Full wwPDB X-ray Structure Validation Report ⓘ

Jun 13, 2024 – 09:46 AM EDT

PDB ID	:	4GTQ
Title	:	FTase in complex with BMS analogue 12
Authors	:	Guo, Z.; Stigter, E.A.; Bon, R.S.; Waldmann, H.; Blankenfeldt, W.; Goody, R.S.
Deposited on	:	2012-08-29
Resolution	:	2.60 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:

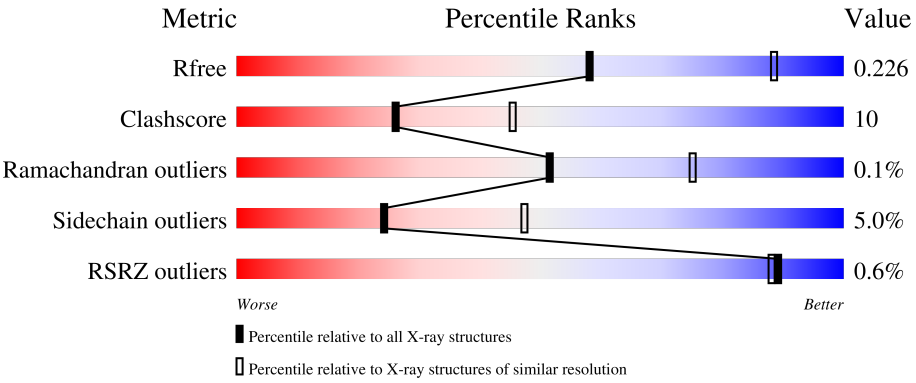
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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 <=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	377	% 65% 16% • 16%
2	B	427	80% 13% • 5%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 6164 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/geranylgeranyltransferase type-1 subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	315	2674	1708	465	496	5	0	1	0

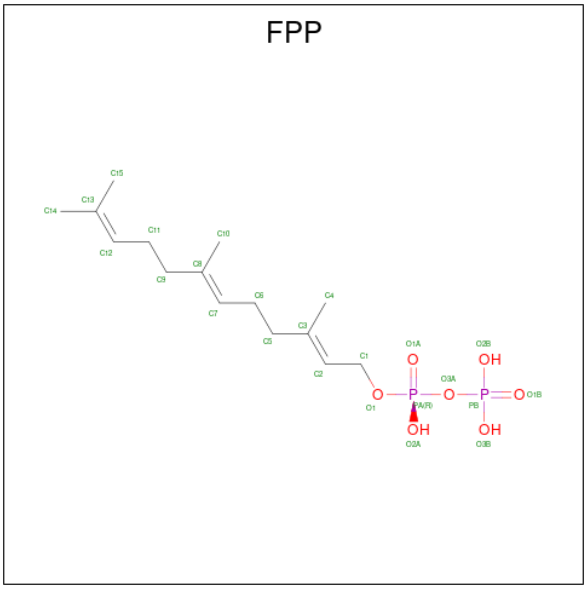
- Molecule 2 is a protein called Protein farnesyltransferase subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	405	3172	2027	545	577	23	0	2	0

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

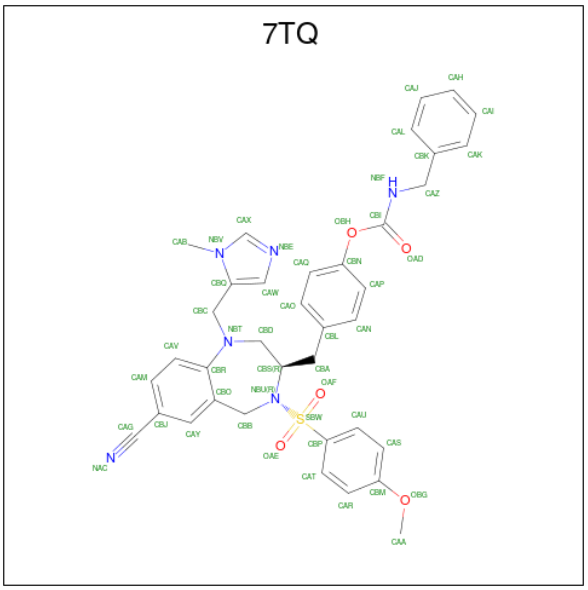
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
3	B	1	1	1	0	0

- Molecule 4 is FARNESYL DIPHOSPHATE (three-letter code: FPP) (formula: $C_{15}H_{28}O_7P_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	O	P	0	0
			24	15	7	2		

- Molecule 5 is 4-({(3R)-7-cyano-4-[(4-methoxyphenyl)sulfonyl]-1-[(1-methyl-1H-imidazol-5-yl)methyl]-2,3,4,5-tetrahydro-1H-1,4-benzodiazepin-3-yl}methyl)phenyl benzylcarbamate (three-letter code: 7TQ) (formula: $C_{37}H_{36}N_6O_5S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	B	1	Total	C	N	O	S	0	0
			49	37	6	5	1		

- Molecule 6 is water.

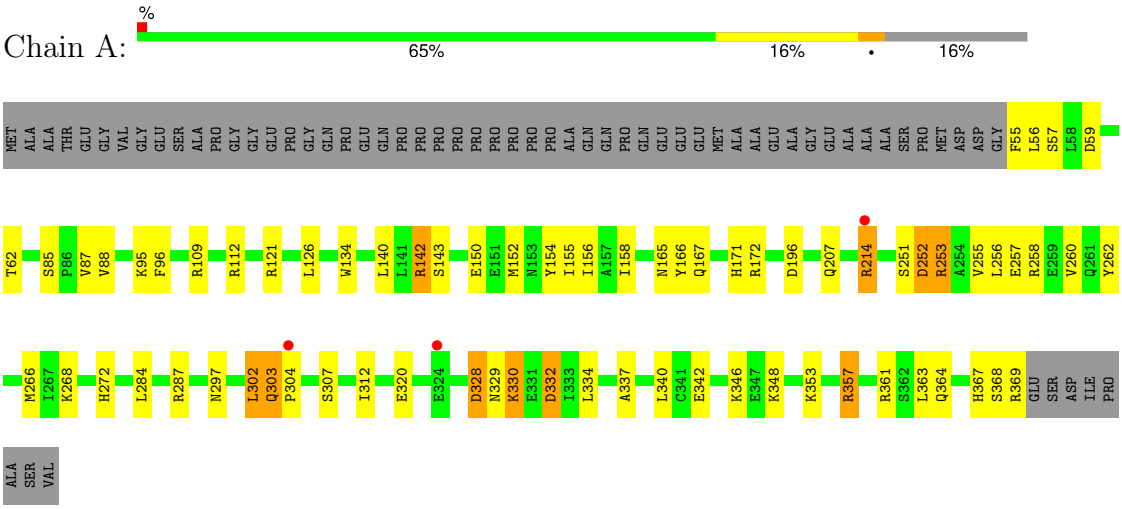
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	123	Total	O	0	0
			123	123		
6	B	121	Total	O	0	0
			121	121		

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.

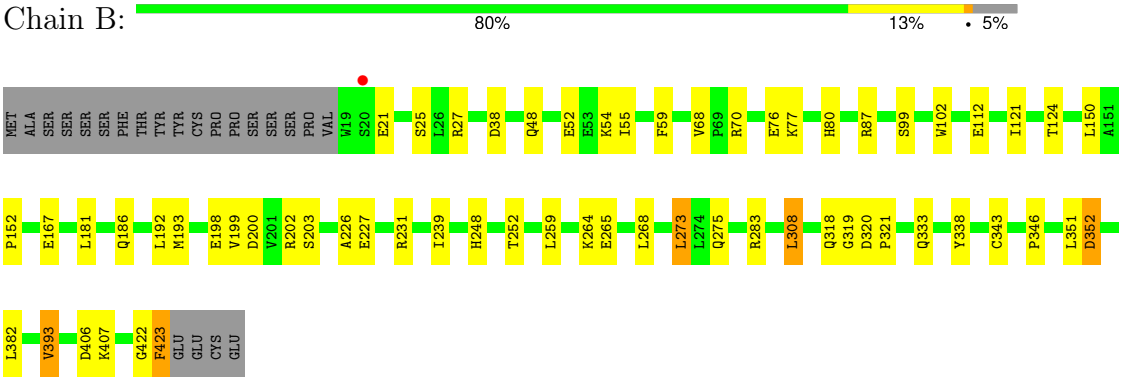
• Molecule 1: Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha

Chain A:



• Molecule 2: Protein farnesyltransferase subunit beta

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α, β, γ	172.40Å 172.40Å 69.78Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.91 – 2.60 29.86 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.9 (29.91-2.60) 99.9 (29.86-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) >$ [1]	5.01 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.171 , 0.223 0.189 , 0.226	Depositor DCC
R_{free} test set	1809 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å^2)	37.3	Xtriage
Anisotropy	0.058	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 40.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.034 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	6164	wwPDB-VP
Average B, all atoms (Å^2)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.74% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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, 7TQ, FPP

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	0.79	0/2744	0.80	5/3729 (0.1%)
2	B	0.80	0/3264	0.77	3/4437 (0.1%)
All	All	0.79	0/6008	0.79	8/8166 (0.1%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	121	ARG	NE-CZ-NH2	-5.87	117.36	120.30
1	A	328	ASP	CB-CA-C	5.75	121.89	110.40
2	B	283	ARG	NE-CZ-NH1	5.71	123.16	120.30
1	A	253	ARG	NE-CZ-NH1	5.68	123.14	120.30
1	A	196	ASP	CB-CG-OD2	5.43	123.19	118.30
2	B	87	ARG	NE-CZ-NH2	-5.34	117.63	120.30
1	A	253	ARG	NE-CZ-NH2	-5.03	117.79	120.30
2	B	283	ARG	NE-CZ-NH2	-5.01	117.80	120.30

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	2674	0	2582	74	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	3172	0	3082	50	0
3	B	1	0	0	0	0
4	B	24	0	25	7	0
5	B	49	0	36	4	0
6	A	123	0	0	23	0
6	B	121	0	0	8	0
All	All	6164	0	5725	121	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 10.

All (121) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:214:ARG:HH11	1:A:214:ARG:HG2	1.11	1.08
1:A:142:ARG:HH11	1:A:142:ARG:HG2	1.06	1.07
1:A:368:SER:HA	6:A:503:HOH:O	1.57	1.04
1:A:152:MET:O	1:A:156:ILE:HG13	1.58	1.02
1:A:59:ASP:HB2	6:A:457:HOH:O	1.59	1.02
1:A:142:ARG:HH11	1:A:142:ARG:CG	1.84	0.90
1:A:142:ARG:HG2	1:A:142:ARG:NH1	1.71	0.88
2:B:319:GLY:O	2:B:321:PRO:HD3	1.75	0.85
2:B:202:ARG:HG2	4:B:502:FPP:H142	1.59	0.83
1:A:302:LEU:HD23	6:A:482:HOH:O	1.78	0.83
2:B:320:ASP:OD1	6:B:633:HOH:O	1.95	0.82
1:A:214:ARG:HH11	1:A:214:ARG:CG	1.95	0.74
1:A:154:TYR:CZ	1:A:158:ILE:HD12	2.22	0.73
2:B:124:THR:HG23	2:B:167:GLU:OE2	1.89	0.73
2:B:21:GLU:OE1	6:B:622:HOH:O	2.08	0.72
1:A:287:ARG:HA	6:A:478:HOH:O	1.90	0.71
1:A:166[B]:TYR:CE1	2:B:202:ARG:NH2	2.59	0.71
2:B:70:ARG:HD3	6:B:653:HOH:O	1.92	0.70
1:A:214:ARG:HG2	1:A:214:ARG:NH1	1.92	0.70
1:A:330:LYS:CE	6:A:471:HOH:O	2.39	0.69
1:A:112:ARG:HA	1:A:140:LEU:HD21	1.74	0.68
1:A:302:LEU:CD2	6:A:482:HOH:O	2.38	0.68
2:B:202:ARG:HD3	4:B:502:FPP:H12	1.73	0.68
1:A:330:LYS:HE2	6:A:471:HOH:O	1.94	0.68
1:A:332:ASP:C	1:A:332:ASP:OD2	2.30	0.67
1:A:368:SER:O	1:A:369:ARG:C	2.33	0.67
1:A:266:MET:HE2	6:A:485:HOH:O	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:202:ARG:CG	4:B:502:FPP:H142	2.25	0.66
1:A:266:MET:CE	6:A:485:HOH:O	2.46	0.63
2:B:273:LEU:HD12	2:B:273:LEU:O	1.99	0.63
2:B:319:GLY:O	2:B:320:ASP:C	2.35	0.63
1:A:251:SER:O	1:A:252:ASP:C	2.38	0.62
2:B:202:ARG:CD	4:B:502:FPP:H142	2.31	0.60
2:B:319:GLY:O	2:B:321:PRO:CD	2.48	0.59
1:A:152:MET:O	1:A:156:ILE:CG1	2.44	0.59
1:A:368:SER:CA	6:A:503:HOH:O	2.32	0.58
6:A:448:HOH:O	5:B:503:7TQ:CAK	2.51	0.58
1:A:251:SER:O	1:A:253:ARG:N	2.36	0.58
1:A:154:TYR:CZ	1:A:158:ILE:CD1	2.87	0.57
1:A:156:ILE:HG12	1:A:172:ARG:HH12	1.69	0.57
1:A:214:ARG:NH1	6:A:497:HOH:O	2.38	0.57
2:B:102:TRP:CD1	5:B:503:7TQ:H36	2.40	0.56
1:A:357:ARG:HB3	1:A:361:ARG:HH12	1.70	0.56
1:A:112:ARG:HA	1:A:140:LEU:CD2	2.35	0.56
1:A:368:SER:C	6:A:503:HOH:O	2.42	0.56
1:A:156:ILE:HG12	1:A:172:ARG:NH1	2.22	0.55
1:A:342:GLU:HA	1:A:342:GLU:OE1	2.07	0.55
2:B:21:GLU:HB2	2:B:27:ARG:HG2	1.89	0.54
1:A:62:THR:CG2	1:A:62:THR:O	2.55	0.54
2:B:264:LYS:O	2:B:265:GLU:C	2.46	0.54
1:A:320:GLU:HG3	1:A:363:LEU:HD21	1.89	0.54
2:B:227:GLU:HG3	6:B:676:HOH:O	2.07	0.54
2:B:192:LEU:HD23	2:B:199:VAL:HG23	1.90	0.53
1:A:272:HIS:ND1	2:B:38:ASP:OD1	2.38	0.53
1:A:96:PHE:HA	1:A:126:LEU:HD13	1.89	0.53
2:B:318:GLN:HB3	6:B:682:HOH:O	2.09	0.53
1:A:312:ILE:CG2	1:A:340:LEU:HD22	2.40	0.52
1:A:134:TRP:CD1	1:A:167:GLN:HG3	2.45	0.51
1:A:348:LYS:HE2	6:A:523:HOH:O	2.09	0.51
2:B:231:ARG:HD3	6:B:674:HOH:O	2.10	0.51
2:B:48:GLN:O	2:B:52:GLU:HG3	2.11	0.51
2:B:186:GLN:NE2	2:B:186:GLN:HA	2.25	0.51
1:A:155:ILE:HD13	1:A:171:HIS:CD2	2.45	0.51
1:A:214:ARG:CG	1:A:214:ARG:NH1	2.61	0.50
1:A:56:LEU:CD2	6:A:498:HOH:O	0.80	0.50
1:A:328:ASP:O	1:A:329:ASN:HB2	2.12	0.49
1:A:332:ASP:OD2	1:A:332:ASP:O	2.30	0.49
2:B:259:LEU:HD12	2:B:268:LEU:HD11	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:VAL:HG21	1:A:284:LEU:HD21	1.94	0.49
2:B:76:GLU:OE2	2:B:80[B]:HIS:NE2	2.46	0.49
1:A:255:VAL:HG13	1:A:258:ARG:HH21	1.77	0.49
1:A:368:SER:O	1:A:369:ARG:O	2.30	0.49
1:A:109:ARG:HD2	6:A:507:HOH:O	2.12	0.49
1:A:166[B]:TYR:CZ	2:B:202:ARG:NH2	2.81	0.48
1:A:142:ARG:CG	1:A:142:ARG:NH1	2.51	0.48
2:B:150:LEU:HD21	2:B:181:LEU:CD2	2.43	0.48
1:A:262:TYR:OH	1:A:266:MET:HE3	2.13	0.48
1:A:207:GLN:HB3	6:A:479:HOH:O	2.14	0.48
2:B:239:ILE:HB	2:B:252:THR:HA	1.96	0.47
2:B:422:GLY:C	2:B:423:PHE:HD2	2.17	0.47
1:A:150:GLU:HG3	6:A:469:HOH:O	2.13	0.47
2:B:99:SER:OG	5:B:503:7TQ:CAL	2.61	0.47
2:B:202:ARG:HG2	4:B:502:FPP:C14	2.38	0.47
1:A:256:LEU:HD12	1:A:256:LEU:O	2.13	0.47
1:A:62:THR:O	1:A:62:THR:HG22	2.13	0.47
1:A:134:TRP:CD1	1:A:167:GLN:CG	2.99	0.46
2:B:54:LYS:HD2	6:B:701:HOH:O	2.15	0.46
2:B:77[A]:LYS:HD2	2:B:346:PRO:O	2.16	0.46
2:B:273:LEU:HD12	2:B:273:LEU:C	2.36	0.46
1:A:166[A]:TYR:OH	2:B:198:GLU:HB2	2.16	0.46
2:B:55:ILE:HG22	2:B:59:PHE:CE1	2.51	0.45
1:A:56:LEU:HD23	6:A:498:HOH:O	0.81	0.45
1:A:268:LYS:HE3	1:A:302:LEU:HD11	1.99	0.45
1:A:334:LEU:O	1:A:337:ALA:HB3	2.17	0.45
1:A:262:TYR:CE1	1:A:266:MET:HE2	2.53	0.44
2:B:259:LEU:HD23	2:B:259:LEU:HA	1.83	0.44
2:B:338:TYR:CE2	2:B:343:CYS:SG	3.11	0.43
2:B:152:PRO:HD3	5:B:503:7TQ:CAH	2.48	0.43
2:B:406:ASP:OD2	2:B:407:LYS:N	2.51	0.43
2:B:393:VAL:O	2:B:393:VAL:CG1	2.66	0.42
1:A:262:TYR:OH	1:A:266:MET:CE	2.68	0.42
1:A:312:ILE:HG23	1:A:340:LEU:HD22	2.02	0.42
2:B:193:MET:SD	2:B:203:SER:HB3	2.59	0.41
1:A:142:ARG:NH2	6:A:447:HOH:O	2.53	0.41
2:B:202:ARG:HD2	4:B:502:FPP:H142	2.02	0.41
1:A:303:GLN:N	1:A:304:PRO:HD2	2.36	0.41
2:B:248:HIS:CE1	4:B:502:FPP:H2	2.56	0.41
1:A:158:ILE:HD11	6:A:402:HOH:O	2.20	0.41
2:B:352:ASP:OD1	2:B:352:ASP:C	2.59	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:TYR:OH	1:A:158:ILE:CD1	2.69	0.41
1:A:156:ILE:CG1	1:A:172:ARG:HH12	2.34	0.41
2:B:226:ALA:HA	2:B:259:LEU:HD21	2.02	0.41
2:B:308:LEU:HD13	2:B:308:LEU:HA	1.72	0.41
1:A:87:VAL:O	1:A:88:VAL:C	2.60	0.40
1:A:109:ARG:HG3	6:A:507:HOH:O	2.21	0.40
2:B:27:ARG:HD3	6:B:640:HOH:O	2.21	0.40
2:B:200:ASP:OD1	2:B:202:ARG:HB2	2.21	0.40
2:B:320:ASP:HA	2:B:321:PRO:HD2	1.85	0.40
1:A:334:LEU:HD22	1:A:367:HIS:O	2.22	0.40
1:A:346:LYS:HE3	1:A:346:LYS:HB2	1.97	0.40
1:A:56:LEU:HD21	6:A:498:HOH:O	0.95	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	314/377 (83%)	293 (93%)	20 (6%)	1 (0%)	41 64
2	B	405/427 (95%)	390 (96%)	15 (4%)	0	100 100
All	All	719/804 (89%)	683 (95%)	35 (5%)	1 (0%)	51 75

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	252	ASP

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	290/338 (86%)	272 (94%)	18 (6%)	18 37
2	B	338/363 (93%)	325 (96%)	13 (4%)	33 59
All	All	628/701 (90%)	597 (95%)	31 (5%)	24 48

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	55	PHE
1	A	57	SER
1	A	85	SER
1	A	95	LYS
1	A	142	ARG
1	A	143	SER
1	A	165	ASN
1	A	214	ARG
1	A	257	GLU
1	A	297	ASN
1	A	302	LEU
1	A	303	GLN
1	A	307	SER
1	A	330	LYS
1	A	332	ASP
1	A	353	LYS
1	A	357	ARG
1	A	364	GLN
2	B	25	SER
2	B	68	VAL
2	B	112	GLU
2	B	121	ILE
2	B	273	LEU
2	B	275	GLN
2	B	308	LEU
2	B	333	GLN
2	B	351	LEU

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Mol	Chain	Res	Type
2	B	352	ASP
2	B	382	LEU
2	B	393	VAL
2	B	423	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	108	GLN
1	A	149	GLN
1	A	167	GLN
1	A	201	HIS
2	B	30	HIS
2	B	170	ASN
2	B	186	GLN
2	B	275	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 monosaccharides 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	7TQ	B	503	3	51,54,54	3.70	11 (21%)	64,76,76	2.21	15 (23%)
4	FPP	B	502	-	22,23,23	2.74	11 (50%)	27,31,31	1.83	5 (18%)

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	7TQ	B	503	3	-	4/33/49/49	0/5/6/6
4	FPP	B	502	-	-	8/25/25/25	-

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	503	7TQ	CBP-SBW	12.63	1.93	1.76
5	B	503	7TQ	OAF-SBW	10.65	1.54	1.43
5	B	503	7TQ	SBW-NBU	10.56	1.79	1.63
5	B	503	7TQ	OAE-SBW	9.37	1.53	1.43
5	B	503	7TQ	CBB-CBO	-8.28	1.39	1.51
5	B	503	7TQ	CAG-NAC	-6.49	1.00	1.14
4	B	502	FPP	PB-O1B	6.42	1.70	1.50
5	B	503	7TQ	CAZ-CBK	-5.78	1.38	1.51
5	B	503	7TQ	CBA-CBL	-5.12	1.39	1.51
4	B	502	FPP	PA-O3A	4.82	1.64	1.59
4	B	502	FPP	PB-O2B	4.40	1.71	1.54
4	B	502	FPP	C1-C2	-3.68	1.38	1.49
5	B	503	7TQ	CBC-CBQ	3.64	1.57	1.51
5	B	503	7TQ	CBR-NBT	-3.34	1.37	1.43
4	B	502	FPP	C12-C13	3.13	1.41	1.32
4	B	502	FPP	C11-C12	-2.89	1.41	1.50
4	B	502	FPP	PA-O1	2.82	1.70	1.59
4	B	502	FPP	C6-C7	-2.79	1.42	1.50
4	B	502	FPP	C7-C8	2.70	1.39	1.33
4	B	502	FPP	C2-C3	2.23	1.38	1.33
4	B	502	FPP	C10-C8	2.04	1.55	1.50
5	B	503	7TQ	CAV-CBR	2.01	1.42	1.39

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	B	503	7TQ	CBN-OBH-CBI	-7.44	105.76	118.03
5	B	503	7TQ	OAF-SBW-OAE	-6.69	109.15	119.59
5	B	503	7TQ	CBB-CBO-CAY	-6.65	110.39	119.17
4	B	502	FPP	C10-C8-C9	5.58	124.91	115.23
5	B	503	7TQ	CAU-CBP-SBW	4.90	124.60	119.73
5	B	503	7TQ	CBB-CBO-CBR	4.63	129.57	122.45
5	B	503	7TQ	CAB-NBV-CBQ	3.93	129.67	124.44
5	B	503	7TQ	CBP-SBW-NBU	3.61	113.66	107.36
4	B	502	FPP	C4-C3-C5	3.49	121.28	115.23
5	B	503	7TQ	OAD-CBI-NBF	-3.20	120.12	124.93
5	B	503	7TQ	OAF-SBW-CBP	2.65	111.40	108.10
4	B	502	FPP	O3B-PB-O2B	2.63	117.67	107.80
5	B	503	7TQ	CBO-CBR-NBT	2.45	125.34	123.79
5	B	503	7TQ	CAT-CBP-SBW	-2.35	117.40	119.73
4	B	502	FPP	C9-C8-C7	-2.28	116.05	121.17
5	B	503	7TQ	NBE-CAX-NBV	-2.26	108.90	112.26
5	B	503	7TQ	CBD-CBS-NBU	2.24	116.62	112.15
5	B	503	7TQ	CBD-NBT-CBR	2.21	121.92	116.96
5	B	503	7TQ	OBH-CBI-OAD	-2.20	119.39	123.63
4	B	502	FPP	C1-C2-C3	-2.01	122.91	126.20

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	502	FPP	PA-O3A-PB-O2B
5	B	503	7TQ	CBL-CBA-CBS-NBU
5	B	503	7TQ	OAD-CBI-OBH-CBN
5	B	503	7TQ	NBF-CBI-OBH-CBN
4	B	502	FPP	C12-C11-C9-C8
5	B	503	7TQ	CBB-NBU-SBW-OAF
4	B	502	FPP	PB-O3A-PA-O1A
4	B	502	FPP	C1-O1-PA-O1A
4	B	502	FPP	C4-C3-C5-C6
4	B	502	FPP	C2-C3-C5-C6
4	B	502	FPP	PB-O3A-PA-O1
4	B	502	FPP	PA-O3A-PB-O3B

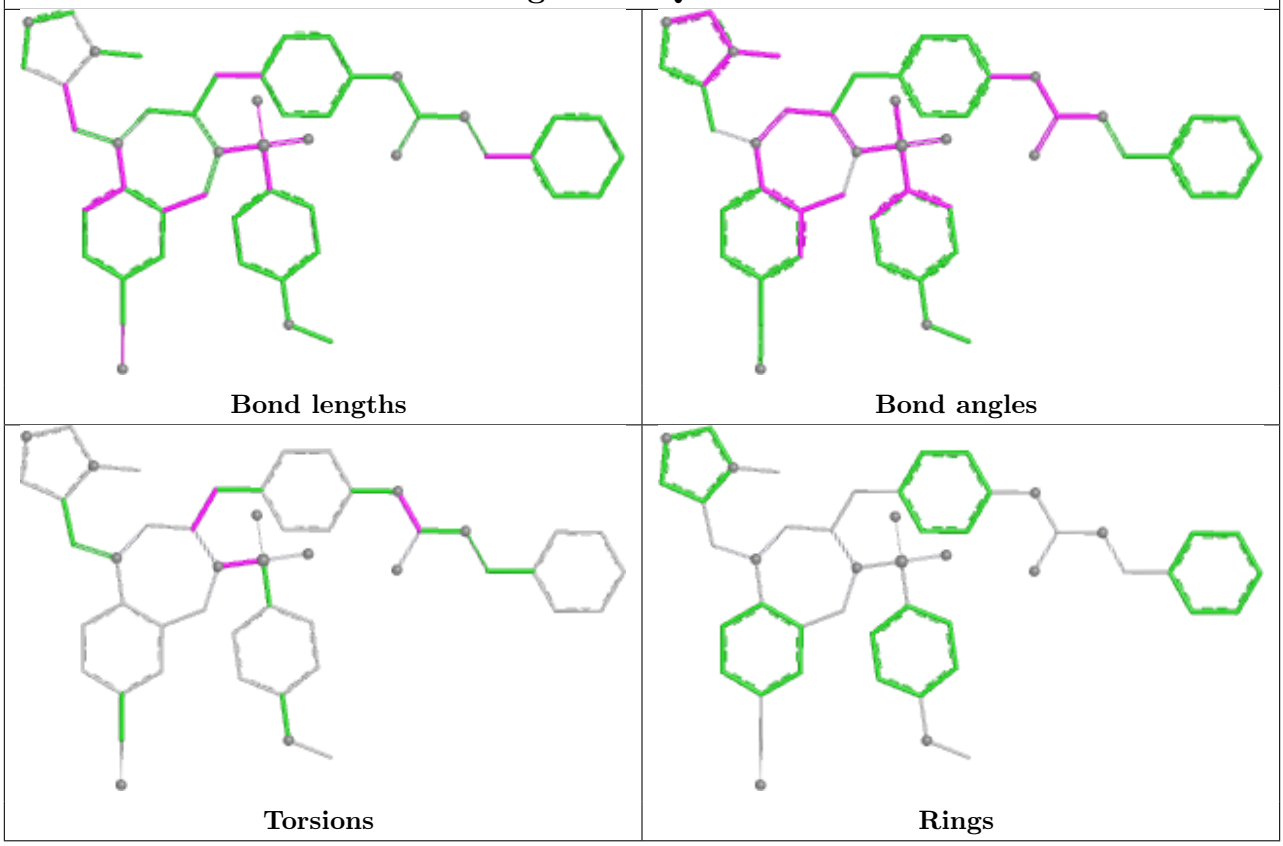
There are no ring outliers.

2 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	503	7TQ	4	0
4	B	502	FPP	7	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 then 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.

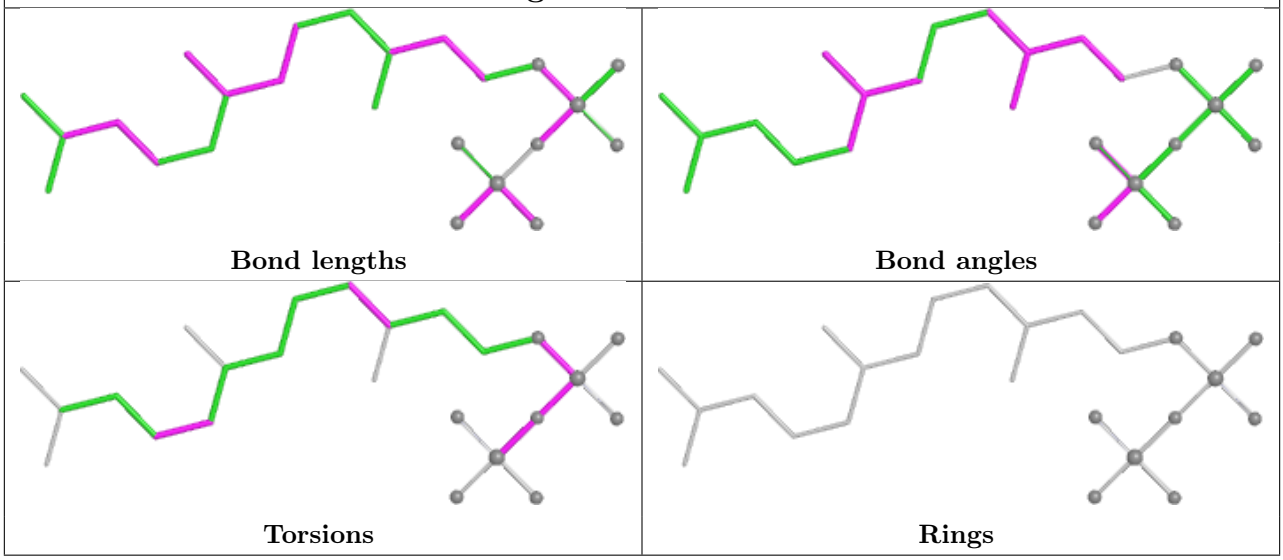
Ligand 7TQ B 503



Bond lengths | **Bond angles**

Torsions | **Rings**

Ligand FPP B 502



5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 95^{th} 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	315/377 (83%)	-0.52	3 (0%)	82	80	26, 44, 80, 99	0
2	B	405/427 (94%)	-0.43	1 (0%)	95	95	27, 38, 74, 89	0
All	All	720/804 (89%)	-0.47	4 (0%)	89	88	26, 41, 76, 99	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	20	SER	2.5
1	A	304	PRO	2.2
1	A	324	GLU	2.1
1	A	214	ARG	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no monosaccharides 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, 95^{th} 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	FPP	B	502	24/24	0.89	0.22	40,47,63,67	0

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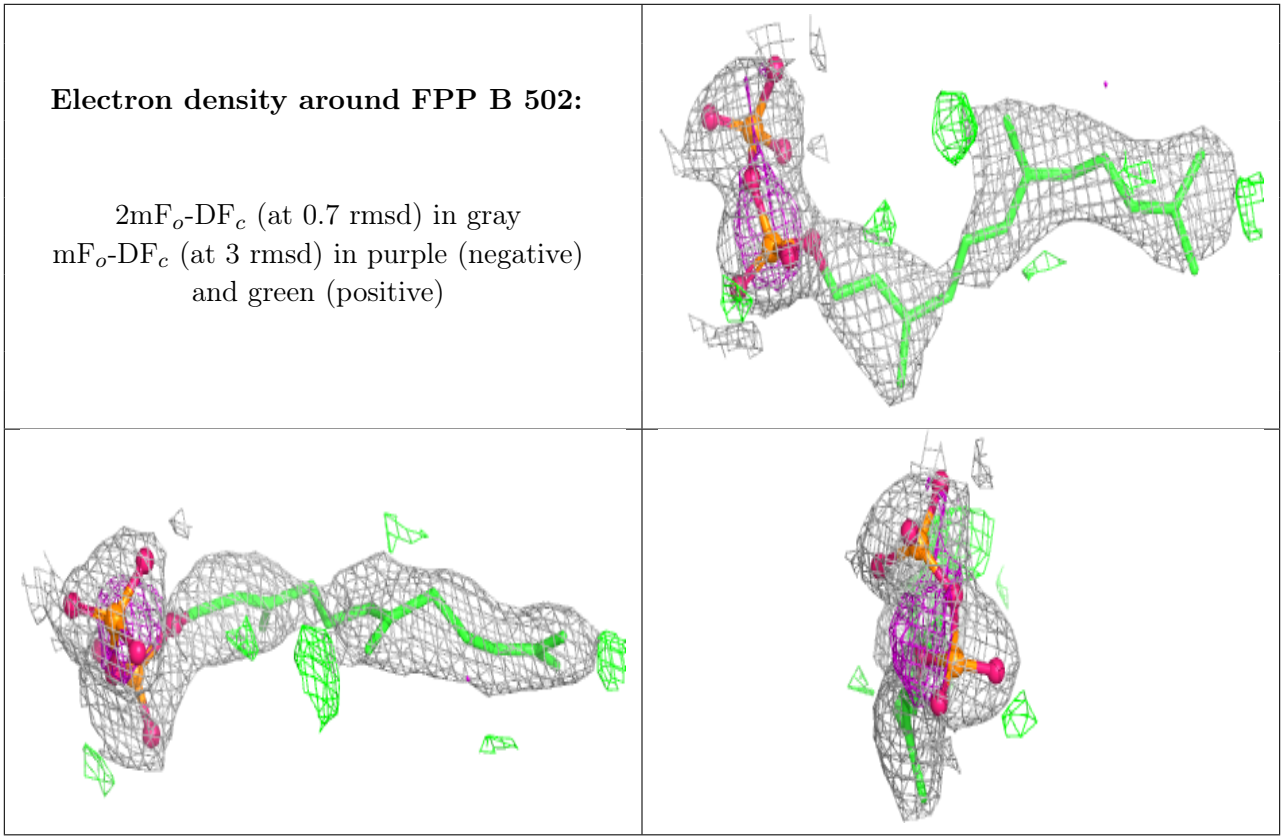
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	7TQ	B	503	49/49	0.93	0.17	33,56,138,146	0
3	ZN	B	501	1/1	0.99	0.08	30,30,30,30	0

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.

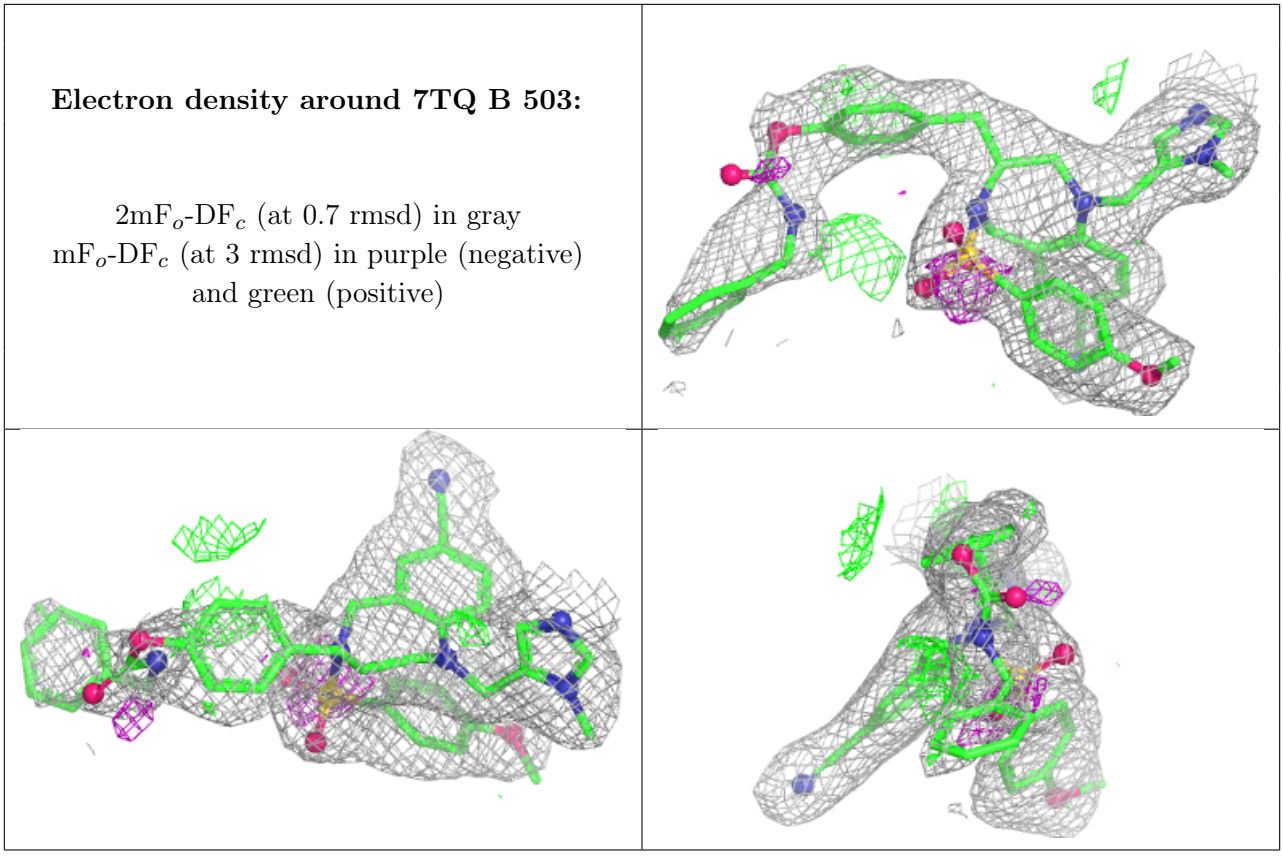
Electron density around FPP B 502:

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



Electron density around 7TQ B 503:

$2mF_o$-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.