Full wwPDB X-ray Structure Validation Report (i)

Apr 27, 2024 – 10:54 am BST

PDB ID	:	4Y6S
Title	:	Structure of Plasmodium falciparum DXR in complex with a beta-substituted fosmidomycin analogue, RC134, and manganese
Authors	:	Sooriyaarachchi, S.; Bergfors, T.; Jones, T.A.; Mowbray, S.L.
Deposited on	:	2015-02-13
Resolution	:	2.10 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 (i) 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 (i)) were used in the production of this report:

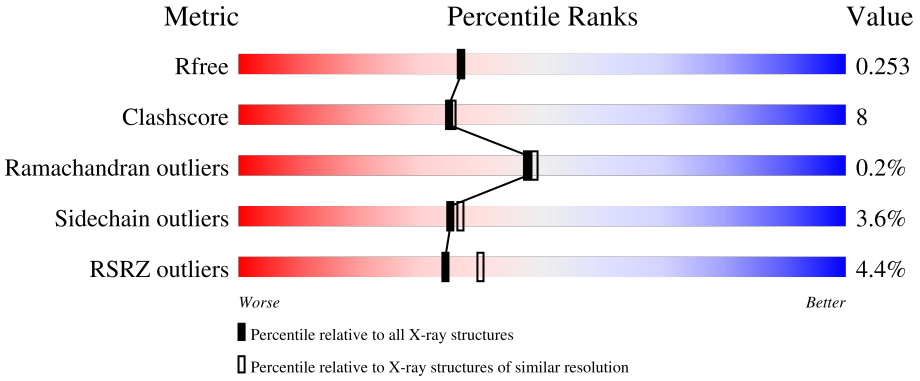
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
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 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	422	2% 77% 19% • •
1	B	422	7% 77% 19% • •

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 6843 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 1-deoxy-D-xylulose 5-phosphate reductoisomerase, apicoplast.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	410	3276	2103	537	616	20	0	0	0
1	B	410	3276	2103	537	616	20	0	0	0

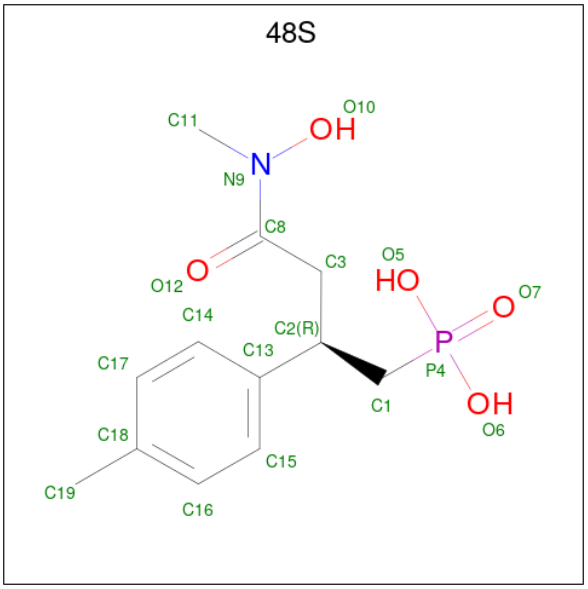
There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	67	MET	-	initiating methionine	UNP Q8IKG4
A	68	ALA	-	expression tag	UNP Q8IKG4
A	69	HIS	-	expression tag	UNP Q8IKG4
A	70	HIS	-	expression tag	UNP Q8IKG4
A	71	HIS	-	expression tag	UNP Q8IKG4
A	72	HIS	-	expression tag	UNP Q8IKG4
A	73	HIS	-	expression tag	UNP Q8IKG4
A	74	HIS	-	expression tag	UNP Q8IKG4
B	67	MET	-	initiating methionine	UNP Q8IKG4
B	68	ALA	-	expression tag	UNP Q8IKG4
B	69	HIS	-	expression tag	UNP Q8IKG4
B	70	HIS	-	expression tag	UNP Q8IKG4
B	71	HIS	-	expression tag	UNP Q8IKG4
B	72	HIS	-	expression tag	UNP Q8IKG4
B	73	HIS	-	expression tag	UNP Q8IKG4
B	74	HIS	-	expression tag	UNP Q8IKG4

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mn		
2	A	1	1	1	0	0
2	B	1	1	1	0	0

- Molecule 3 is [(2R)-4-[hydroxy(methyl)amino]-2-(4-methylphenyl)-4-oxobutyl]phosphonic acid (three-letter code: 48S) (formula: $C_{12}H_{18}NO_5P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	A	1	19	12	1	5	1	0	0
			Total	C	N	O	P		
3	B	1	19	12	1	5	1	0	0

- Molecule 4 is water.

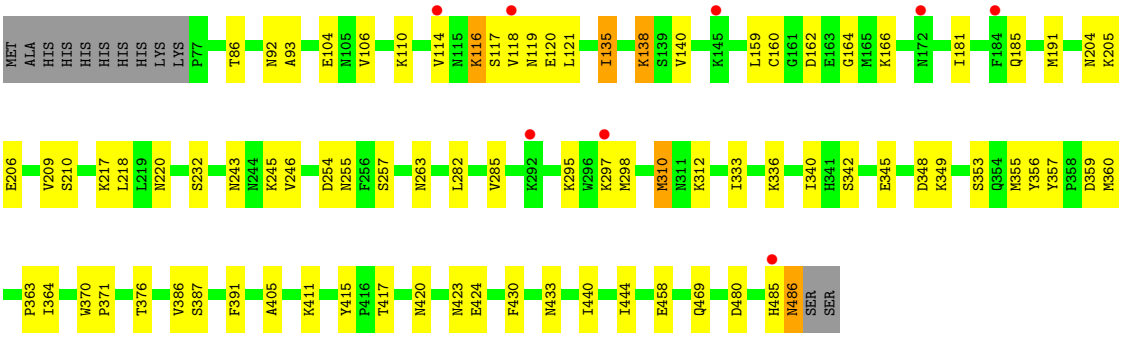
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	144	144	144	0	0
			Total	O		
4	B	107	107	107	0	0

3 Residue-property plots (i)

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

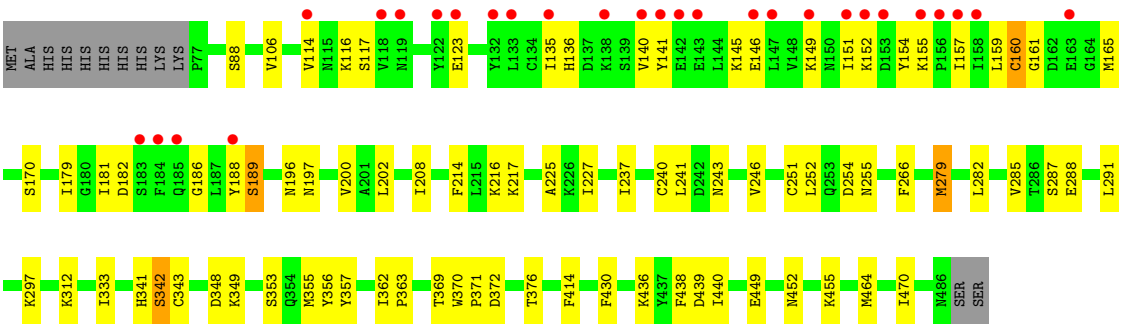
• Molecule 1: 1-deoxy-D-xylulose 5-phosphate reductoisomerase, apicoplast

Chain A:



• Molecule 1: 1-deoxy-D-xylulose 5-phosphate reductoisomerase, apicoplast

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	51.40Å 54.96Å 85.05Å 89.41° 105.52° 107.28°	Depositor
Resolution (Å)	47.15 – 2.10 47.16 – 2.10	Depositor EDS
% Data completeness (in resolution range)	93.9 (47.15-2.10) 93.9 (47.16-2.10)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.21 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.217 , 0.252 0.221 , 0.253	Depositor DCC
R_{free} test set	2377 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å^2)	23.4	Xtriage
Anisotropy	1.172	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 38.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	6843	wwPDB-VP
Average B, all atoms (Å^2)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.20% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: MN, 48S

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	0.45	1/3339 (0.0%)	0.69	1/4509 (0.0%)
1	B	0.43	0/3339	0.67	0/4509
All	All	0.44	1/6678 (0.0%)	0.68	1/9018 (0.0%)

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
1	B	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	486	ASN	C-O	5.64	1.34	1.23

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	310	MET	CG-SD-CE	5.31	108.69	100.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	181	ILE	Peptide

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	3276	0	3322	65	0
1	B	3276	0	3322	54	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	19	0	17	4	0
3	B	19	0	17	0	0
4	A	144	0	0	11	0
4	B	107	0	0	1	0
All	All	6843	0	6678	110	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 8.

All (110) 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:486:ASN:O	4:A:601:HOH:O	1.79	1.00
1:A:364:ILE:HD12	4:A:728:HOH:O	1.75	0.87
1:A:106:VAL:HG13	4:A:719:HOH:O	1.79	0.80
1:B:279:MET:CE	1:B:438:PHE:CZ	2.67	0.77
1:B:279:MET:CE	1:B:438:PHE:HZ	2.01	0.73
1:A:104:GLU:O	1:A:106:VAL:HG23	1.90	0.71
1:B:146:GLU:OE1	1:B:149:LYS:HE2	1.90	0.71
1:B:202:LEU:HD23	1:B:208:ILE:HD11	1.73	0.71
1:A:116:LYS:HA	1:A:135:ILE:HD11	1.73	0.69
1:A:295:LYS:NZ	1:A:336:LYS:O	2.23	0.67
1:A:206:GLU:HG2	1:A:420:ASN:HD21	1.60	0.66
1:A:340:ILE:HD12	1:A:391:PHE:HZ	1.61	0.66
1:A:310:MET:HE1	1:A:405:ALA:HB2	1.78	0.64
1:A:217:LYS:HE2	1:A:458:GLU:O	1.98	0.63
1:B:254:ASP:O	1:B:255:ASN:HB2	1.97	0.63
1:A:245:LYS:NZ	1:B:372:ASP:OD1	2.32	0.62
1:A:355:MET:HE1	1:B:353:SER:CB	2.30	0.61
1:A:106:VAL:CG1	4:A:719:HOH:O	2.45	0.61
1:B:279:MET:HE3	1:B:438:PHE:HZ	1.64	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:355:MET:HE1	1:B:353:SER:OG	2.01	0.60
1:B:362:ILE:HB	1:B:363:PRO:HD3	1.82	0.60
1:A:359:ASP:O	4:A:727:HOH:O	2.17	0.59
1:B:200:VAL:HB	1:B:227:ILE:HD13	1.84	0.59
1:B:123:GLU:HA	1:B:123:GLU:OE1	2.02	0.59
1:B:251:CYS:O	1:B:252:LEU:HB2	2.02	0.59
1:A:355:MET:CE	1:B:353:SER:OG	2.51	0.59
1:A:355:MET:HE1	1:B:353:SER:HB3	1.84	0.58
1:A:92:ASN:HB3	4:A:728:HOH:O	2.04	0.57
1:A:424:GLU:OE2	4:A:686:HOH:O	2.18	0.57
1:A:364:ILE:CD1	4:A:728:HOH:O	2.43	0.57
1:A:263:ASN:ND2	1:A:345:GLU:OE2	2.35	0.57
1:B:186:GLY:HA2	4:B:634:HOH:O	2.05	0.57
1:B:430:PHE:CG	1:B:440:ILE:HD11	2.40	0.57
1:B:279:MET:HE1	1:B:438:PHE:CZ	2.39	0.57
1:B:135:ILE:O	1:B:160:CYS:HA	2.05	0.56
1:B:282:LEU:O	1:B:285:VAL:HG22	2.06	0.56
1:B:370:TRP:CD1	1:B:371:PRO:HA	2.41	0.56
1:B:114:VAL:HG23	1:B:135:ILE:HD12	1.88	0.55
1:B:136:HIS:CD2	1:B:161:GLY:HA2	2.42	0.54
1:A:355:MET:O	1:A:356:TYR:HB2	2.08	0.53
1:A:210:SER:OG	1:A:417:THR:HG23	2.09	0.52
1:A:298:MET:CE	3:A:502:48S:H3	2.39	0.52
1:B:179:ILE:HB	1:B:202:LEU:HD12	1.92	0.52
1:B:165:MET:SD	1:B:189:SER:HA	2.51	0.51
1:A:430:PHE:CG	1:A:440:ILE:HD11	2.46	0.51
1:B:157:ILE:CG2	1:B:159:LEU:HD21	2.41	0.51
1:A:310:MET:CE	1:A:405:ALA:HB2	2.39	0.51
1:A:191:MET:HG3	1:A:218:LEU:HD21	1.92	0.50
1:B:266:PHE:HB2	1:B:343:CYS:HB2	1.94	0.50
1:B:414:PHE:CG	1:B:470:ILE:HD13	2.47	0.50
1:A:162:ASP:O	1:A:166:LYS:HG3	2.12	0.49
1:A:353:SER:OG	1:B:355:MET:HE2	2.11	0.49
1:B:287:SER:O	1:B:291:LEU:HG	2.13	0.49
1:A:370:TRP:CD1	1:A:371:PRO:HA	2.47	0.48
1:B:430:PHE:CB	1:B:440:ILE:HD11	2.43	0.47
1:B:356:TYR:CG	1:B:357:TYR:N	2.82	0.47
1:A:86:THR:HB	1:A:120:GLU:OE1	2.15	0.47
1:A:92:ASN:HB3	1:A:364:ILE:HD12	1.97	0.46
1:B:116:LYS:HA	1:B:135:ILE:HD11	1.97	0.46
1:A:118:VAL:CG1	1:A:140:VAL:HB	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:282:LEU:O	1:A:285:VAL:HG22	2.16	0.46
1:A:297:LYS:HA	4:A:669:HOH:O	2.15	0.46
1:B:197:ASN:HA	1:B:225:ALA:HB2	1.98	0.46
1:A:298:MET:HE1	3:A:502:48S:H3	1.97	0.45
1:A:114:VAL:HG23	1:A:121:LEU:HD13	1.99	0.45
1:A:110:LYS:HA	1:A:110:LYS:HD2	1.74	0.45
1:A:433:ASN:ND2	4:A:657:HOH:O	2.35	0.45
1:A:159:LEU:HD13	1:A:164:GLY:HA2	1.99	0.44
1:B:214:PHE:CZ	1:B:464:MET:HG2	2.52	0.44
1:A:181:ILE:HG21	1:A:185:GLN:HG3	2.00	0.44
1:B:436:LYS:O	1:B:439:ASP:HB2	2.17	0.44
1:B:312:LYS:HA	1:B:312:LYS:HE2	2.00	0.44
1:A:118:VAL:HG23	1:A:119:ASN:H	1.81	0.44
1:A:411:LYS:HD3	1:A:415:TYR:CE2	2.52	0.44
1:B:237:ILE:O	1:B:241:LEU:HG	2.17	0.44
1:A:340:ILE:HD12	1:A:391:PHE:CZ	2.47	0.43
1:A:376:THR:HG23	1:B:348:ASP:HA	2.01	0.43
1:B:135:ILE:HG12	1:B:140:VAL:HG23	2.00	0.43
1:B:369:THR:O	1:B:370:TRP:C	2.56	0.43
1:A:356:TYR:CG	1:A:357:TYR:N	2.86	0.43
1:A:348:ASP:O	1:A:349:LYS:HB2	2.19	0.43
1:A:430:PHE:CB	1:A:440:ILE:HD11	2.48	0.43
1:A:480:ASP:HA	4:A:608:HOH:O	2.18	0.42
1:B:151:ILE:HG22	1:B:154:TYR:HB3	2.00	0.42
1:A:376:THR:O	1:B:349:LYS:NZ	2.45	0.42
1:A:360:MET:O	1:A:363:PRO:HD2	2.19	0.42
1:B:370:TRP:CG	1:B:371:PRO:HA	2.54	0.42
1:A:93:ALA:HA	1:A:364:ILE:HG21	2.02	0.42
1:A:114:VAL:CG2	1:A:121:LEU:HD13	2.50	0.42
1:A:217:LYS:CE	1:A:458:GLU:O	2.66	0.42
1:A:254:ASP:O	1:A:255:ASN:HB2	2.20	0.42
1:B:141:TYR:CE2	1:B:145:LYS:HE3	2.55	0.42
1:A:423:ASN:HA	1:A:444:ILE:HD11	2.02	0.42
1:A:360:MET:C	1:A:363:PRO:HD2	2.40	0.42
1:B:243:ASN:HA	1:B:246:VAL:HB	2.01	0.42
1:A:243:ASN:HA	1:A:246:VAL:HB	2.02	0.41
1:A:349:LYS:NZ	1:B:376:THR:O	2.51	0.41
1:A:386:VAL:O	1:A:387:SER:HB3	2.20	0.41
1:B:341:HIS:O	1:B:342:SER:CB	2.68	0.41
1:A:298:MET:HE3	3:A:502:48S:H3	2.02	0.41
1:B:216:LYS:HG3	1:B:252:LEU:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:502:48S:H5	3:A:502:48S:H10	1.83	0.41
1:B:182:ASP:OD1	1:B:182:ASP:N	2.49	0.41
1:A:355:MET:HE2	1:B:353:SER:OG	2.21	0.40
1:B:240:CYS:SG	1:B:353:SER:HA	2.60	0.40
1:B:141:TYR:CZ	1:B:145:LYS:HE2	2.56	0.40
1:A:138:LYS:HD2	1:A:160:CYS:SG	2.61	0.40
1:A:232:SER:HB3	1:A:360:MET:SD	2.61	0.40
1:A:205:LYS:O	1:A:209:VAL:HG23	2.21	0.40
1:B:170:SER:HA	1:B:196:ASN:OD1	2.22	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	408/422 (97%)	385 (94%)	22 (5%)	1 (0%)	47	49
1	B	408/422 (97%)	386 (95%)	21 (5%)	1 (0%)	47	49
All	All	816/844 (97%)	771 (94%)	43 (5%)	2 (0%)	47	49

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	485	HIS
1	B	342	SER

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	377/388 (97%)	366 (97%)	11 (3%)	42	46
1	B	377/388 (97%)	361 (96%)	16 (4%)	30	30
All	All	754/776 (97%)	727 (96%)	27 (4%)	35	36

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	116	LYS
1	A	117	SER
1	A	135	ILE
1	A	138	LYS
1	A	204	ASN
1	A	220	ASN
1	A	257	SER
1	A	312	LYS
1	A	333	ILE
1	A	342	SER
1	A	469	GLN
1	B	88	SER
1	B	106	VAL
1	B	117	SER
1	B	152	LYS
1	B	155	LYS
1	B	160	CYS
1	B	188	TYR
1	B	189	SER
1	B	217	LYS
1	B	279	MET
1	B	288	GLU
1	B	297	LYS
1	B	333	ILE
1	B	449	GLU
1	B	452	ASN
1	B	455	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	185	GLN

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Mol	Chain	Res	Type
1	A	255	ASN
1	A	420	ASN
1	B	115	ASN
1	B	136	HIS
1	B	150	ASN
1	B	420	ASN

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 4 ligands modelled in this entry, 2 are 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	$\#\|Z\| > 2$
3	48S	A	502	2	16,19,19	0.92	0	19,27,27	1.52	1 (5%)
3	48S	B	502	2	16,19,19	0.84	0	19,27,27	1.55	3 (15%)

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	48S	A	502	2	-	3/17/17/17	0/1/1/1
3	48S	B	502	2	-	3/17/17/17	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	502	48S	C3-C2-C13	-5.11	102.75	111.93
3	B	502	48S	C3-C2-C13	-4.55	103.75	111.93
3	B	502	48S	C3-C8-N9	2.71	120.94	117.63
3	B	502	48S	O12-C8-C3	-2.44	117.80	122.20

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	502	48S	C14-C13-C2-C1
3	A	502	48S	C15-C13-C2-C1
3	B	502	48S	C14-C13-C2-C1
3	B	502	48S	C15-C13-C2-C1
3	A	502	48S	O12-C8-N9-O10
3	B	502	48S	O12-C8-N9-O10

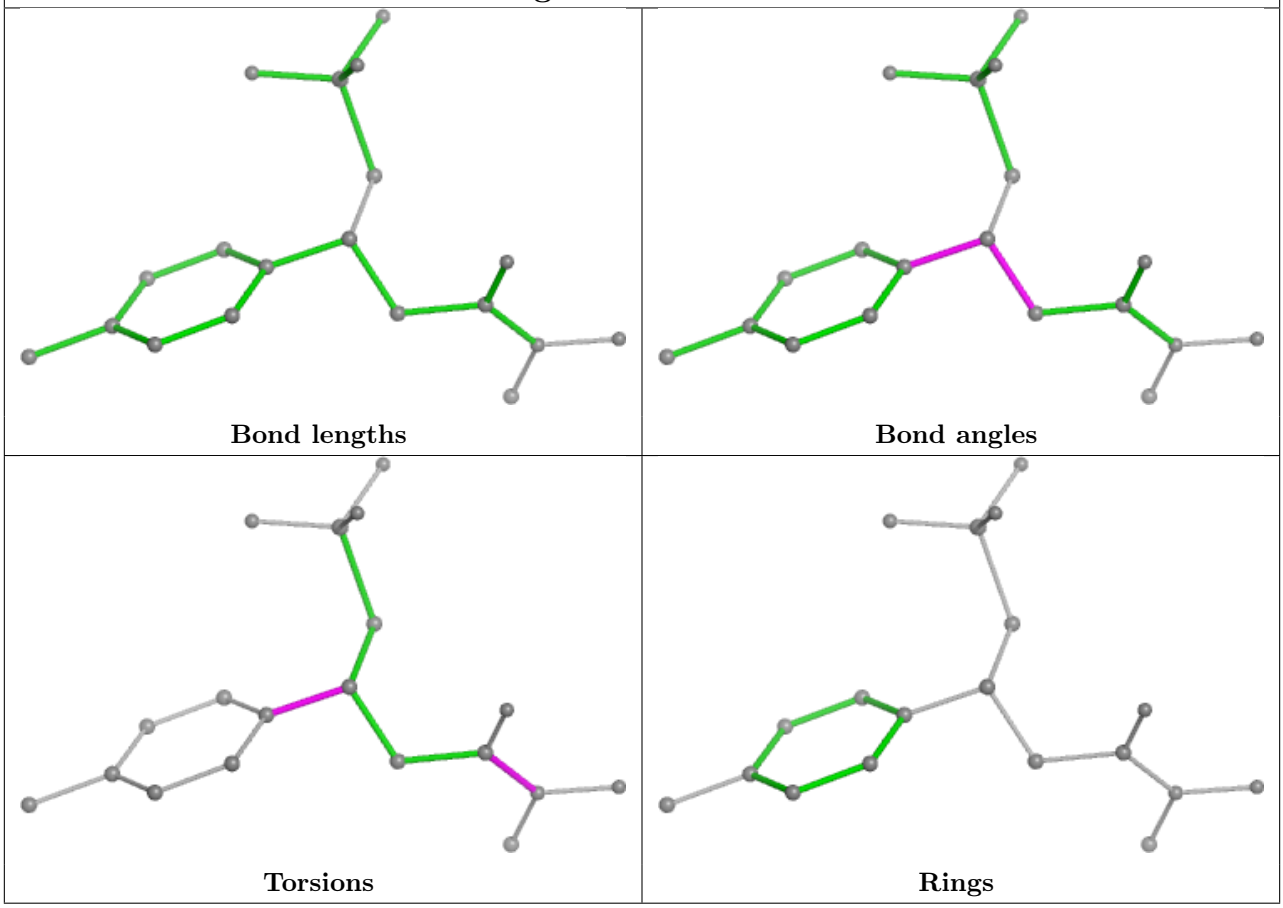
There are no ring outliers.

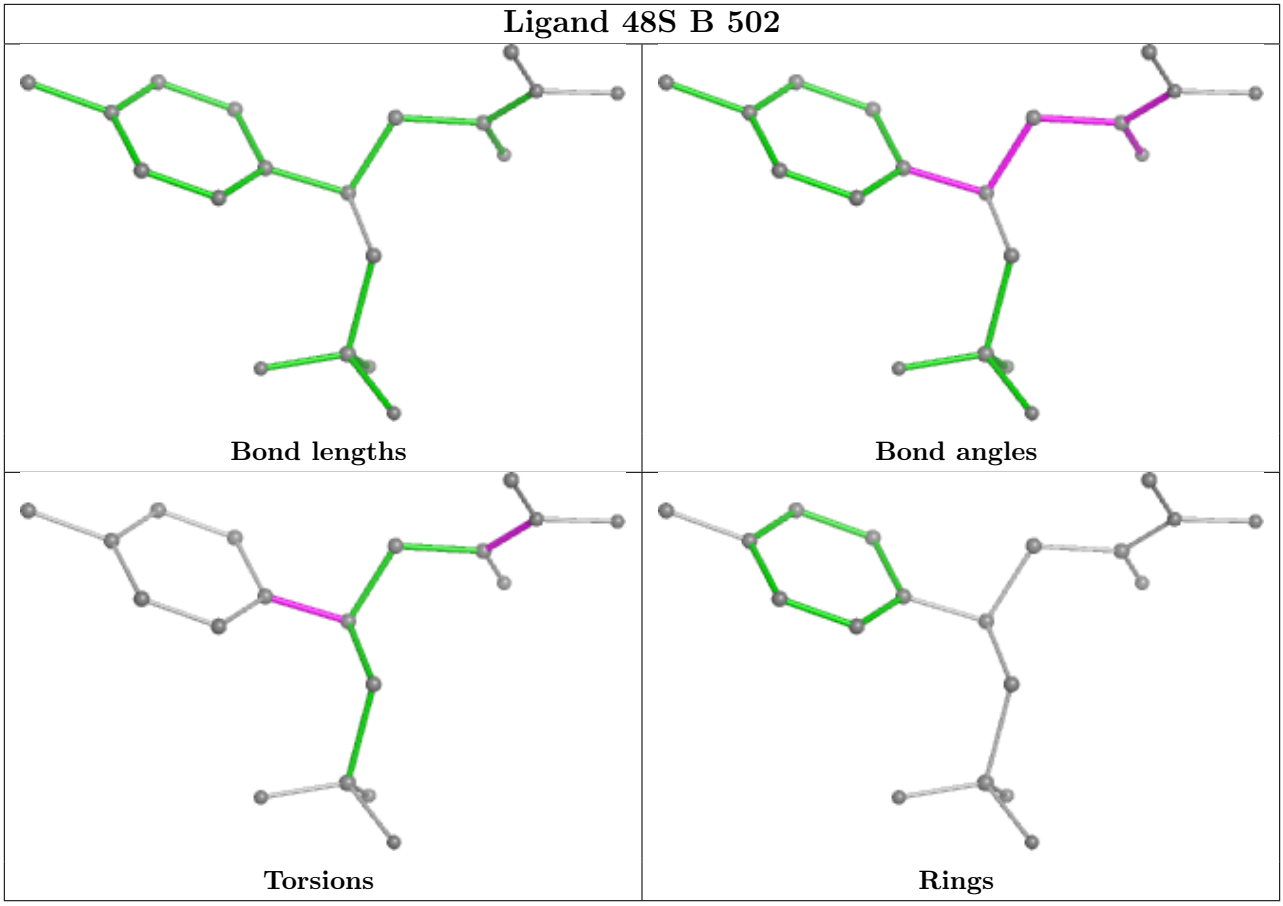
1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	502	48S	4	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 48S A 502





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	410/422 (97%)	0.11	8 (1%)	65	69	19, 29, 47, 73	0
1	B	410/422 (97%)	0.31	28 (6%)	17	21	18, 31, 66, 78	0
All	All	820/844 (97%)	0.21	36 (4%)	34	40	18, 30, 59, 78	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	183	SER	4.8
1	B	147	LEU	3.7
1	B	118	VAL	3.5
1	B	184	PHE	3.5
1	B	157	ILE	3.4
1	A	485	HIS	3.3
1	B	158	ILE	3.2
1	B	149	LYS	3.1
1	B	152	LYS	3.0
1	B	119	ASN	3.0
1	B	146	GLU	2.9
1	B	138	LYS	2.9
1	A	184	PHE	2.7
1	A	292	LYS	2.7
1	B	133	LEU	2.6
1	B	142	GLU	2.6
1	B	135	ILE	2.6
1	B	143	GLU	2.6
1	B	114	VAL	2.5
1	B	156	PRO	2.5
1	B	151	ILE	2.4
1	B	155	LYS	2.4
1	A	297	LYS	2.4
1	A	114	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	188	TYR	2.3
1	B	153	ASP	2.3
1	A	145	LYS	2.3
1	B	132	TYR	2.3
1	B	123	GLU	2.3
1	B	163	GLU	2.2
1	B	141	TYR	2.1
1	B	185	GLN	2.0
1	B	140	VAL	2.0
1	A	172	ASN	2.0
1	A	118	VAL	2.0
1	B	122	TYR	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 monosaccharides in this entry.

6.4 Ligands (i)

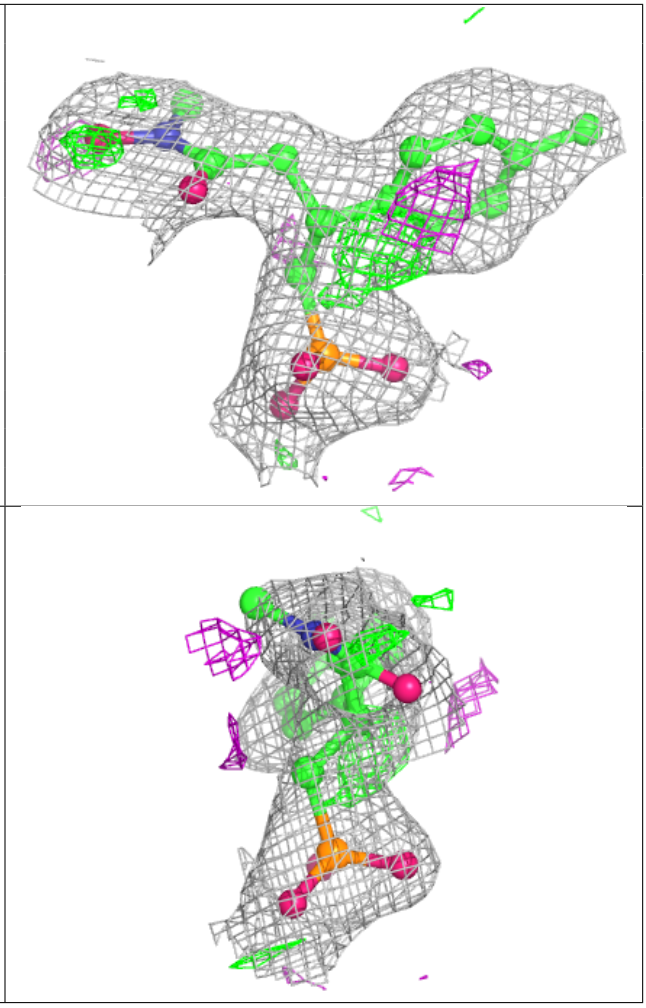
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	48S	B	502	19/19	0.94	0.15	22,25,27,28	0
3	48S	A	502	19/19	0.96	0.13	25,28,30,30	0
2	MN	B	501	1/1	0.98	0.10	25,25,25,25	0
2	MN	A	501	1/1	0.99	0.09	25,25,25,25	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.

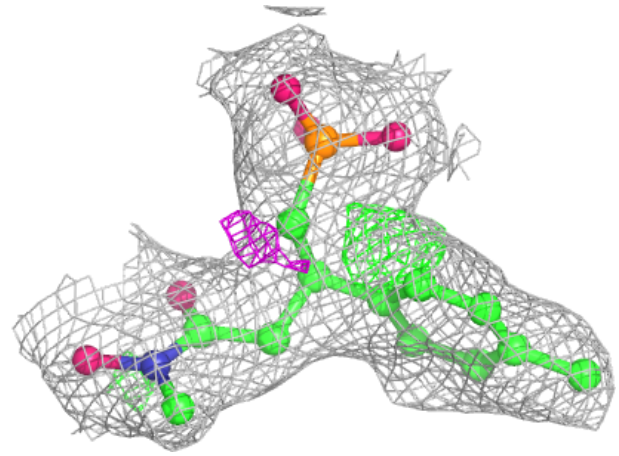
Electron density around 48S B 502:

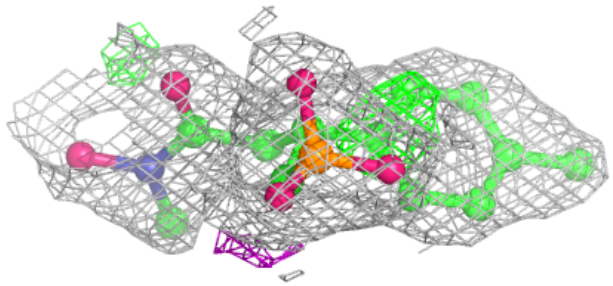
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

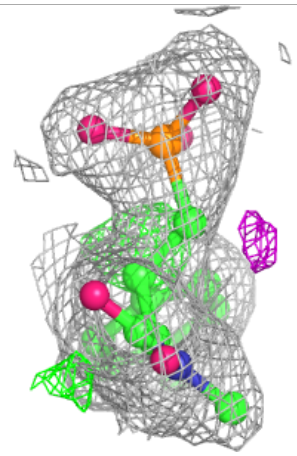


Electron density around 48S A 502:

$2mF_o$-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.