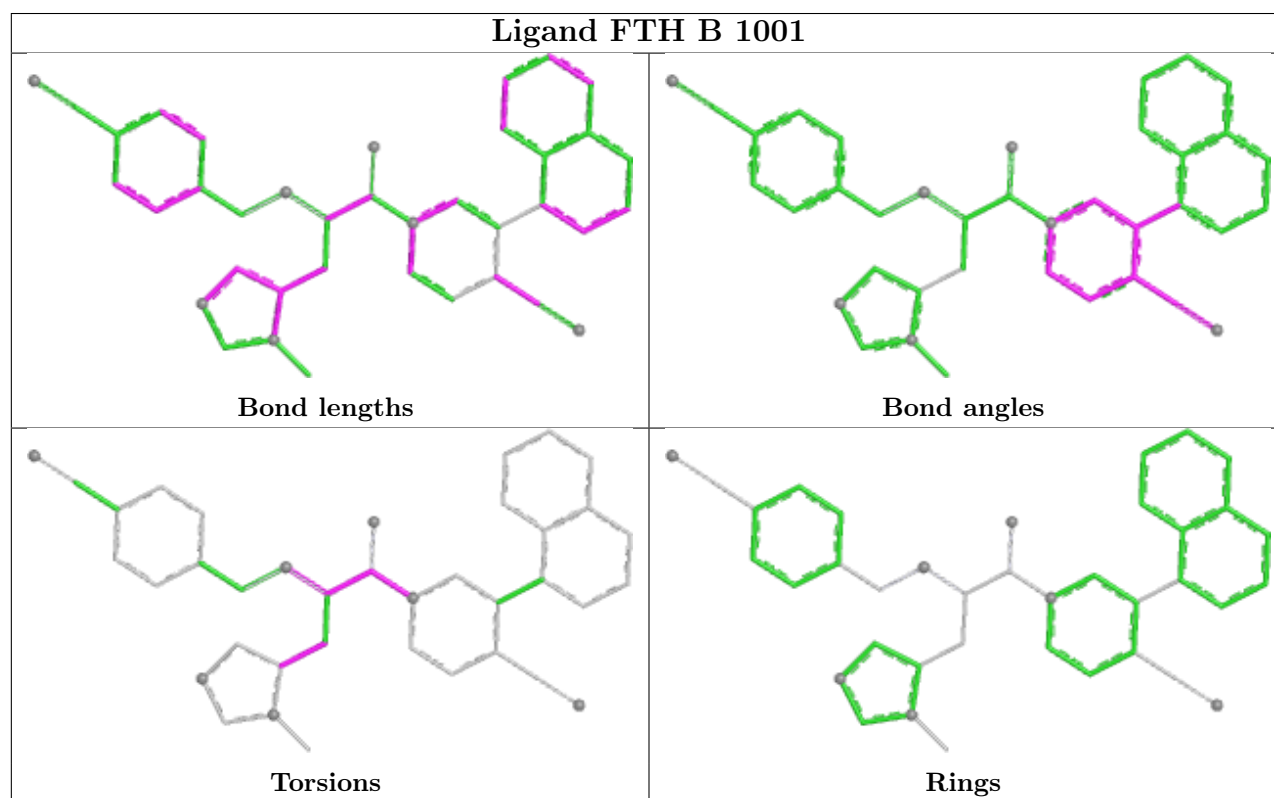
Mol	Chain	Res	Type	Atoms
4	B	501	HFP	O1-C1-P-O1P
4	B	501	HFP	P-C1-C2-C3
4	B	501	HFP	C1-C2-C3-C4
4	B	501	HFP	C6-C7-C8-C9
5	B	1001	FTH	C8-C19-N21-C22
5	B	1001	FTH	C8-C19-N21-C26
5	B	1001	FTH	O20-C19-N21-C22
5	B	1001	FTH	O20-C19-N21-C26
4	B	501	HFP	C11-C12-C13-C14
4	B	501	HFP	O1-C1-C2-C3
4	B	501	HFP	C11-C10-C8-C9
5	B	1001	FTH	N21-C19-C8-C7
5	B	1001	FTH	C7-C8-N9-C10
5	B	1001	FTH	O20-C19-C8-N9
5	B	1001	FTH	C19-C8-N9-C10
5	B	1001	FTH	C5-C6-C7-C8
5	B	1001	FTH	O20-C19-C8-C7
4	B	501	HFP	C2-C3-C5-C6
4	B	501	HFP	C2-C1-P-O1P
4	B	501	HFP	C4-C3-C5-C6
5	B	1001	FTH	N21-C19-C8-N9

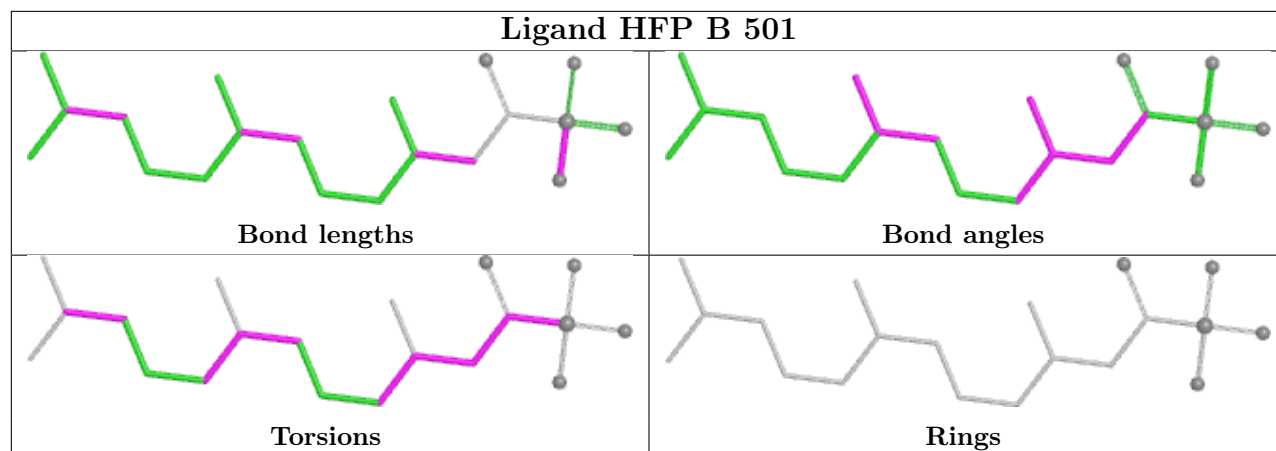
There are no ring outliers.

2 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	1001	FTH	14	0
4	B	501	HFP	10	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	312/315 (99%)	-0.88	1 (0%) 90 90	13, 41, 82, 100	0
2	B	401/402 (99%)	-1.02	0 100 100	11, 35, 72, 100	0
All	All	713/717 (99%)	-0.95	1 (0%) 92 91	11, 37, 78, 100	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	55	PHE	3.1

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

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

6.3 Carbohydrates [i](#)

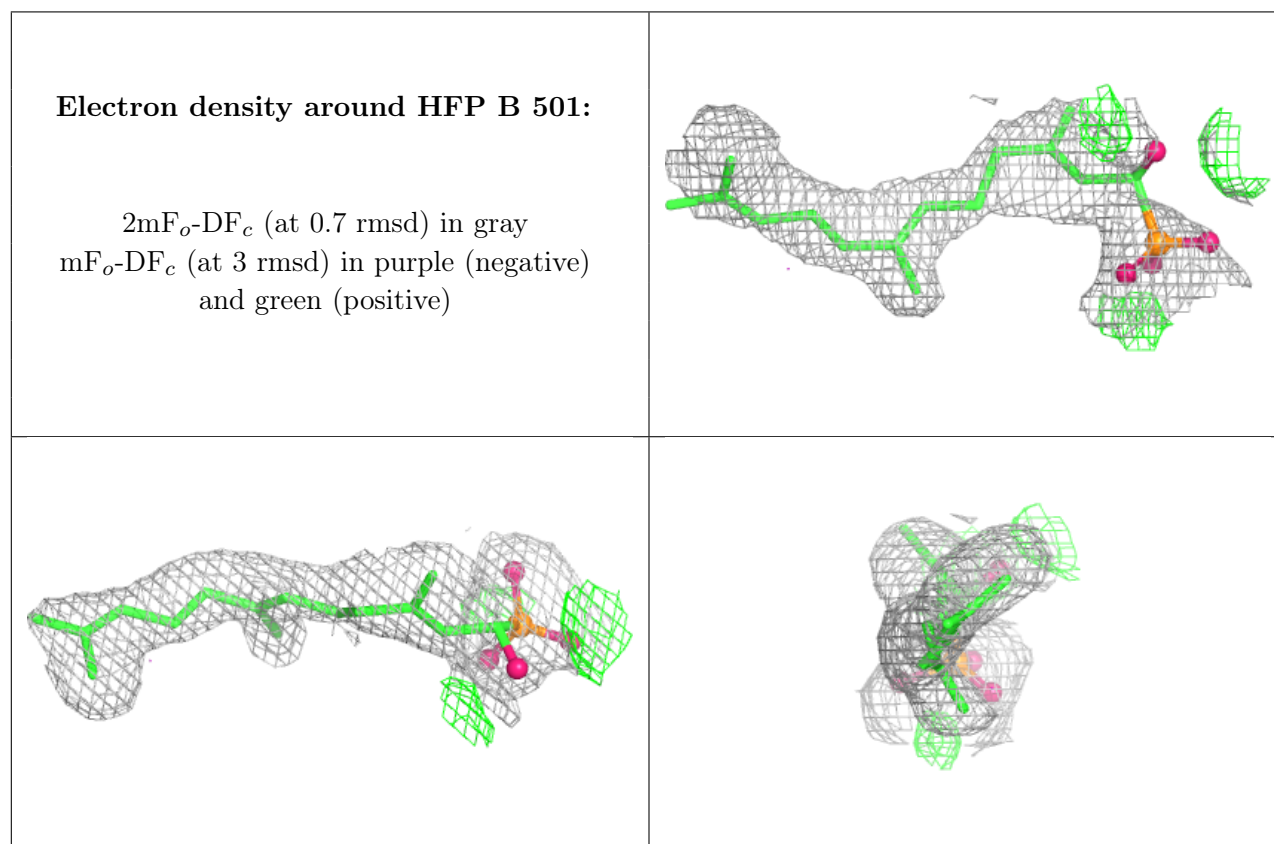
There are no oligosaccharides in this entry.

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.

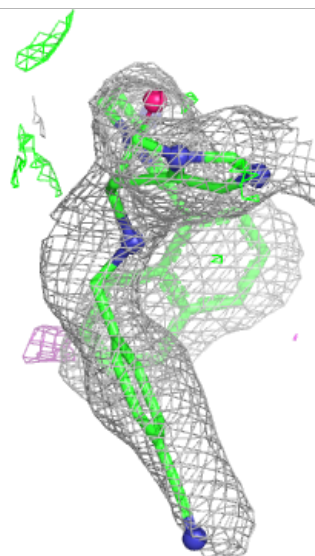
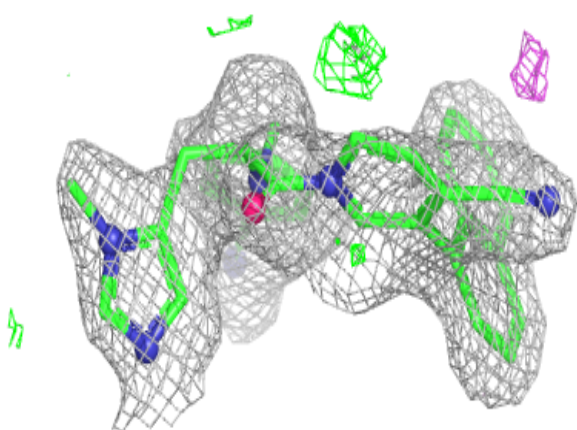
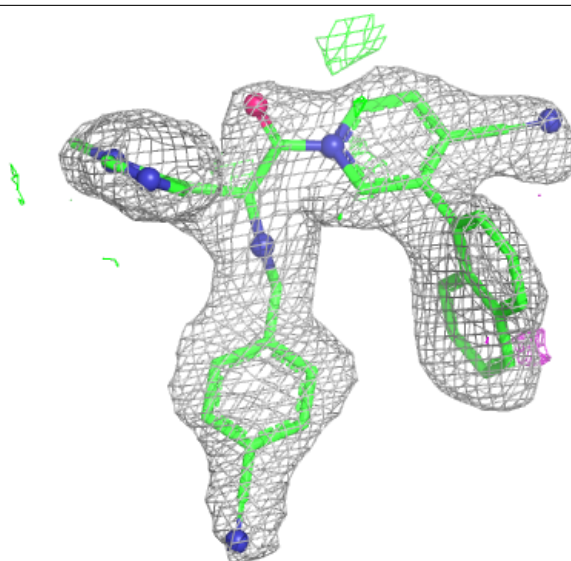
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	HFP	B	501	20/20	0.99	0.05	30,30,30,30	0
5	FTH	B	1001	38/38	0.99	0.05	30,30,30,30	0
3	ZN	B	500	1/1	1.00	0.01	30,30,30,30	0

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 FTH B 1001:

$2mF_o-DF_c$ (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.