



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:22 AM GMT

PDB ID : 3EEK
Title : Candida glabrata Dihydrofolate Reductase complexed with 2,4-diamino-5-[3-methyl-3-(3-methoxy-5-(4-methylphenyl)phenyl)prop-1-ynyl]-6-methylpyrimidine(UCP111D4M) and NADPH
Authors : Liu, J.; Anderson, A.
Deposited on : 2008-09-04
Resolution : 2.03 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

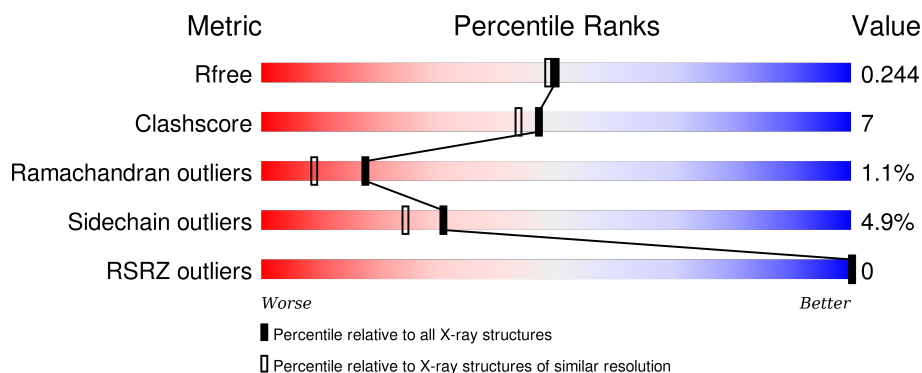
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 2.03 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}	91344	7858 (2.04-2.00)
Clashscore	102246	9060 (2.04-2.00)
Ramachandran outliers	100387	8952 (2.04-2.00)
Sidechain outliers	100360	8951 (2.04-2.00)
RSRZ outliers	91569	7873 (2.04-2.00)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	227	 77% 20% ..
1	B	227	 75% 16% 5% ..

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3981 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 Dihydrofolate reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	225	Total	C	N	O	S	0	0	0
			1846	1180	325	334	7			
1	B	225	Total	C	N	O	S	0	0	0
			1846	1180	325	334	7			

There are 20 discrepancies between the modelled and reference sequences:

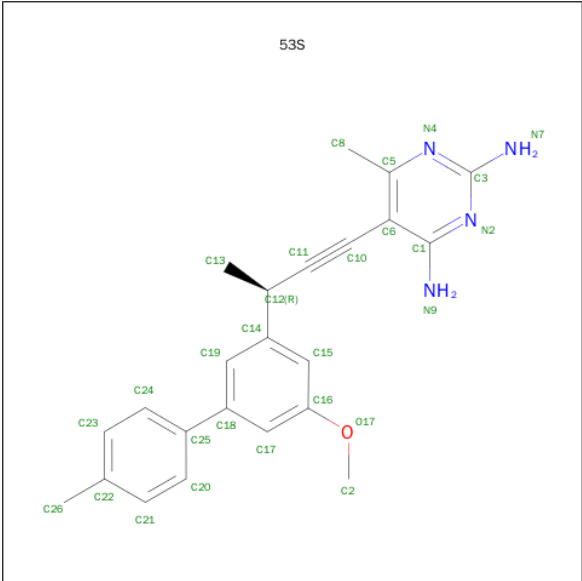
Chain	Residue	Modelled	Actual	Comment	Reference
A	218	LEU	-	EXPRESSION TAG	UNP Q6FPH0
A	219	GLU	-	EXPRESSION TAG	UNP Q6FPH0
A	220	HIS	-	EXPRESSION TAG	UNP Q6FPH0
A	221	HIS	-	EXPRESSION TAG	UNP Q6FPH0
A	222	HIS	-	EXPRESSION TAG	UNP Q6FPH0
A	223	HIS	-	EXPRESSION TAG	UNP Q6FPH0
A	224	HIS	-	EXPRESSION TAG	UNP Q6FPH0
A	225	HIS	-	EXPRESSION TAG	UNP Q6FPH0
A	226	HIS	-	EXPRESSION TAG	UNP Q6FPH0
A	227	HIS	-	EXPRESSION TAG	UNP Q6FPH0
B	218	LEU	-	EXPRESSION TAG	UNP Q6FPH0
B	219	GLU	-	EXPRESSION TAG	UNP Q6FPH0
B	220	HIS	-	EXPRESSION TAG	UNP Q6FPH0
B	221	HIS	-	EXPRESSION TAG	UNP Q6FPH0
B	222	HIS	-	EXPRESSION TAG	UNP Q6FPH0
B	223	HIS	-	EXPRESSION TAG	UNP Q6FPH0
B	224	HIS	-	EXPRESSION TAG	UNP Q6FPH0
B	225	HIS	-	EXPRESSION TAG	UNP Q6FPH0
B	226	HIS	-	EXPRESSION TAG	UNP Q6FPH0
B	227	HIS	-	EXPRESSION TAG	UNP Q6FPH0

- Molecule 2 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 3 is 5-[(3R)-3-(5-METHOXY-4'-METHYLBIPHENYL-3-YL)BUT-1-YN-1-YL]-6-METHYLPYRIMIDINE-2,4-DIAMINE (three-letter code: 53S) (formula: C₂₃H₂₄N₄O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			28	23	4	1		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			28	23	4	1		

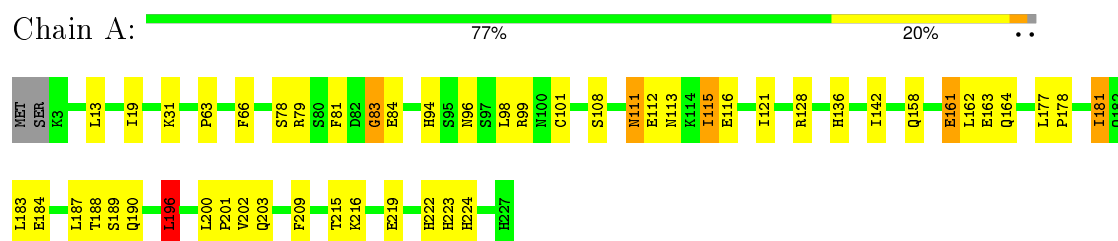
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	71	Total	O	0	0
			71	71		
4	B	66	Total	O	0	0
			66	66		

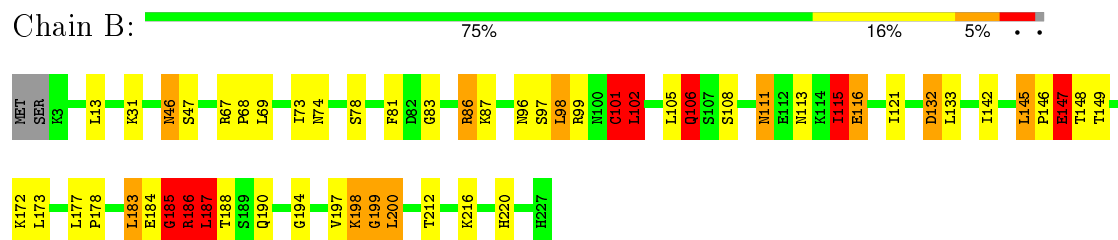
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Dihydrofolate reductase



- Molecule 1: Dihydrofolate reductase



4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	42.75Å 42.75Å 230.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.76 – 2.03 42.75 – 2.03	Depositor EDS
% Data completeness (in resolution range)	90.9 (42.76-2.03) 90.9 (42.75-2.03)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.81 (at 2.03Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.175 , 0.243 0.177 , 0.244	Depositor DCC
R_{free} test set	1223 reflections (5.38%)	DCC
Wilson B-factor (Å ²)	23.1	Xtriage
Anisotropy	0.075	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 21.1	EDS
Estimated twinning fraction	0.487 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 23937 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3981	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.62% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: NDP, 53S

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	1.04	1/1891 (0.1%)	1.01	11/2556 (0.4%)
1	B	1.14	3/1891 (0.2%)	1.14	15/2556 (0.6%)
All	All	1.09	4/3782 (0.1%)	1.08	26/5112 (0.5%)

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	A	0	7
1	B	0	16
All	All	0	23

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	101	CYS	CB-SG	-8.36	1.68	1.82
1	B	101	CYS	CB-SG	-7.77	1.69	1.82
1	B	147	GLU	CG-CD	6.33	1.61	1.51
1	B	185	GLY	N-CA	5.52	1.54	1.46

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	102	LEU	N-CA-C	-8.77	87.33	111.00
1	B	86	ARG	NE-CZ-NH1	8.57	124.59	120.30
1	B	106	GLN	N-CA-C	7.67	131.72	111.00
1	B	187	LEU	N-CA-C	7.55	131.40	111.00
1	A	116	GLU	N-CA-C	7.00	129.89	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	128	ARG	NE-CZ-NH2	-6.87	116.86	120.30
1	B	116	GLU	N-CA-C	6.81	129.38	111.00
1	B	86	ARG	NE-CZ-NH2	-6.71	116.94	120.30
1	B	99	ARG	N-CA-C	-6.62	93.11	111.00
1	A	164	GLN	N-CA-C	6.54	128.65	111.00
1	B	47	SER	N-CA-C	6.41	128.30	111.00
1	A	115	ILE	N-CA-C	-6.14	94.41	111.00
1	B	194	GLY	N-CA-C	-6.10	97.84	113.10
1	A	128	ARG	NE-CZ-NH1	6.07	123.33	120.30
1	A	84	GLU	N-CA-C	-5.87	95.16	111.00
1	B	115	ILE	N-CA-C	-5.68	95.67	111.00
1	A	224	HIS	N-CA-C	5.50	125.85	111.00
1	A	196	LEU	CA-CB-CG	5.48	127.91	115.30
1	A	188	THR	N-CA-CB	5.47	120.69	110.30
1	B	46	ASN	CB-CA-C	-5.46	99.48	110.40
1	A	99	ARG	NE-CZ-NH1	5.46	123.03	120.30
1	B	198	LYS	N-CA-CB	5.45	120.40	110.60
1	B	188	THR	N-CA-CB	5.32	120.41	110.30
1	B	199	GLY	N-CA-C	-5.16	100.21	113.10
1	B	145	LEU	CA-CB-CG	5.11	127.06	115.30
1	A	83	GLY	N-CA-C	-5.05	100.48	113.10

There are no chirality outliers.

All (23) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	115	ILE	Peptide
1	A	161	GLU	Peptide
1	A	163	GLU	Peptide
1	A	187	LEU	Peptide
1	A	201	PRO	Peptide
1	A	223	HIS	Peptide
1	A	83	GLY	Peptide
1	B	101	CYS	Peptide
1	B	105	LEU	Peptide
1	B	111	ASN	Peptide
1	B	115	ILE	Peptide
1	B	148	THR	Peptide
1	B	185	GLY	Peptide
1	B	186	ARG	Peptide
1	B	187	LEU	Peptide
1	B	197	VAL	Peptide

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Mol	Chain	Res	Type	Group
1	B	199	GLY	Peptide
1	B	200	LEU	Mainchain,Peptide
1	B	46	ASN	Peptide
1	B	81	PHE	Peptide
1	B	83	GLY	Peptide
1	B	98	LEU	Peptide

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	1846	0	1846	30	1
1	B	1846	0	1846	28	1
2	A	48	0	26	1	0
2	B	48	0	26	0	0
3	A	28	0	24	4	0
3	B	28	0	24	1	0
4	A	71	0	0	3	0
4	B	66	0	0	6	0
All	All	3981	0	3792	57	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (57) 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:190:GLN:HG2	4:A:269:HOH:O	1.32	1.26
1:A:183:LEU:HD13	1:A:200:LEU:HD12	1.24	1.09
1:B:190:GLN:HG2	4:B:260:HOH:O	1.56	1.03
1:B:186:ARG:N	1:B:186:ARG:HD3	1.68	1.01
1:A:183:LEU:HD13	1:A:200:LEU:CD1	1.91	1.00
1:A:121:ILE:HD12	3:A:229:53S:H13	1.61	0.82
1:B:132:ASP:HB3	4:B:272:HOH:O	1.81	0.80
1:A:183:LEU:CD1	1:A:200:LEU:HD12	2.10	0.80
1:B:173:LEU:HD23	1:B:200:LEU:HD12	1.69	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:LEU:CD1	1:A:200:LEU:CD1	2.66	0.71
1:A:158:GLN:HB3	1:A:161:GLU:OE1	1.95	0.67
1:A:111:ASN:ND2	1:A:113:ASN:H	1.94	0.65
1:B:69:LEU:H	1:B:74:ASN:HD21	1.43	0.65
1:A:111:ASN:C	1:A:111:ASN:HD22	1.99	0.65
1:A:184:GLU:HG3	4:A:279:HOH:O	1.98	0.62
1:B:31:LYS:NZ	1:B:184:GLU:HG3	2.15	0.62
1:B:186:ARG:HD3	1:B:186:ARG:H	1.65	0.57
1:B:108:SER:HB2	1:B:113:ASN:HD21	1.70	0.57
1:A:78:SER:O	1:A:96:ASN:HA	2.06	0.56
1:B:108:SER:HB2	1:B:113:ASN:ND2	2.22	0.55
1:A:222:HIS:HE1	4:B:264:HOH:O	1.89	0.54
1:A:121:ILE:HD12	3:A:229:53S:C13	2.34	0.54
1:A:111:ASN:HD22	1:A:112:GLU:N	2.06	0.53
1:B:198:LYS:O	1:B:212:THR:HG22	2.09	0.53
1:A:111:ASN:HD22	1:A:113:ASN:H	1.55	0.53
1:A:136:HIS:HD2	1:A:215:THR:OG1	1.91	0.53
1:B:78:SER:O	1:B:96:ASN:HA	2.09	0.53
1:A:178:PRO:HG2	1:A:181:ILE:HD11	1.89	0.53
1:A:108:SER:HA	1:A:111:ASN:ND2	2.24	0.52
1:B:121:ILE:HD12	3:B:229:53S:H13	1.91	0.52
1:A:66:PHE:CD2	3:A:229:53S:H26A	2.44	0.52
1:A:31:LYS:HD2	1:A:202:VAL:HG11	1.93	0.51
1:B:67:ARG:HA	1:B:68:PRO:C	2.33	0.49
1:B:147:GLU:HG2	1:B:147:GLU:O	2.13	0.49
1:B:183:LEU:HG	1:B:200:LEU:HD13	1.96	0.48
1:B:190:GLN:CG	4:B:260:HOH:O	2.36	0.48
1:A:81:PHE:CD2	1:A:94:HIS:HB3	2.48	0.48
1:B:13:LEU:HD12	1:B:142:ILE:HG22	1.96	0.48
1:A:189:SER:HB3	1:A:196:LEU:HD21	1.97	0.47
1:B:102:LEU:CD2	1:B:133:LEU:HD13	2.46	0.45
1:B:132:ASP:CB	4:B:272:HOH:O	2.52	0.45
1:A:202:VAL:HG12	1:A:203:GLN:N	2.32	0.45
1:B:177:LEU:HB3	1:B:178:PRO:HD2	1.97	0.44
1:A:79:ARG:NE	1:B:97:SER:HB2	2.33	0.44
1:A:66:PHE:CE2	3:A:229:53S:H26A	2.53	0.44
1:B:102:LEU:O	1:B:106:GLN:HG2	2.18	0.43
1:B:108:SER:HA	1:B:111:ASN:OD1	2.17	0.43
1:A:13:LEU:HD12	1:A:142:ILE:HG22	2.02	0.42
1:B:31:LYS:HZ3	1:B:184:GLU:HG3	1.85	0.42
1:B:190:GLN:CB	4:B:260:HOH:O	2.64	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:106:GLN:HG2	1:B:106:GLN:H	1.62	0.42
1:A:202:VAL:HB	1:A:209:PHE:CE2	2.56	0.41
1:B:187:LEU:N	1:B:200:LEU:HD23	2.35	0.41
1:A:190:GLN:CG	4:A:269:HOH:O	2.19	0.41
1:B:73:ILE:HD12	1:B:115:ILE:CD1	2.51	0.41
1:A:19:ILE:O	2:A:228:NDP:H2N	2.21	0.41
1:A:63:PRO:HB2	1:A:66:PHE:HD2	1.87	0.40

All (1) 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:219:GLU:OE1	1:B:87:LYS:NZ[1_545]	2.16	0.04

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	223/227 (98%)	215 (96%)	7 (3%)	1 (0%)	39	32
1	B	223/227 (98%)	209 (94%)	10 (4%)	4 (2%)	11	4
All	All	446/454 (98%)	424 (95%)	17 (4%)	5 (1%)	17	9

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	162	LEU
1	B	187	LEU
1	B	106	GLN
1	B	116	GLU
1	B	185	GLY

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	205/207 (99%)	199 (97%)	6 (3%)	50	48
1	B	205/207 (99%)	191 (93%)	14 (7%)	20	13
All	All	410/414 (99%)	390 (95%)	20 (5%)	31	24

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	98	LEU
1	A	111	ASN
1	A	177	LEU
1	A	181	ILE
1	A	196	LEU
1	A	216	LYS
1	B	86	ARG
1	B	98	LEU
1	B	101	CYS
1	B	102	LEU
1	B	132	ASP
1	B	145	LEU
1	B	146	PRO
1	B	147	GLU
1	B	149	THR
1	B	172	LYS
1	B	183	LEU
1	B	186	ARG
1	B	216	LYS
1	B	220	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	111	ASN
1	A	136	HIS

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Mol	Chain	Res	Type
1	A	193	ASN
1	A	203	GLN
1	A	208	GLN
1	A	222	HIS
1	B	74	ASN
1	B	113	ASN
1	B	136	HIS

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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NDP	A	228	-	42,52,52	1.60	5 (11%)	55,80,80	2.26	10 (18%)
3	53S	A	229	-	28,30,30	1.47	5 (17%)	33,42,42	2.25	13 (39%)
2	NDP	B	228	-	42,52,52	1.62	6 (14%)	55,80,80	2.33	11 (20%)
3	53S	B	229	-	28,30,30	1.56	4 (14%)	33,42,42	2.28	9 (27%)

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
2	NDP	A	228	-	-	0/30/77/77	0/5/5/5
3	53S	A	229	-	-	0/12/15/15	0/3/3/3
2	NDP	B	228	-	-	0/30/77/77	0/5/5/5
3	53S	B	229	-	-	0/12/15/15	0/3/3/3

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	228	NDP	C4N-C5N	-3.66	1.41	1.49
2	A	228	NDP	C4N-C5N	-3.38	1.41	1.49
3	B	229	53S	C18-C25	-3.32	1.40	1.49
3	A	229	53S	C18-C25	-2.81	1.41	1.49
3	B	229	53S	C10-C11	-2.33	1.17	1.19
2	B	228	NDP	C2N-C3N	2.04	1.39	1.34
3	A	229	53S	O17-C2	2.10	1.49	1.42
3	A	229	53S	C19-C18	2.14	1.43	1.39
3	A	229	53S	C17-C18	2.14	1.43	1.39
2	A	228	NDP	C2A-N1A	2.21	1.38	1.33
2	B	228	NDP	C2A-N1A	2.27	1.38	1.33
3	B	229	53S	C6-C1	2.77	1.45	1.42
2	B	228	NDP	C2A-N3A	3.12	1.37	1.32
3	A	229	53S	C8-C5	3.68	1.57	1.50
2	A	228	NDP	C6N-C5N	3.87	1.40	1.33
2	A	228	NDP	C2A-N3A	3.90	1.39	1.32
3	B	229	53S	C8-C5	4.03	1.58	1.50
2	B	228	NDP	C6N-C5N	4.27	1.41	1.33
2	B	228	NDP	O7N-C7N	5.41	1.38	1.24
2	A	228	NDP	O7N-C7N	5.75	1.38	1.24

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	228	NDP	N3A-C2A-N1A	-13.33	118.69	128.89
2	A	228	NDP	N3A-C2A-N1A	-13.22	118.77	128.89
2	B	228	NDP	C4A-C5A-N7A	-4.29	105.53	109.48
2	B	228	NDP	O7N-C7N-N7N	-3.56	113.92	122.76
3	A	229	53S	N2-C3-N4	-3.38	119.99	125.53
3	A	229	53S	C24-C23-C22	-3.38	116.84	121.39
3	B	229	53S	N2-C3-N4	-2.90	120.77	125.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	228	NDP	C4A-C5A-N7A	-2.74	106.96	109.48
3	A	229	53S	C21-C20-C25	-2.55	117.41	121.14
3	A	229	53S	C17-C18-C25	-2.49	116.67	120.90
2	A	228	NDP	C1D-N1N-C2N	-2.48	116.58	120.91
3	A	229	53S	C2-O17-C16	-2.27	112.19	117.51
3	B	229	53S	C24-C25-C18	-2.24	117.37	121.39
3	B	229	53S	C15-C16-C17	-2.17	117.24	120.99
3	B	229	53S	C17-C18-C25	-2.11	117.30	120.90
3	A	229	53S	C15-C16-C17	-2.08	117.40	120.99
2	B	228	NDP	C1D-N1N-C2N	-2.08	117.28	120.91
2	A	228	NDP	O7N-C7N-N7N	-2.08	117.60	122.76
2	A	228	NDP	O3D-C3D-C2D	-2.04	105.20	111.83
3	A	229	53S	C6-C1-N2	-2.03	118.09	121.60
2	B	228	NDP	O2B-P2B-O1X	-2.02	102.06	107.11
3	A	229	53S	N9-C1-N2	2.04	119.90	116.95
2	B	228	NDP	C4B-O4B-C1B	2.09	112.01	109.72
3	A	229	53S	N7-C3-N2	2.21	120.86	117.20
2	B	228	NDP	O4D-C1D-N1N	2.29	112.91	108.07
2	B	228	NDP	O2X-P2B-O1X	2.34	118.12	110.58
2	A	228	NDP	O2N-PN-O3	2.40	115.96	105.09
3	A	229	53S	C16-C15-C14	2.48	122.78	120.09
2	B	228	NDP	C5N-C4N-C3N	2.48	119.36	112.52
2	A	228	NDP	C5N-C4N-C3N	2.50	119.40	112.52
3	B	229	53S	C15-C14-C19	2.51	121.94	118.13
2	B	228	NDP	C2A-N1A-C6A	2.56	123.33	118.77
3	B	229	53S	N7-C3-N2	2.73	121.72	117.20
2	B	228	NDP	PN-O3-PA	2.93	140.95	132.73
2	A	228	NDP	C2A-N1A-C6A	2.93	124.00	118.77
2	A	228	NDP	PN-O3-PA	2.98	141.10	132.73
3	B	229	53S	C3-N2-C1	3.02	120.47	117.04
3	A	229	53S	C8-C5-C6	3.10	124.32	122.09
2	A	228	NDP	O4D-C1D-N1N	3.70	115.89	108.07
3	B	229	53S	C8-C5-C6	4.18	125.11	122.09
3	A	229	53S	C3-N2-C1	4.62	122.30	117.04
3	A	229	53S	C3-N4-C5	7.03	122.96	117.01
3	B	229	53S	C3-N4-C5	8.67	124.34	117.01

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	228	NDP	1	0
3	A	229	53S	4	0
3	B	229	53S	1	0

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	225/227 (99%)	-0.46	0 100 100	10, 21, 36, 46	0
1	B	225/227 (99%)	-0.46	0 100 100	11, 21, 35, 49	0
All	All	450/454 (99%)	-0.46	0 100 100	10, 21, 36, 49	0

There are no RSRZ outliers to report.

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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
3	53S	B	229	28/28	0.93	0.14	1.36	13,22,34,34	0
3	53S	A	229	28/28	0.95	0.12	0.84	10,21,30,31	0
2	NDP	A	228	48/48	0.98	0.08	-0.59	10,15,20,23	0
2	NDP	B	228	48/48	0.98	0.07	-0.91	9,16,19,22	0

6.5 Other polymers

There are no such residues in this entry.