



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 02:51 pm GMT

PDB ID : 2RH4
Title : Actinorhodin ketoreductase, actKR, with NADPH and Inhibitor Emodin
Authors : Korman, T.P.; Tsai, S.-C.
Deposited on : 2007-10-05
Resolution : 2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

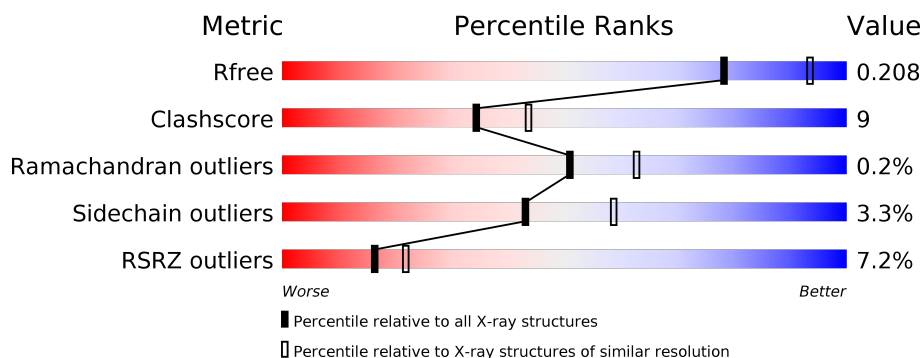
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	4130 (2.30-2.30)
Clashscore	112137	4751 (2.30-2.30)
Ramachandran outliers	110173	4705 (2.30-2.30)
Sidechain outliers	110143	4704 (2.30-2.30)
RSRZ outliers	101464	4156 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	277	
1	B	277	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	EMO	A	401	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4234 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 Actinorhodin Polyketide Ketoreductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	257	Total	C	N	O	S	0	0	0
			1884	1176	337	364	7			
1	B	268	Total	C	N	O	S	0	0	0
			1966	1226	354	378	8			

There are 32 discrepancies between the modelled and reference sequences:

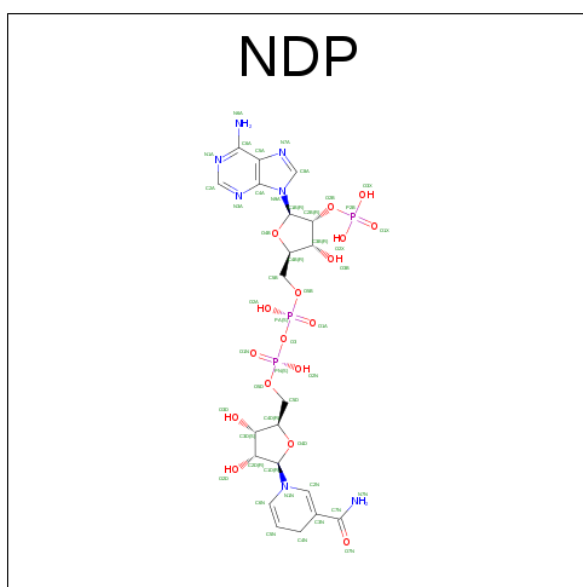
Chain	Residue	Modelled	Actual	Comment	Reference
A	-15	HIS	-	EXPRESSION TAG	UNP P16544
A	-14	HIS	-	EXPRESSION TAG	UNP P16544
A	-13	HIS	-	EXPRESSION TAG	UNP P16544
A	-12	HIS	-	EXPRESSION TAG	UNP P16544
A	-11	HIS	-	EXPRESSION TAG	UNP P16544
A	-10	HIS	-	EXPRESSION TAG	UNP P16544
A	-9	SER	-	EXPRESSION TAG	UNP P16544
A	-8	SER	-	EXPRESSION TAG	UNP P16544
A	-7	GLY	-	EXPRESSION TAG	UNP P16544
A	-6	LEU	-	EXPRESSION TAG	UNP P16544
A	-5	VAL	-	EXPRESSION TAG	UNP P16544
A	-4	PRO	-	EXPRESSION TAG	UNP P16544
A	-3	ARG	-	EXPRESSION TAG	UNP P16544
A	-2	GLY	-	EXPRESSION TAG	UNP P16544
A	-1	SER	-	EXPRESSION TAG	UNP P16544
A	0	HIS	-	EXPRESSION TAG	UNP P16544
B	-15	HIS	-	EXPRESSION TAG	UNP P16544
B	-14	HIS	-	EXPRESSION TAG	UNP P16544
B	-13	HIS	-	EXPRESSION TAG	UNP P16544
B	-12	HIS	-	EXPRESSION TAG	UNP P16544
B	-11	HIS	-	EXPRESSION TAG	UNP P16544
B	-10	HIS	-	EXPRESSION TAG	UNP P16544
B	-9	SER	-	EXPRESSION TAG	UNP P16544
B	-8	SER	-	EXPRESSION TAG	UNP P16544
B	-7	GLY	-	EXPRESSION TAG	UNP P16544

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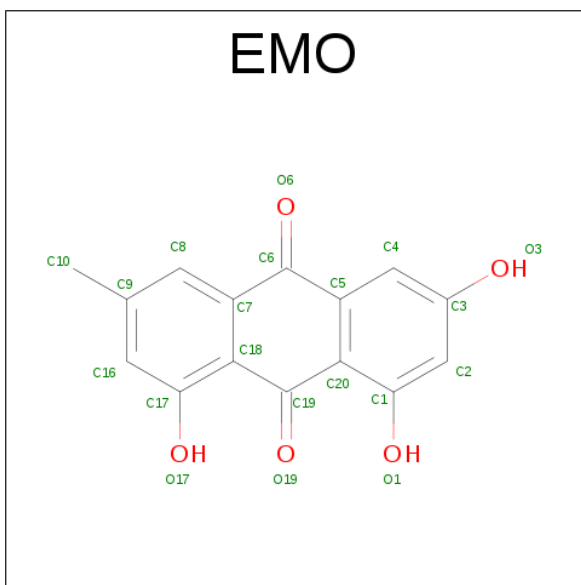
Chain	Residue	Modelled	Actual	Comment	Reference
B	-6	LEU	-	EXPRESSION TAG	UNP P16544
B	-5	VAL	-	EXPRESSION TAG	UNP P16544
B	-4	PRO	-	EXPRESSION TAG	UNP P16544
B	-3	ARG	-	EXPRESSION TAG	UNP P16544
B	-2	GLY	-	EXPRESSION TAG	UNP P16544
B	-1	SER	-	EXPRESSION TAG	UNP P16544
B	0	HIS	-	EXPRESSION TAG	UNP P16544

- 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 3-METHYL-1,6,8-TRIHIDROXYANTHRAQUINONE (three-letter code: EMO) (formula: $C_{15}H_{10}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			20	15	5		

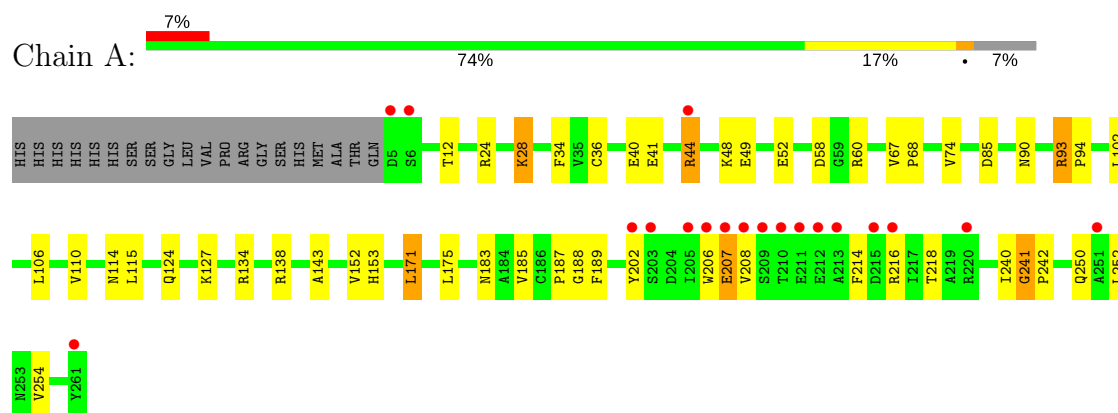
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	145	Total	O	0	0
			145	145		
4	B	123	Total	O	0	0
			123	123		

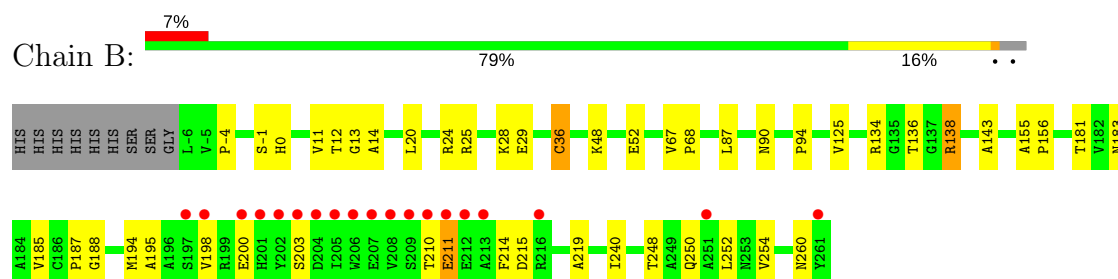
3 Residue-property plots

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



• Molecule 1: Actinorhodin Polyketide Ketoreductase



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	104.00Å 104.00Å 123.40Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.30 42.30 – 2.30	Depositor EDS
% Data completeness (in resolution range)	96.7 (50.00-2.30) 96.8 (42.30-2.30)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.71 (at 2.29Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.179 , 0.204 0.182 , 0.208	Depositor DCC
R_{free} test set	3355 reflections (9.97%)	DCC
Wilson B-factor (Å ²)	34.0	Xtriage
Anisotropy	0.340	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 44.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.024 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4234	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.68% 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: NDP, EMO

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	0.29	0/1910	0.56	0/2594
1	B	0.31	0/1994	0.57	0/2708
All	All	0.30	0/3904	0.56	0/5302

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	2
1	B	0	2
All	All	0	4

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	241	GLY	Peptide
1	A	254	VAL	Peptide
1	B	254	VAL	Peptide
1	B	36	CYS	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	1884	0	1900	38	0
1	B	1966	0	1987	37	1
2	A	48	0	26	2	0
2	B	48	0	26	3	0
3	A	20	0	9	0	0
4	A	145	0	0	2	0
4	B	123	0	0	0	0
All	All	4234	0	3948	75	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 9.

All (75) 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:28:LYS:HE3	1:A:28:LYS:HA	1.49	0.91
1:B:134:ARG:HE	1:B:136:THR:CG2	1.97	0.77
1:A:93:ARG:H	1:A:114:ASN:HD21	1.32	0.77
1:A:40:GLU:HG2	4:A:535:HOH:O	1.89	0.71
1:A:28:LYS:HE3	1:A:28:LYS:CA	2.23	0.69
1:A:28:LYS:HA	1:A:28:LYS:CE	2.24	0.68
1:B:138:ARG:HG2	1:B:240:ILE:HA	1.76	0.66
1:B:200:GLU:HA	1:B:203:SER:HB3	1.80	0.64
1:A:206:TRP:C	1:A:208:VAL:H	2.01	0.64
1:B:20:LEU:O	1:B:24:ARG:HG2	1.97	0.63
1:A:202:TYR:OH	1:A:216:ARG:HD2	1.98	0.62
1:B:134:ARG:HE	1:B:136:THR:HG23	1.63	0.62
1:B:134:ARG:HE	1:B:136:THR:HG22	1.65	0.61
1:A:252:LEU:N	1:A:252:LEU:HD12	2.18	0.59
1:B:134:ARG:HG2	1:B:136:THR:HG22	1.83	0.59
1:A:24:ARG:NH1	1:A:49:GLU:OE2	2.36	0.58
1:B:-1:SER:OG	1:B:0:HIS:HD2	1.89	0.56
1:B:195:ALA:O	1:B:198:VAL:HG22	2.05	0.56
1:B:-4:PRO:O	1:B:0:HIS:HB2	2.06	0.55
1:A:48:LYS:O	1:A:52:GLU:HG3	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:188:GLY:O	2:B:301:NDP:H42N	2.07	0.54
1:B:183:ASN:HD21	1:B:248:THR:HA	1.73	0.54
1:B:48:LYS:O	1:B:52:GLU:HG3	2.06	0.54
1:B:67:VAL:N	1:B:68:PRO:HD2	2.22	0.54
1:A:127:LYS:HE2	1:A:127:LYS:HA	1.90	0.54
1:B:138:ARG:HD2	1:B:181:THR:OG1	2.07	0.53
1:A:189:PHE:HB2	4:A:531:HOH:O	2.07	0.53
1:B:252:LEU:N	1:B:252:LEU:HD12	2.24	0.53
1:A:138:ARG:HG3	1:A:240:ILE:HA	1.91	0.52
1:B:194:MET:O	1:B:198:VAL:HG13	2.09	0.52
1:A:138:ARG:HB3	1:A:240:ILE:HG22	1.92	0.52
1:B:143:ALA:O	2:B:301:NDP:H6N	2.10	0.51
1:B:12:THR:O	1:B:90:ASN:HB3	2.11	0.51
1:A:93:ARG:HD2	1:A:110:VAL:HG22	1.91	0.51
1:A:41:GLU:OE1	1:A:44:ARG:NH1	2.44	0.50
1:A:143:ALA:O	2:A:301:NDP:H6N	2.10	0.50
1:A:206:TRP:O	1:A:208:VAL:N	2.45	0.49
1:A:206:TRP:C	1:A:208:VAL:N	2.65	0.49
1:A:183:ASN:HD22	1:A:250:GLN:H	1.60	0.49
1:B:134:ARG:NE	1:B:136:THR:CG2	2.72	0.48
1:A:93:ARG:HD3	1:A:94:PRO:O	2.12	0.48
1:A:67:VAL:N	1:A:68:PRO:HD2	2.30	0.47
1:B:155:ALA:N	1:B:156:PRO:HD2	2.30	0.47
1:B:183:ASN:HD22	1:B:250:GLN:H	1.61	0.47
1:B:13:GLY:HA2	2:B:301:NDP:H1B	1.96	0.46
1:A:241:GLY:HA2	1:A:242:PRO:HD2	1.63	0.46
1:A:214:PHE:O	1:A:218:THR:HG23	2.16	0.46
1:A:34:PHE:HA	1:A:58:ASP:O	2.17	0.45
1:B:94:PRO:HG3	1:B:194:MET:SD	2.56	0.45
1:A:188:GLY:O	2:A:301:NDP:H42N	2.17	0.45
1:A:85:ASP:HA	1:A:134:ARG:NH1	2.32	0.45
1:B:200:GLU:O	1:B:203:SER:HB3	2.17	0.44
1:A:74:VAL:HG21	1:A:124:GLN:HB3	2.00	0.44
1:A:138:ARG:CB	1:A:240:ILE:HG22	2.47	0.44
1:A:206:TRP:CD1	1:A:206:TRP:N	2.86	0.43
1:A:152:VAL:HG12	1:A:153:HIS:CD2	2.53	0.43
1:A:171:LEU:HD22	1:A:175:LEU:HG	2.01	0.43
1:A:93:ARG:CD	1:A:94:PRO:O	2.67	0.43
1:B:210:THR:HG22	1:B:211:GLU:N	2.34	0.42
1:B:25:ARG:NH1	1:B:29:GLU:OE2	2.52	0.42
1:A:185:VAL:O	1:A:187:PRO:HD3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:44:ARG:CG	1:A:44:ARG:HH11	2.31	0.42
1:B:134:ARG:NE	1:B:136:THR:HG22	2.30	0.42
1:B:211:GLU:O	1:B:214:PHE:HB3	2.20	0.42
1:B:11:VAL:HG12	1:B:14:ALA:HB2	2.02	0.42
1:A:114:ASN:N	1:A:114:ASN:HD22	2.18	0.41
1:B:24:ARG:O	1:B:28:LYS:HG3	2.20	0.41
1:B:87:LEU:HD22	1:B:125:VAL:HG21	2.01	0.41
1:B:183:ASN:HD21	1:B:248:THR:CA	2.32	0.41
1:A:12:THR:O	1:A:90:ASN:HB3	2.21	0.41
1:B:185:VAL:O	1:B:187:PRO:HD3	2.20	0.41
1:B:183:ASN:ND2	1:B:248:THR:HA	2.36	0.41
1:B:134:ARG:CG	1:B:136:THR:HG22	2.51	0.41
1:A:93:ARG:N	1:A:114:ASN:HD21	2.09	0.40
1:B:215:ASP:O	1:B:219:ALA:HB2	2.21	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:B:260:ASN:ND2	1:B:260:ASN:ND2[5_554]	2.14	0.06

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	255/277 (92%)	240 (94%)	14 (6%)	1 (0%)	38	47
1	B	266/277 (96%)	248 (93%)	18 (7%)	0	100	100
All	All	521/554 (94%)	488 (94%)	32 (6%)	1 (0%)	51	63

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	207	GLU

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	192/209 (92%)	182 (95%)	10 (5%)	27	36
1	B	201/209 (96%)	198 (98%)	3 (2%)	70	83
All	All	393/418 (94%)	380 (97%)	13 (3%)	43	59

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	LYS
1	A	36	CYS
1	A	44	ARG
1	A	60	ARG
1	A	93	ARG
1	A	102	LEU
1	A	106	LEU
1	A	115	LEU
1	A	171	LEU
1	A	207	GLU
1	B	36	CYS
1	B	138	ARG
1	B	211	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	89	ASN
1	A	114	ASN
1	A	153	HIS
1	A	162	HIS
1	A	183	ASN

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Mol	Chain	Res	Type
1	B	0	HIS
1	B	89	ASN
1	B	124	GLN
1	B	162	HIS
1	B	183	ASN
1	B	228	GLN

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 ⓘ

3 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	301	-	43,52,52	1.27	4 (9%)	49,80,80	1.58	5 (10%)
3	EMO	A	401	-	22,22,22	2.57	17 (77%)	34,34,34	1.31	5 (14%)
2	NDP	B	301	-	43,52,52	1.27	4 (9%)	49,80,80	1.63	5 (10%)

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	301	-	-	0/30/77/77	0/5/5/5
3	EMO	A	401	-	-	0/0/16/16	0/3/3/3
2	NDP	B	301	-	-	0/30/77/77	0/5/5/5

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	301	NDP	C4N-C5N	-4.39	1.39	1.49
2	B	301	NDP	C4N-C5N	-4.39	1.39	1.49
3	A	401	EMO	C10-C9	-4.18	1.36	1.51
3	A	401	EMO	C8-C9	2.00	1.42	1.39
3	A	401	EMO	C8-C7	2.01	1.43	1.39
3	A	401	EMO	C18-C19	2.04	1.52	1.47
2	B	301	NDP	O4B-C1B	2.05	1.44	1.41
3	A	401	EMO	C20-C19	2.06	1.52	1.47
3	A	401	EMO	C16-C9	2.06	1.42	1.39
2	A	301	NDP	O4B-C1B	2.19	1.44	1.41
3	A	401	EMO	C2-C3	2.20	1.42	1.39
3	A	401	EMO	C7-C6	2.33	1.53	1.48
3	A	401	EMO	C18-C17	2.35	1.45	1.41
3	A	401	EMO	C4-C3	2.42	1.42	1.39
3	A	401	EMO	C5-C6	2.52	1.53	1.48
3	A	401	EMO	C20-C1	2.62	1.45	1.41
3	A	401	EMO	C2-C1	2.81	1.42	1.38
3	A	401	EMO	C7-C18	2.82	1.45	1.41
3	A	401	EMO	C16-C17	2.92	1.42	1.38
3	A	401	EMO	C5-C20	3.01	1.45	1.41
2	A	301	NDP	P2B-O1X	3.14	1.61	1.50
2	B	301	NDP	P2B-O1X	3.18	1.61	1.50
2	A	301	NDP	C6N-C5N	3.39	1.39	1.33
2	B	301	NDP	C6N-C5N	3.43	1.39	1.33
3	A	401	EMO	O3-C3	5.94	1.50	1.37

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	301	NDP	N3A-C2A-N1A	-8.93	121.08	128.86
2	A	301	NDP	N3A-C2A-N1A	-8.93	121.08	128.86
3	A	401	EMO	C16-C17-C18	-2.58	117.94	120.99
3	A	401	EMO	C2-C1-C20	-2.47	118.07	120.99
3	A	401	EMO	C7-C6-C5	-2.35	113.55	117.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	301	NDP	C4B-O4B-C1B	-2.23	107.40	109.77
2	A	301	NDP	C3B-C2B-C1B	-2.21	98.43	102.75
2	A	301	NDP	C3N-C2N-N1N	-2.21	119.87	123.08
2	B	301	NDP	C3N-C2N-N1N	-2.20	119.89	123.08
2	B	301	NDP	C3B-C2B-C1B	-2.14	98.55	102.75
2	A	301	NDP	C4A-C5A-N7A	-2.00	107.48	109.41
3	A	401	EMO	C17-C16-C9	2.37	123.18	121.00
2	A	301	NDP	O4D-C1D-N1N	2.61	113.33	108.07
2	B	301	NDP	O4D-C1D-N1N	2.65	113.40	108.07
3	A	401	EMO	C1-C2-C3	3.09	122.45	119.65

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	NDP	2	0
2	B	301	NDP	3	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

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, 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	257/277 (92%)	0.19	19 (7%) 15 21	24, 34, 66, 93	0
1	B	268/277 (96%)	-0.02	19 (7%) 17 22	22, 35, 80, 99	0
All	All	525/554 (94%)	0.08	38 (7%) 16 22	22, 35, 73, 99	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	204	ASP	6.6
1	B	202	TYR	6.3
1	A	207	GLU	6.3
1	A	206	TRP	5.8
1	B	206	TRP	5.6
1	B	212	GLU	5.1
1	B	210	THR	5.0
1	B	213	ALA	4.4
1	B	207	GLU	4.2
1	B	201	HIS	4.1
1	A	205	ILE	3.9
1	B	261	TYR	3.8
1	B	205	ILE	3.6
1	A	5	ASP	3.6
1	B	203	SER	3.6
1	A	208	VAL	3.5
1	A	209	SER	3.4
1	B	211	GLU	3.3
1	A	216	ARG	3.3
1	B	216	ARG	3.3
1	A	261	TYR	3.2
1	A	202	TYR	3.0
1	B	209	SER	3.0
1	B	208	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	212	GLU	2.9
1	A	251	ALA	2.9
1	A	6	SER	2.7
1	A	210	THR	2.4
1	A	215	ASP	2.4
1	A	220	ARG	2.3
1	A	211	GLU	2.3
1	B	200	GLU	2.3
1	B	198	VAL	2.2
1	B	251	ALA	2.2
1	A	213	ALA	2.1
1	B	197	SER	2.1
1	A	203	SER	2.1
1	A	44	ARG	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 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	EMO	A	401	20/20	0.73	0.30	3.65	72,73,74,75	0
2	NDP	A	301	48/48	0.98	0.13	-0.30	27,30,33,36	0
2	NDP	B	301	48/48	0.96	0.10	-0.30	37,41,45,48	0

6.5 Other polymers [i](#)

There are no such residues in this entry.