



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 02:09 PM UTC

PDB ID : 6M8Q / pdb_00006m8q
Title : Cleavage and Polyadenylation Specificity Factor Subunit 3 (CPSF3) in complex with NVP-LTM531
Authors : Weihofen, W.A.; Salcius, M.; Michaud, G.
Deposited on : 2018-08-22
Resolution : 2.49 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

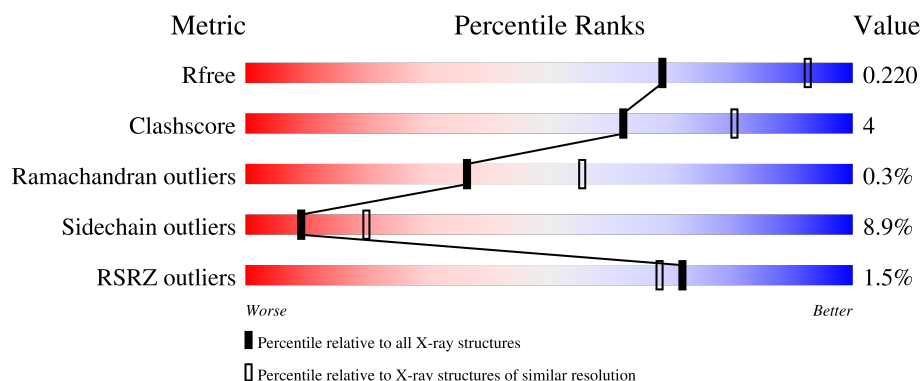
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.49 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	478	78% 15% • 6%
1	B	478	2% 76% 17% • 5%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7824 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 Cleavage and polyadenylation specificity factor subunit 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	451	Total	C	N	O	S	0	1	0
			3620	2305	621	668	26			
1	B	453	Total	C	N	O	S	0	1	0
			3635	2314	622	673	26			

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	GLY	-	expression tag	UNP Q9UKF6
A	-17	SER	-	expression tag	UNP Q9UKF6
A	-16	SER	-	expression tag	UNP Q9UKF6
A	-15	HIS	-	expression tag	UNP Q9UKF6
A	-14	HIS	-	expression tag	UNP Q9UKF6
A	-13	HIS	-	expression tag	UNP Q9UKF6
A	-12	HIS	-	expression tag	UNP Q9UKF6
A	-11	HIS	-	expression tag	UNP Q9UKF6
A	-10	HIS	-	expression tag	UNP Q9UKF6
A	-9	SER	-	expression tag	UNP Q9UKF6
A	-8	SER	-	expression tag	UNP Q9UKF6
A	-7	GLY	-	expression tag	UNP Q9UKF6
A	-6	LEU	-	expression tag	UNP Q9UKF6
A	-5	VAL	-	expression tag	UNP Q9UKF6
A	-4	PRO	-	expression tag	UNP Q9UKF6
A	-3	ARG	-	expression tag	UNP Q9UKF6
A	-2	GLY	-	expression tag	UNP Q9UKF6
A	-1	SER	-	expression tag	UNP Q9UKF6
A	0	HIS	-	expression tag	UNP Q9UKF6
B	-18	GLY	-	expression tag	UNP Q9UKF6
B	-17	SER	-	expression tag	UNP Q9UKF6
B	-16	SER	-	expression tag	UNP Q9UKF6
B	-15	HIS	-	expression tag	UNP Q9UKF6
B	-14	HIS	-	expression tag	UNP Q9UKF6
B	-13	HIS	-	expression tag	UNP Q9UKF6

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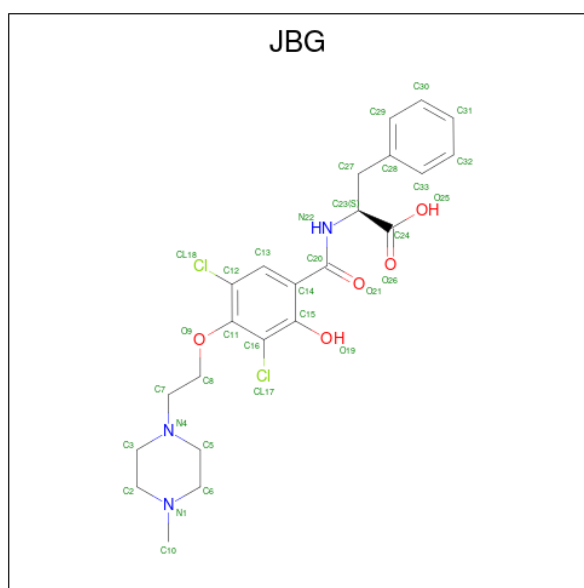
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Chain	Residue	Modelled	Actual	Comment	Reference
B	-12	HIS	-	expression tag	UNP Q9UKF6
B	-11	HIS	-	expression tag	UNP Q9UKF6
B	-10	HIS	-	expression tag	UNP Q9UKF6
B	-9	SER	-	expression tag	UNP Q9UKF6
B	-8	SER	-	expression tag	UNP Q9UKF6
B	-7	GLY	-	expression tag	UNP Q9UKF6
B	-6	LEU	-	expression tag	UNP Q9UKF6
B	-5	VAL	-	expression tag	UNP Q9UKF6
B	-4	PRO	-	expression tag	UNP Q9UKF6
B	-3	ARG	-	expression tag	UNP Q9UKF6
B	-2	GLY	-	expression tag	UNP Q9UKF6
B	-1	SER	-	expression tag	UNP Q9UKF6
B	0	HIS	-	expression tag	UNP Q9UKF6

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

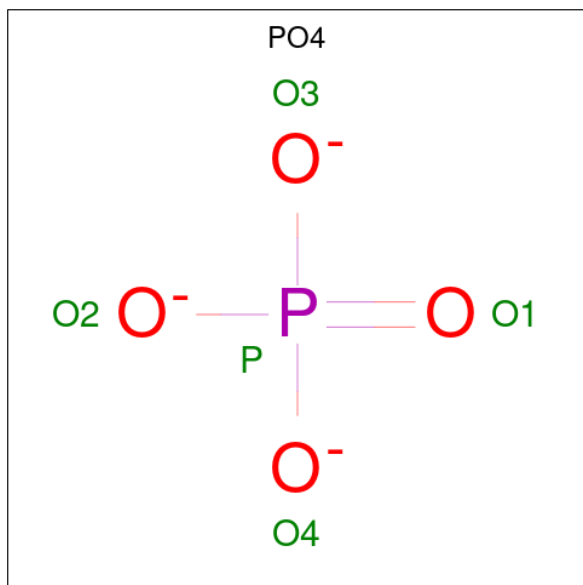
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Zn 2 2	0	0
2	B	2	Total Zn 2 2	0	0

- Molecule 3 is N-{3,5-dichloro-2-hydroxy-4-[2-(4-methylpiperazin-1-yl)ethoxy]benzene-1-carbonyl}-L-phenylalanine (CCD ID: JBG) (formula: C₂₃H₂₇Cl₂N₃O₅) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	Cl	N	O	0	0
			33	23	2	3	5		
3	B	1	Total	C	Cl	N	O	0	0
			33	23	2	3	5		

- Molecule 4 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	P	0	0
			5	4	1		
4	A	1	Total	O	P	0	0
			5	4	1		
4	B	1	Total	O	P	0	0
			5	4	1		

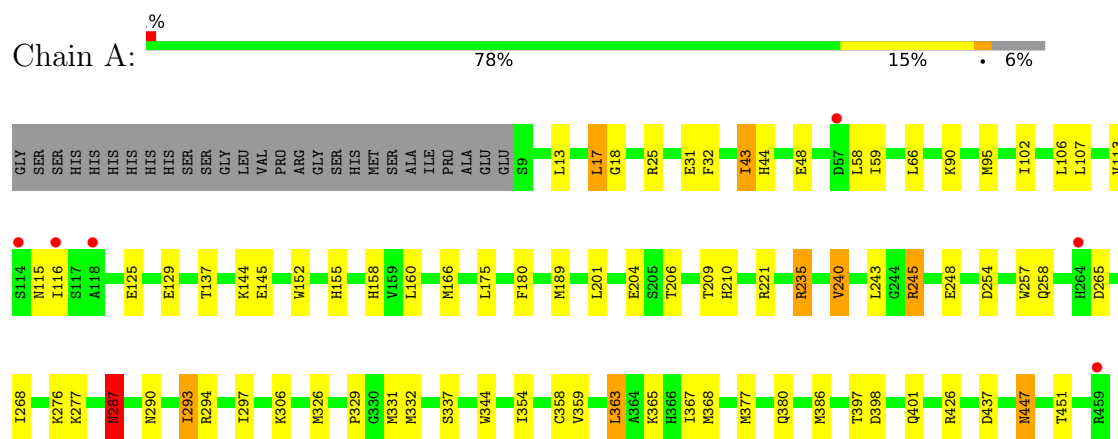
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	265	Total	O	0	0
			265	265		
5	B	219	Total	O	0	0
			219	219		

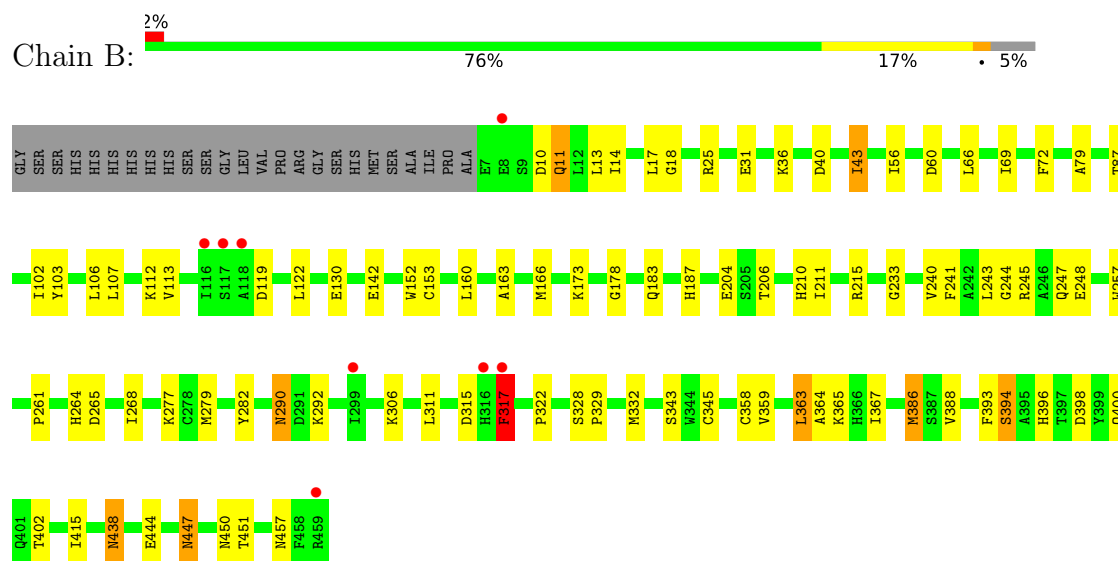
3 Residue-property plots [i](#)

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: Cleavage and polyadenylation specificity factor subunit 3



- Molecule 1: Cleavage and polyadenylation specificity factor subunit 3



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	106.22Å 106.22Å 206.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	73.95 – 2.49 73.95 – 2.49	Depositor EDS
% Data completeness (in resolution range)	99.4 (73.95-2.49) 93.9 (73.95-2.49)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.70 (at 2.48Å)	Xtriage
Refinement program	BUSTER 2.11.4	Depositor
R, R_{free}	0.163 , 0.221 0.163 , 0.220	Depositor DCC
R_{free} test set	2110 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	39.2	Xtriage
Anisotropy	0.595	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 77.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7824	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.35% 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, PO4, JBG

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	0.87	1/3704 (0.0%)	1.30	8/5010 (0.2%)
1	B	0.88	1/3722 (0.0%)	1.34	14/5034 (0.3%)
All	All	0.87	2/7426 (0.0%)	1.32	22/10044 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	332	MET	SD-CE	-7.75	1.60	1.79
1	A	332	MET	SD-CE	-5.58	1.65	1.79

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	17	LEU	N-CA-C	-6.41	105.76	113.97
1	B	393	PHE	CA-C-N	6.41	129.16	120.38
1	B	393	PHE	C-N-CA	6.41	129.16	120.38
1	B	103	TYR	CA-C-N	5.99	128.59	120.38
1	B	103	TYR	C-N-CA	5.99	128.59	120.38
1	A	17	LEU	N-CA-C	-5.88	105.94	113.23
1	A	447	ASN	CA-CB-CG	5.82	118.42	112.60
1	A	180	PHE	CA-CB-CG	5.73	119.53	113.80
1	B	317	PHE	CA-CB-CG	5.63	119.43	113.80
1	B	60	ASP	CA-CB-CG	5.61	118.20	112.60
1	A	32	PHE	CA-C-N	5.49	130.16	122.36
1	A	32	PHE	C-N-CA	5.49	130.16	122.36
1	B	438	ASN	CA-CB-CG	5.38	117.98	112.60
1	B	402	THR	CA-C-N	5.34	127.74	120.54
1	B	402	THR	C-N-CA	5.34	127.74	120.54
1	B	112	LYS	CA-C-N	5.28	127.98	120.53
1	B	112	LYS	C-N-CA	5.28	127.98	120.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	72	PHE	CA-CB-CG	5.23	119.03	113.80
1	A	245	ARG	CA-C-N	5.22	127.28	120.28
1	A	245	ARG	C-N-CA	5.22	127.28	120.28
1	B	178	GLY	N-CA-C	-5.16	101.37	110.86
1	A	287	ASN	CA-CB-CG	5.09	117.69	112.60

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	3620	0	3574	28	0
1	B	3635	0	3587	32	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	33	0	0	2	0
3	B	33	0	0	3	0
4	A	10	0	0	0	0
4	B	5	0	0	0	0
5	A	265	0	0	0	0
5	B	219	0	0	1	0
All	All	7824	0	7161	60	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 4.

All (60) 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:367:ILE:HG22	1:B:388:VAL:HG11	1.75	0.69
1:A:240:VAL:HG21	1:A:326:MET:HE3	1.77	0.67
1:B:233:GLY:HA2	1:B:322:PRO:HG3	1.79	0.63
1:B:187:HIS:HE1	1:B:282:TYR:OH	1.82	0.62
1:B:102:ILE:HG23	1:B:243:LEU:HD13	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:244:GLY:H	1:B:247:GLN:HE22	1.51	0.58
1:A:152:TRP:CZ2	1:A:166:MET:HG2	2.38	0.58
1:A:115:ASN:HD21	1:A:377:MET:HE3	1.68	0.57
1:B:31:GLU:HG2	1:B:36:LYS:HG2	1.86	0.57
1:B:363:LEU:O	1:B:367:ILE:HG12	2.05	0.56
1:A:209:THR:HG21	1:A:426:ARG:HB3	1.88	0.54
1:A:257:TRP:CD2	1:A:268:ILE:HD11	2.42	0.54
1:B:210:HIS:O	1:B:398:ASP:HB2	2.07	0.54
1:B:152:TRP:CZ2	1:B:166:MET:HG2	2.43	0.53
1:B:43:ILE:CD1	3:B:503:JBG:CL18	2.93	0.53
1:A:25:ARG:HG2	1:A:44:HIS:HB2	1.91	0.53
1:A:287:ASN:HA	1:A:294:ARG:HE	1.74	0.53
1:A:43:ILE:CD1	3:A:503:JBG:CL18	2.94	0.52
1:B:450:ASN:O	1:B:451:THR:HB	2.09	0.52
1:B:11:GLN:HE21	1:B:457:ASN:HD21	1.59	0.50
1:A:397:THR:HA	1:A:401:GLN:NE2	2.25	0.50
1:A:397:THR:HA	1:A:401:GLN:HE21	1.76	0.49
1:A:290:ASN:HB2	1:A:293:ILE:HG22	1.94	0.49
1:A:58:LEU:HD11	1:A:451:THR:HG22	1.95	0.49
1:B:447:ASN:HD22	1:B:447:ASN:H	1.62	0.47
1:A:95:MET:O	1:A:137:THR:HA	2.14	0.47
1:A:102:ILE:HG23	1:A:243:LEU:HD13	1.96	0.47
1:B:153:CYS:HB2	1:B:163:ALA:HB1	1.95	0.47
1:B:18:GLY:HA3	1:B:25:ARG:O	2.15	0.46
1:B:257:TRP:CD2	1:B:268:ILE:HD11	2.50	0.46
1:B:241:PHE:HA	1:B:328:SER:HB2	1.97	0.46
1:B:290:ASN:C	1:B:290:ASN:HD22	2.24	0.46
1:A:245:ARG:NH2	1:A:248:GLU:HG3	2.30	0.46
1:A:235:ARG:HG3	1:A:344:TRP:CE2	2.52	0.45
1:B:394:SER:HB3	1:B:396:HIS:CD2	2.51	0.45
1:A:254:ASP:O	1:A:258:GLN:HG3	2.17	0.44
1:A:155:HIS:CE1	1:A:189:MET:HE1	2.52	0.44
1:B:345:CYS:HA	1:B:386:MET:HB3	1.99	0.44
1:B:279:MET:HA	1:B:279:MET:HE2	1.99	0.44
1:B:329:PRO:HB2	3:B:503:JBG:CL17	2.54	0.43
1:A:58:LEU:CD1	1:A:451:THR:HG22	2.48	0.43
1:A:363:LEU:HD22	1:A:367:ILE:HG23	2.01	0.43
1:B:14:ILE:HD13	1:B:415:ILE:HD13	1.99	0.43
1:B:43:ILE:HD12	3:B:503:JBG:CL18	2.55	0.43
1:A:329:PRO:HD2	1:A:337:SER:OG	2.18	0.43
1:A:331:MET:HB2	3:A:503:JBG:CL17	2.56	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:125:GLU:O	1:A:129:GLU:HG3	2.19	0.43
1:B:261:PRO:HA	1:B:264:HIS:CE1	2.53	0.43
1:B:40:ASP:HA	1:B:69:ILE:HD13	2.00	0.42
1:A:18:GLY:HA3	1:A:25:ARG:O	2.19	0.42
1:A:13:LEU:HB3	1:A:31:GLU:HB2	2.00	0.42
1:B:358:CYS:SG	1:B:364:ALA:HB1	2.60	0.42
1:A:354:ILE:HG21	1:A:358:CYS:SG	2.60	0.42
1:A:175:LEU:HD23	1:A:201:LEU:HD13	2.02	0.41
1:B:394:SER:HB3	1:B:396:HIS:HD2	1.85	0.41
1:B:43:ILE:HG23	1:B:79:ALA:HB2	2.03	0.41
1:B:215:ARG:HD2	5:B:604:HOH:O	2.21	0.41
1:B:13:LEU:HB3	1:B:31:GLU:HB2	2.03	0.40
1:A:210:HIS:O	1:A:398:ASP:HB2	2.21	0.40
1:B:311:LEU:HD11	1:B:317:PHE:HB2	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	450/478 (94%)	432 (96%)	17 (4%)	1 (0%)	43	63
1	B	452/478 (95%)	428 (95%)	22 (5%)	2 (0%)	30	49
All	All	902/956 (94%)	860 (95%)	39 (4%)	3 (0%)	36	55

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	119	ASP
1	A	158	HIS
1	B	245	ARG

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	395/416 (95%)	362 (92%)	33 (8%)	10	22
1	B	397/416 (95%)	360 (91%)	37 (9%)	8	18
All	All	792/832 (95%)	722 (91%)	70 (9%)	9	20

All (70) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	LEU
1	A	43	ILE
1	A	48	GLU
1	A	59	ILE
1	A	66	LEU
1	A	90	LYS
1	A	106	LEU
1	A	107	LEU
1	A	113	VAL
1	A	116	ILE
1	A	144	LYS
1	A	145	GLU
1	A	160	LEU
1	A	204	GLU
1	A	206	THR
1	A	221	ARG
1	A	235	ARG
1	A	240	VAL
1	A	265	ASP
1	A	276	LYS
1	A	277	LYS
1	A	287	ASN
1	A	293	ILE
1	A	297	ILE
1	A	306	LYS
1	A	359	VAL
1	A	363	LEU

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Mol	Chain	Res	Type
1	A	365	LYS
1	A	368	MET
1	A	380	GLN
1	A	386	MET
1	A	437	ASP
1	A	447	ASN
1	B	10	ASP
1	B	11	GLN
1	B	43	ILE
1	B	56	ILE
1	B	66	LEU
1	B	87	THR
1	B	106	LEU
1	B	107	LEU
1	B	113	VAL
1	B	122	LEU
1	B	130	GLU
1	B	142	GLU
1	B	160	LEU
1	B	173	LYS
1	B	183	GLN
1	B	204	GLU
1	B	206	THR
1	B	211	ILE
1	B	240	VAL
1	B	248	GLU
1	B	265	ASP
1	B	277	LYS
1	B	290	ASN
1	B	292	LYS
1	B	306	LYS
1	B	315	ASP
1	B	317	PHE
1	B	343	SER
1	B	359	VAL
1	B	363	LEU
1	B	365	LYS
1	B	386	MET
1	B	394	SER
1	B	400	GLN
1	B	438	ASN
1	B	444	GLU

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Mol	Chain	Res	Type
1	B	447	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	11	GLN
1	A	97	HIS
1	A	115	ASN
1	A	139	ASN
1	A	155	HIS
1	A	183	GLN
1	A	283	GLN
1	A	287	ASN
1	A	300	ASN
1	A	301	ASN
1	A	401	GLN
1	B	97	HIS
1	B	115	ASN
1	B	187	HIS
1	B	247	GLN
1	B	259	ASN
1	B	283	GLN
1	B	290	ASN
1	B	298	ASN
1	B	300	ASN
1	B	310	ASN
1	B	380	GLN
1	B	401	GLN
1	B	447	ASN
1	B	457	ASN

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 9 ligands modelled in this entry, 4 are monoatomic - leaving 5 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$
4	PO4	A	505	2	4,4,4	2.52	2 (50%)	6,6,6	0.38	0
4	PO4	A	504	-	4,4,4	2.56	1 (25%)	6,6,6	0.41	0
3	JBG	B	503	-	35,35,35	1.16	1 (2%)	48,48,48	1.36	6 (12%)
4	PO4	B	504	2	4,4,4	2.56	1 (25%)	6,6,6	0.40	0
3	JBG	A	503	-	35,35,35	1.05	1 (2%)	48,48,48	1.41	8 (16%)

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	JBG	B	503	-	-	1/22/32/32	0/3/3/3
3	JBG	A	503	-	-	1/22/32/32	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	504	PO4	P-O1	4.33	1.60	1.50
4	A	504	PO4	P-O1	4.28	1.60	1.50
4	A	505	PO4	P-O1	4.17	1.60	1.50
3	A	503	JBG	C16-CL17	2.11	1.77	1.72
4	A	505	PO4	P-O3	2.04	1.60	1.54
3	B	503	JBG	C29-C28	2.00	1.42	1.38

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	503	JBG	C6-N1-C2	4.43	116.59	109.54
3	A	503	JBG	C15-C16-CL17	3.53	122.37	118.09
3	A	503	JBG	C14-C15-C16	3.09	120.89	118.49
3	A	503	JBG	O21-C20-C14	-2.99	115.56	121.03
3	A	503	JBG	C7-N4-C5	2.80	118.69	111.24
3	A	503	JBG	C6-N1-C2	2.73	113.89	109.54
3	B	503	JBG	C14-C15-C16	2.64	120.53	118.49
3	B	503	JBG	C23-N22-C20	2.49	127.55	121.56
3	A	503	JBG	C5-N4-C3	2.49	114.20	108.84
3	B	503	JBG	O21-C20-C14	-2.29	116.84	121.03
3	B	503	JBG	C5-N4-C3	2.27	113.74	108.84
3	A	503	JBG	O9-C8-C7	-2.24	102.14	107.79
3	A	503	JBG	C10-N1-C6	2.10	114.64	110.63
3	B	503	JBG	C7-N4-C5	2.01	116.59	111.24

There are no chirality outliers.

All (2) torsion outliers are listed below:

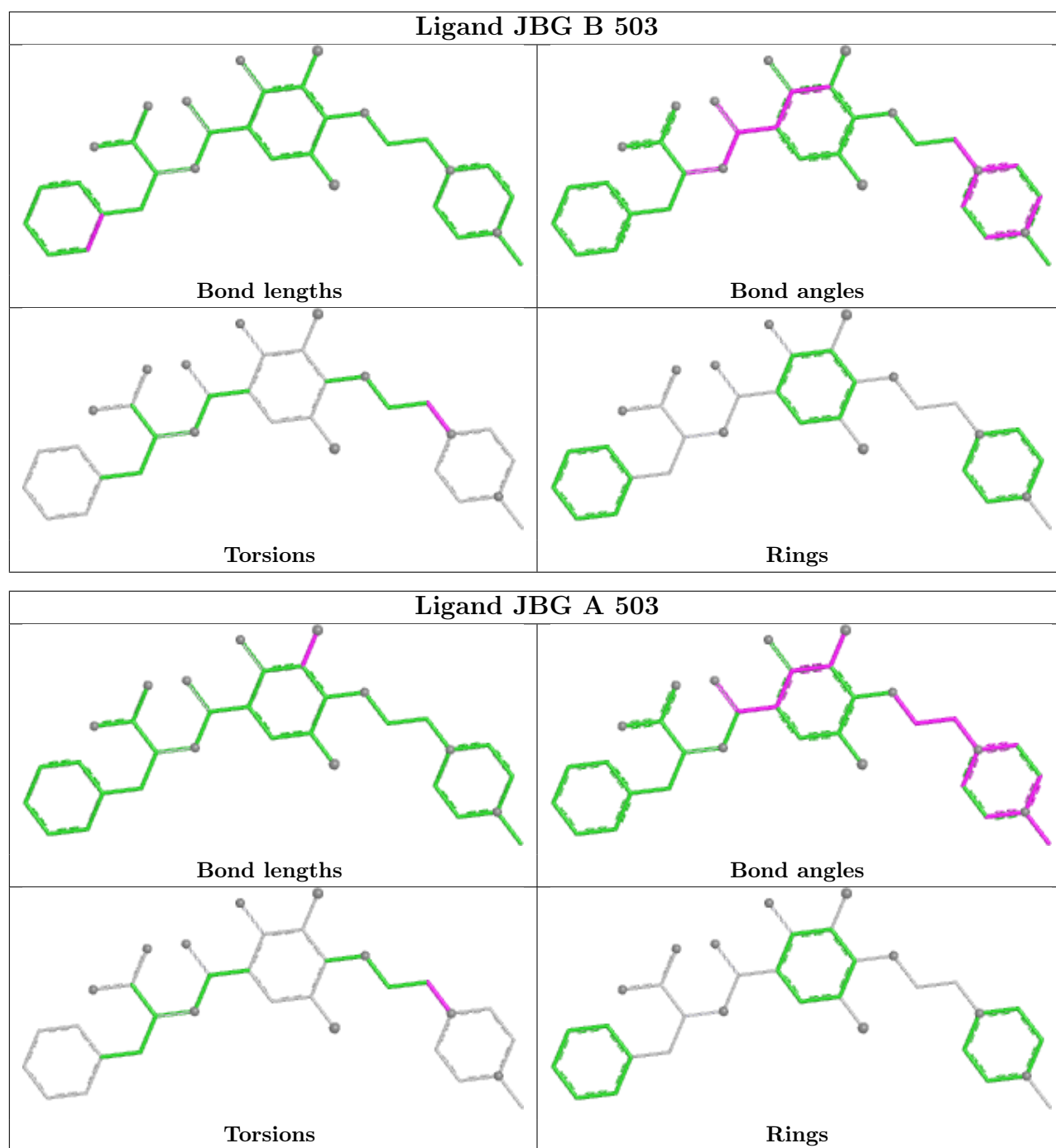
Mol	Chain	Res	Type	Atoms
3	B	503	JBG	C8-C7-N4-C3
3	A	503	JBG	C8-C7-N4-C3

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	503	JBG	3	0
3	A	503	JBG	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.



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	451/478 (94%)	-0.21	6 (1%) 75 71	23, 44, 71, 107	1 (0%)
1	B	453/478 (94%)	-0.01	8 (1%) 67 64	29, 51, 85, 116	1 (0%)
All	All	904/956 (94%)	-0.11	14 (1%) 72 68	23, 47, 81, 116	2 (0%)

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	116	ILE	5.3
1	A	264[A]	HIS	4.3
1	A	116	ILE	3.4
1	A	118	ALA	3.3
1	B	118	ALA	3.0
1	A	459	ARG	2.9
1	B	317	PHE	2.6
1	A	114	SER	2.5
1	B	459	ARG	2.5
1	A	57	ASP	2.4
1	B	117	SER	2.3
1	B	8	GLU	2.2
1	B	299	ILE	2.1
1	B	316	HIS	2.1

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](#)

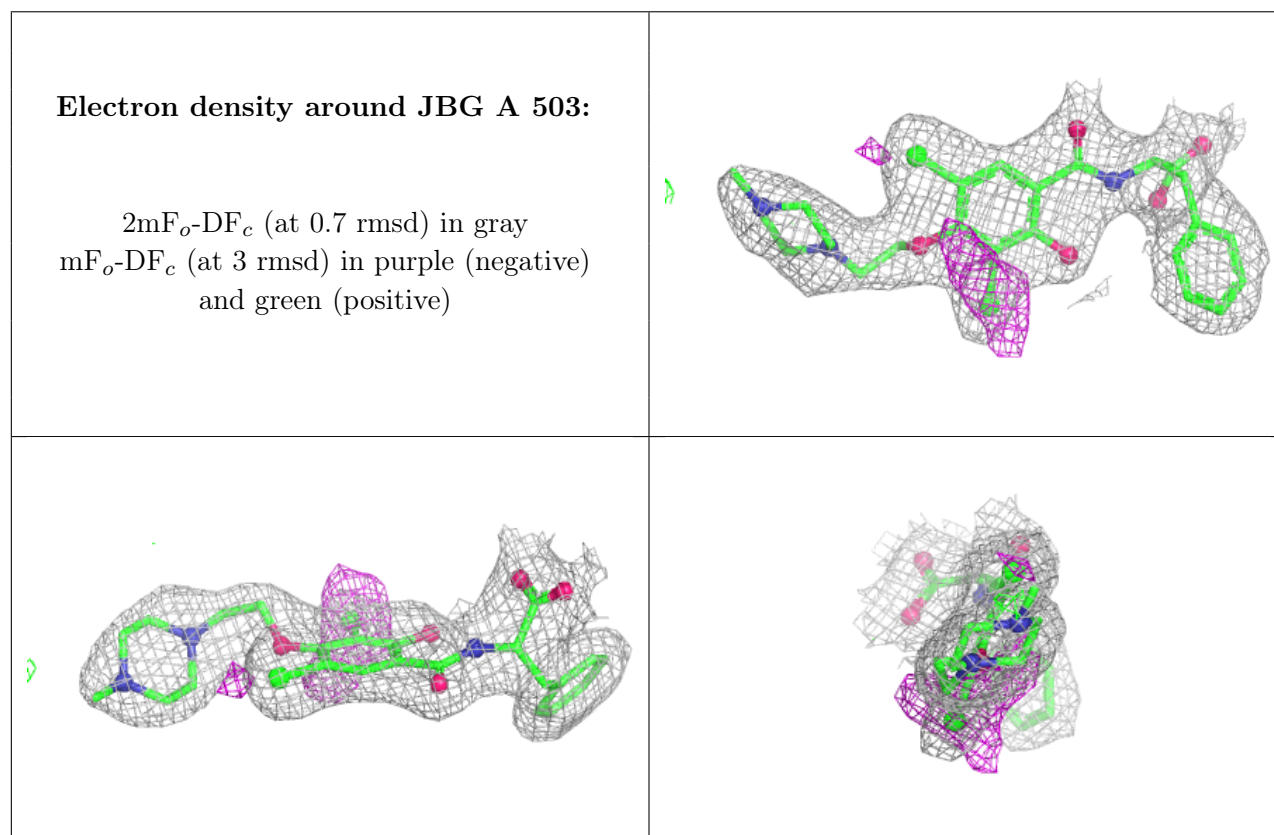
There are no oligosaccharides in this entry.

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.

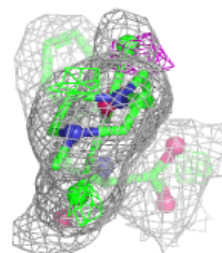
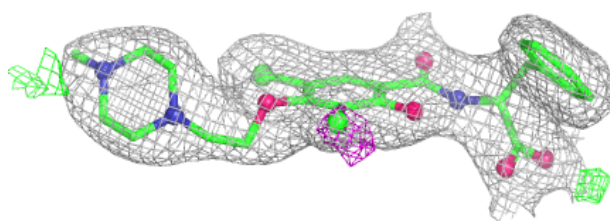
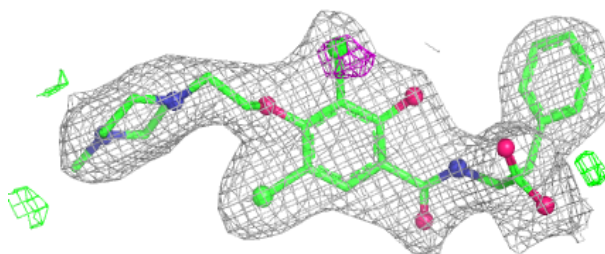
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	JBG	A	503	33/33	0.94	0.09	37,48,61,67	0
3	JBG	B	503	33/33	0.95	0.08	42,51,56,71	0
4	PO4	A	504	5/5	0.97	0.07	59,59,62,62	0
4	PO4	B	504	5/5	0.97	0.08	48,49,50,50	0
4	PO4	A	505	5/5	0.98	0.06	45,47,53,53	0
2	ZN	A	502	1/1	1.00	0.01	41,41,41,41	0
2	ZN	B	501	1/1	1.00	0.01	47,47,47,47	0
2	ZN	B	502	1/1	1.00	0.01	45,45,45,45	0
2	ZN	A	501	1/1	1.00	0.02	45,45,45,45	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 JBG 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.