wwPDB X-ray Structure Validation Summary Report (i)

Jun 18, 2024 – 02:07 AM EDT

PDB ID	:	2XAX
Title	:	Ribonucleotide reductase Y730NO2Y and Y731A modified R1 subunit of E. coli
Authors	:	Yokoyama, K.; Uhlin, U.; Stubbe, J.
Deposited on	:	2010-04-01
Resolution	:	2.75 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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:

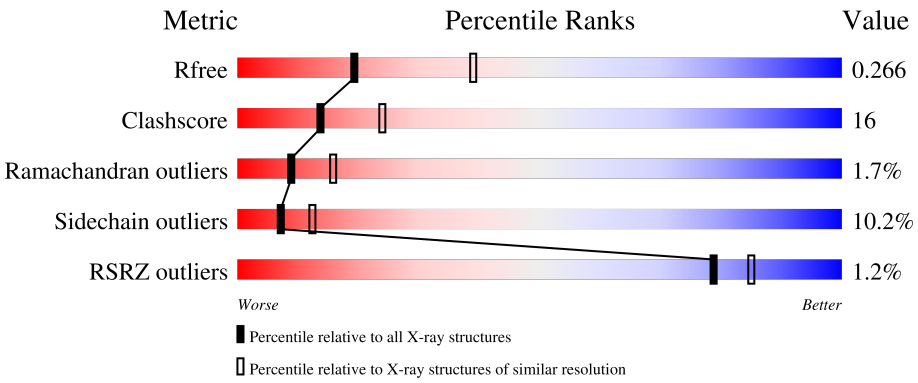
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 2.75 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	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)
RSRZ outliers	127900	1207 (2.78-2.74)

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	761	% 67% 24% • •
1	B	761	% 62% 29% 5% •
1	C	761	% 67% 23% 5% • •
2	D	20	15% 30% 40% 10% 20%
2	E	20	10% 45% 25% 5% 5% 20%

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Mol	Chain	Length	Quality of chain
2	F	20	10%, 60%, 15%, 5%, 20%
2	P	20	5%, 10%, 85%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 18431 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 RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE 1 SUBUNIT ALPHA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	728	5800	3682	996	1098	24	0	0	0
1	B	728	5800	3682	996	1098	24	0	0	0
1	C	728	5788	3668	998	1099	23	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	731	ALA	TYR	engineered mutation	UNP P00452
B	731	ALA	TYR	engineered mutation	UNP P00452
C	731	ALA	TYR	engineered mutation	UNP P00452

- Molecule 2 is a protein called RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE 1 SUBUNIT BETA.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	D	16	129	77	19	33	0	0	0
2	E	16	129	77	19	33	0	0	0
2	F	16	129	77	19	33	0	0	0
2	P	3	27	20	3	4	0	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	187	187	187	0	0

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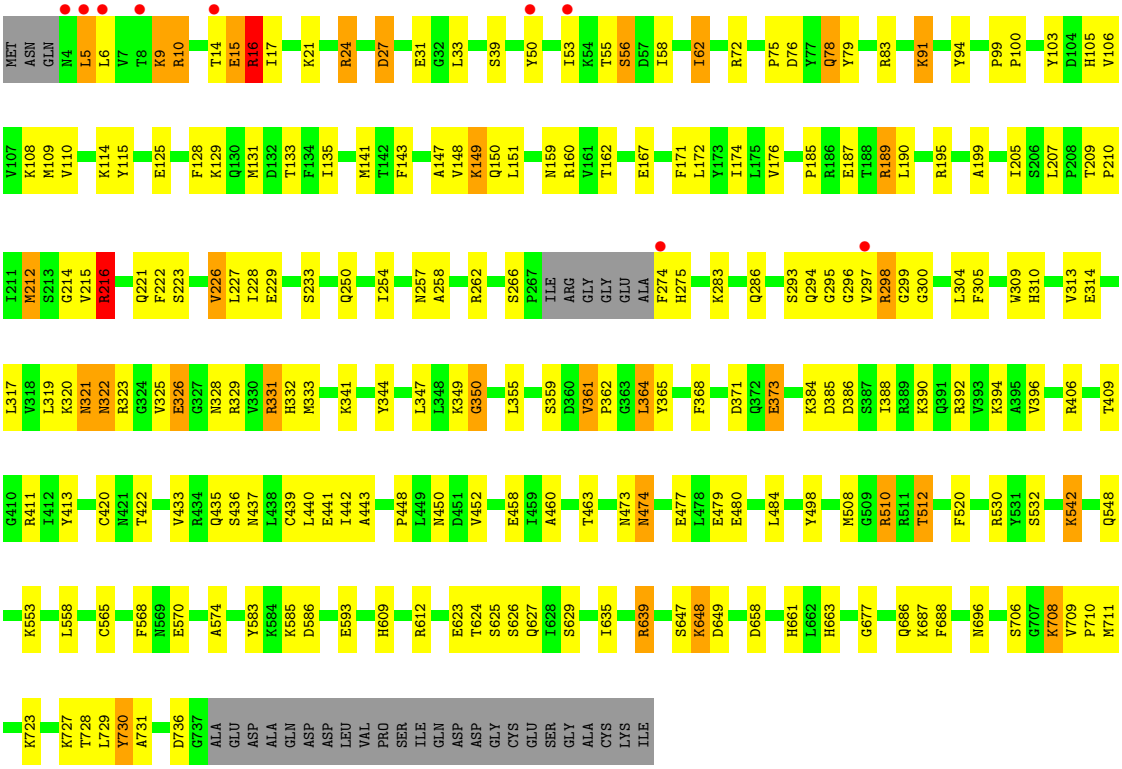
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	B	172	172	172	0	0
			Total	O		
3	C	258	258	258	0	0
			Total	O		
3	D	4	4	4	0	0
			Total	O		
3	E	2	2	2	0	0
			Total	O		
3	F	2	2	2	0	0
			Total	O		
3	P	4	4	4	0	0

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.

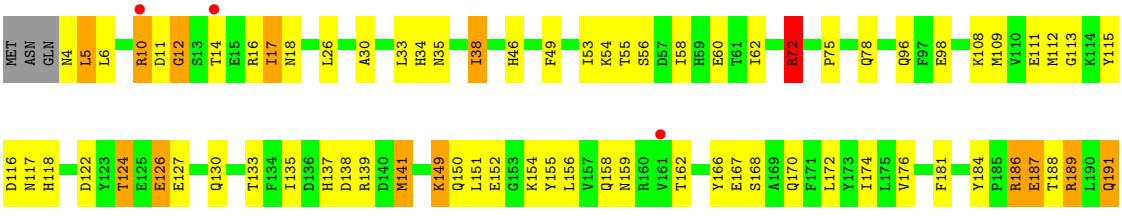
• Molecule 1: RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE 1 SUBUNIT ALPHA

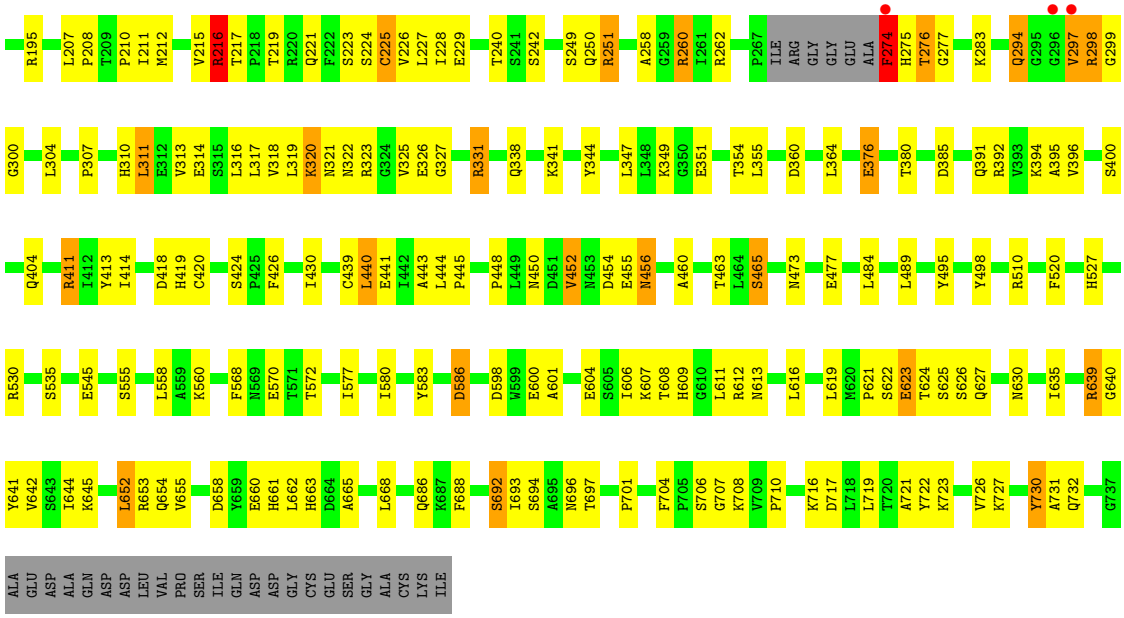
Chain A:



• Molecule 1: RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE 1 SUBUNIT ALPHA

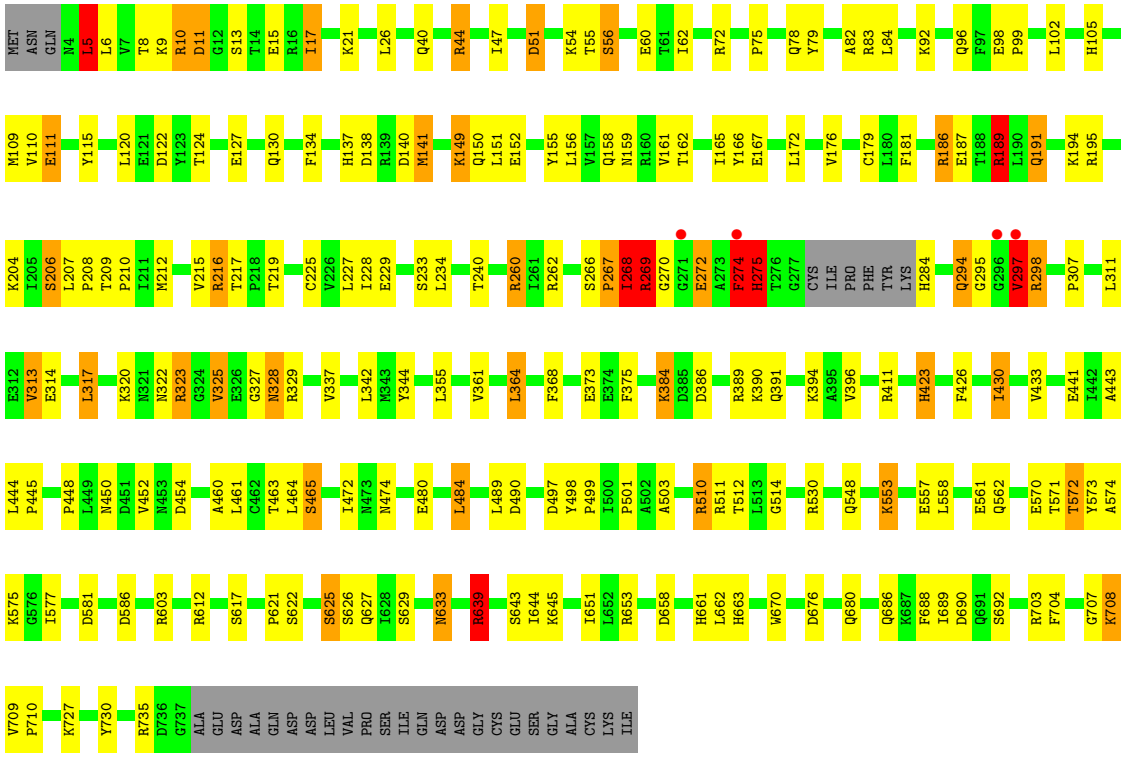
Chain B:





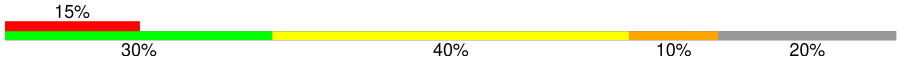
- Molecule 1: RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE 1 SUBUNIT ALPHA

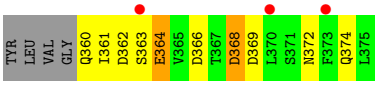
Chain C:



- Molecule 2: RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE 1 SUBUNIT BETA

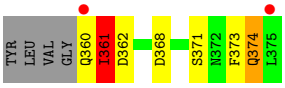
Chain D:





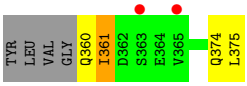
• Molecule 2: RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE 1 SUBUNIT BETA

Chain E:



• Molecule 2: RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE 1 SUBUNIT BETA

Chain F:



• Molecule 2: RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE 1 SUBUNIT BETA

Chain P:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α, β, γ	224.86Å 224.86Å 336.40Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	169.03 – 2.75 79.40 – 2.75	Depositor EDS
% Data completeness (in resolution range)	88.9 (169.03-2.75) 73.7 (79.40-2.75)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.96 (at 2.73Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.182 , 0.261 0.186 , 0.266	Depositor DCC
R_{free} test set	3124 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	46.0	Xtriage
Anisotropy	0.019	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 58.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	18431	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 5.14% 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: NIY

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	0.73	0/5909	0.81	2/8001 (0.0%)
1	B	0.71	0/5909	0.80	2/8001 (0.0%)
1	C	0.85	3/5894 (0.1%)	0.88	4/7979 (0.1%)
2	D	0.69	0/129	0.70	0/173
2	E	0.57	0/129	0.73	0/173
2	F	0.65	0/129	0.82	0/173
2	P	1.11	0/27	1.11	0/36
All	All	0.76	3/18126 (0.0%)	0.83	8/24536 (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
1	C	0	3
All	All	0	4

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	225	CYS	CB-SG	-6.08	1.72	1.82
1	C	179	CYS	CB-SG	-5.52	1.72	1.81
1	C	297	VAL	CA-CB	5.24	1.65	1.54

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	639	ARG	NE-CZ-NH1	7.71	124.16	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	639	ARG	NE-CZ-NH2	-6.77	116.91	120.30
1	C	497	ASP	CB-CG-OD1	6.05	123.75	118.30
1	B	72	ARG	NE-CZ-NH2	-5.80	117.40	120.30
1	B	652	LEU	CA-CB-CG	5.35	127.61	115.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	274	PHE	Peptide
1	C	274	PHE	Peptide
1	C	294	GLN	Peptide
1	C	423	HIS	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	5800	0	5722	168	0
1	B	5800	0	5722	190	0
1	C	5788	0	5709	191	0
2	D	129	0	111	6	0
2	E	129	0	111	5	0
2	F	129	0	111	2	0
2	P	27	0	31	4	0
3	A	187	0	0	47	0
3	B	172	0	0	38	1
3	C	258	0	0	51	1
3	D	4	0	0	1	0
3	E	2	0	0	3	0
3	F	2	0	0	0	0
3	P	4	0	0	5	0
All	All	18431	0	17517	560	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 16.

The worst 5 of 560 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:C:111:GLU:HG2	3:C:2045:HOH:O	1.33	1.28
1:C:430:ILE:HB	3:C:2203:HOH:O	1.36	1.19
1:B:159:ASN:ND2	1:B:162:THR:H	1.40	1.17
1:B:299:GLY:HA3	3:B:2063:HOH:O	1.42	1.15
1:B:262:ARG:HG3	1:B:274:PHE:HB2	1.33	1.10

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)
3:B:2009:HOH:O	3:C:2016:HOH:O[15_554]	2.17	0.03

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	723/761 (95%)	662 (92%)	50 (7%)	11 (2%)	10 18
1	B	723/761 (95%)	662 (92%)	52 (7%)	9 (1%)	13 23
1	C	723/761 (95%)	661 (91%)	48 (7%)	14 (2%)	8 14
2	D	14/20 (70%)	9 (64%)	3 (21%)	2 (14%)	0 0
2	E	14/20 (70%)	9 (64%)	4 (29%)	1 (7%)	1 1
2	F	14/20 (70%)	13 (93%)	1 (7%)	0	100 100
2	P	1/20 (5%)	1 (100%)	0	0	100 100
All	All	2212/2363 (94%)	2017 (91%)	158 (7%)	37 (2%)	9 16

5 of 37 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	216	ARG

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Mol	Chain	Res	Type
1	B	294	GLN
1	B	623	GLU
1	C	10	ARG
1	C	216	ARG

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	624/649 (96%)	562 (90%)	62 (10%)	8 13
1	B	624/649 (96%)	558 (89%)	66 (11%)	6 11
1	C	621/649 (96%)	563 (91%)	58 (9%)	9 15
2	D	16/19 (84%)	12 (75%)	4 (25%)	0 1
2	E	16/19 (84%)	13 (81%)	3 (19%)	1 2
2	F	16/19 (84%)	13 (81%)	3 (19%)	1 2
2	P	3/19 (16%)	3 (100%)	0	100 100
All	All	1920/2023 (95%)	1724 (90%)	196 (10%)	7 12

5 of 196 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	530	ARG
1	C	149	LYS
1	B	607	LYS
1	C	11	ASP
1	C	206	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	663	HIS
1	C	456	ASN
1	B	696	ASN

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Mol	Chain	Res	Type
1	C	183	ASN
1	C	630	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)

3 non-standard protein/DNA/RNA residues 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	$\#\|Z\| > 2$
1	NIY	A	730	1	14,15,16	1.26	1 (7%)	11,20,22	1.31	3 (27%)
1	NIY	C	730	1	14,15,16	1.29	1 (7%)	11,20,22	1.46	2 (18%)
1	NIY	B	730	1	14,15,16	1.60	1 (7%)	11,20,22	1.53	3 (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
1	NIY	A	730	1	-	4/7/10/12	0/1/1/1
1	NIY	C	730	1	-	3/7/10/12	0/1/1/1
1	NIY	B	730	1	-	5/7/10/12	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	730	NIY	CE1-NN	-4.82	1.36	1.45
1	A	730	NIY	CE1-NN	-3.41	1.39	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	730	NIY	CE1-NN	-3.33	1.39	1.45

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	730	NIY	CB-CG-CD1	-3.49	114.43	120.43
1	B	730	NIY	CD2-CE2-CZ	-2.91	117.59	120.50
1	B	730	NIY	CD1-CE1-CZ	2.73	124.91	121.42
1	A	730	NIY	CD2-CG-CD1	2.31	121.73	118.55
1	A	730	NIY	CD2-CE2-CZ	-2.29	118.21	120.50

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	730	NIY	O-C-CA-CB
1	A	730	NIY	CZ-CE1-NN-O2
1	B	730	NIY	O-C-CA-CB
1	B	730	NIY	CD1-CE1-NN-O2
1	B	730	NIY	CZ-CE1-NN-O2

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	730	NIY	1	0
1	B	730	NIY	2	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

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	727/761 (95%)	0.15	9 (1%) 79 85	21, 39, 63, 82	0
1	B	727/761 (95%)	0.09	6 (0%) 86 90	26, 41, 62, 88	0
1	C	727/761 (95%)	-0.05	4 (0%) 89 92	17, 30, 55, 72	0
2	D	16/20 (80%)	1.24	3 (18%) 1 1	68, 85, 87, 87	0
2	E	16/20 (80%)	1.13	2 (12%) 3 4	71, 85, 90, 90	0
2	F	16/20 (80%)	1.23	2 (12%) 3 4	65, 81, 86, 86	0
2	P	3/20 (15%)	0.09	0 100 100	27, 27, 33, 41	0
All	All	2232/2363 (94%)	0.09	26 (1%) 79 85	17, 37, 68, 90	0

The worst 5 of 26 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	296	GLY	6.7
1	C	271	GLY	5.5
1	B	297	VAL	4.0
1	A	4	ASN	3.8
1	A	6	LEU	3.4

6.2 Non-standard residues in protein, DNA, RNA chains (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
1	NIY	B	730	15/16	0.96	0.17	32,34,43,45	0
1	NIY	A	730	15/16	0.97	0.18	31,34,43,44	0
1	NIY	C	730	15/16	0.98	0.15	23,29,39,39	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.