



wwPDB X-ray Structure Validation Summary Report

Feb 27, 2014 – 01:25 PM GMT

PDB ID : 2GR9
Title : Crystal structure of P5CR complexed with NADH
Authors : Meng, Z.; Lou, Z.; Liu, Z.; Rao, Z.
Deposited on : 2006-04-23
Resolution : 3.10 Å(reported)

This is a wwPDB validation summary 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/ValidationPDFNotes.html>

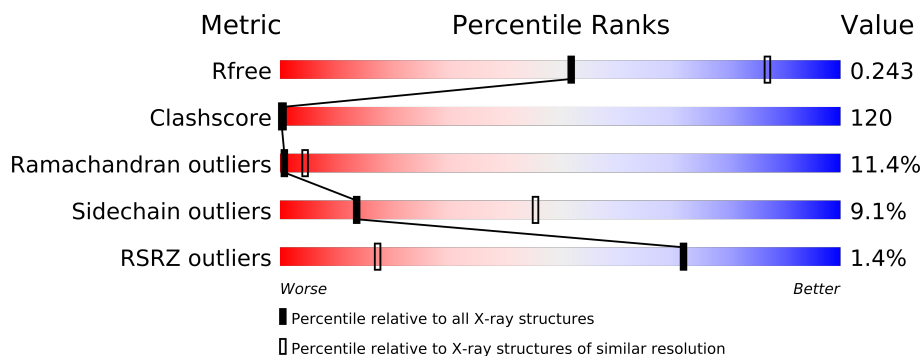
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 3.10 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}	66092	1007 (3.18-3.02)
Clashscore	79885	1078 (3.16-3.04)
Ramachandran outliers	78287	1044 (3.16-3.04)
Sidechain outliers	78261	1044 (3.16-3.04)
RSRZ outliers	66119	1008 (3.18-3.02)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	277	
1	B	277	
1	C	277	
1	D	277	
1	E	277	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	NAI	A	1300	-	X
2	NAI	B	2300	-	X
2	NAI	C	3300	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
2	NAI	D	4300	-	X
2	NAI	E	5300	-	X
3	GLU	B	2301	-	X
3	GLU	C	3301	-	X
3	GLU	E	5301	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11077 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

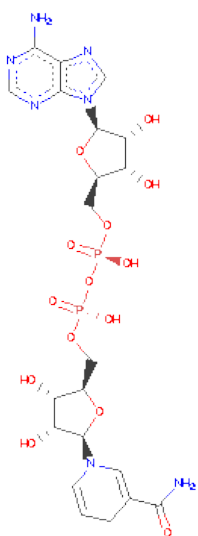
- Molecule 1 is a protein called Pyrroline-5-carboxylatereductase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	277	Total	C	N	O	S	0	0	0
			2038	1279	363	383	13			
1	B	276	Total	C	N	O	S	0	0	0
			2023	1270	358	382	13			
1	C	277	Total	C	N	O	S	0	0	0
			2032	1276	360	383	13			
1	D	277	Total	C	N	O	S	0	0	0
			2038	1279	363	383	13			
1	E	277	Total	C	N	O	S	0	0	0
			2038	1279	363	383	13			

There are 10 discrepancies between the modelled and reference sequences:

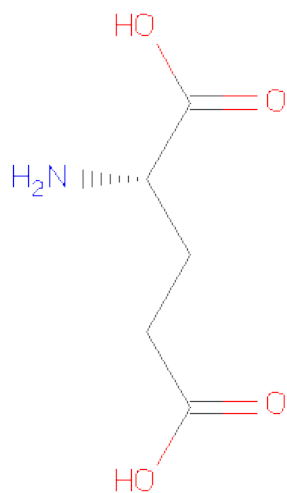
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	ARG	-	CLONING ARTIFACT	UNP P32322
A	0	GLY	-	CLONING ARTIFACT	UNP P32322
B	-1	ARG	-	CLONING ARTIFACT	UNP P32322
B	0	GLY	-	CLONING ARTIFACT	UNP P32322
C	-1	ARG	-	CLONING ARTIFACT	UNP P32322
C	0	GLY	-	CLONING ARTIFACT	UNP P32322
D	-1	ARG	-	CLONING ARTIFACT	UNP P32322
D	0	GLY	-	CLONING ARTIFACT	UNP P32322
E	-1	ARG	-	CLONING ARTIFACT	UNP P32322
E	0	GLY	-	CLONING ARTIFACT	UNP P32322

- Molecule 2 is 1,4-DIHYDRONICOTINAMIDEADENINE DINUCLEOTIDE (three-letter code: NAI) (formula: C₂₁H₂₉N₇O₁₄P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			43	21	6	14	2		
2	B	1	Total	C	N	O	P	0	0
			43	21	6	14	2		
2	C	1	Total	C	N	O	P	0	0
			43	21	6	14	2		
2	D	1	Total	C	N	O	P	0	0
			43	21	6	14	2		
2	E	1	Total	C	N	O	P	0	0
			43	21	6	14	2		

- Molecule 3 is GLUTAMIC ACID (three-letter code: GLU) (formula: C₅H₉NO₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			10	5	1	4		
3	B	1	Total	C	N	O	0	0
			10	5	1	4		
3	C	1	Total	C	N	O	0	0
			10	5	1	4		
3	D	1	Total	C	N	O	0	0
			10	5	1	4		
3	E	1	Total	C	N	O	0	0
			10	5	1	4		

- Molecule 4 is water.

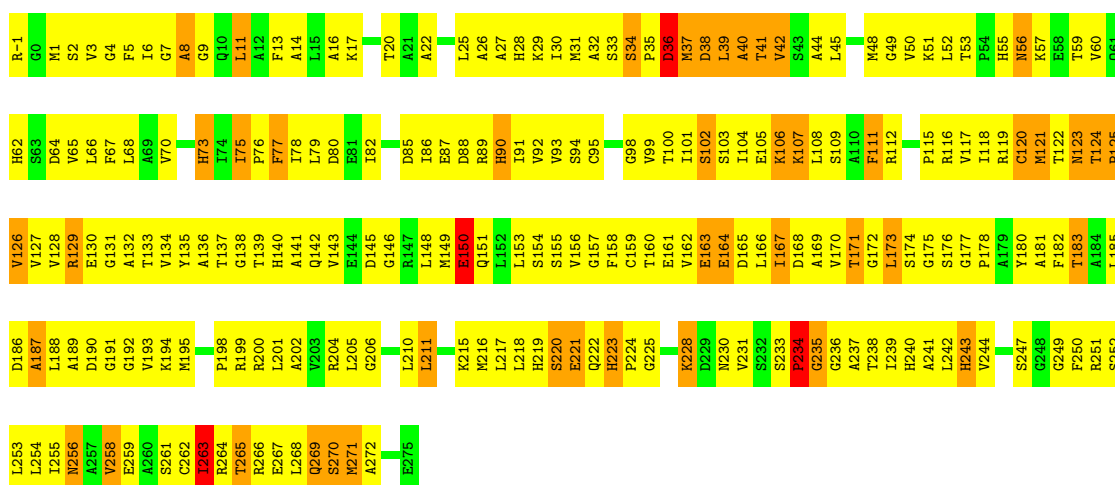
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	141	Total	O	0	0
			141	141		
4	B	93	Total	O	0	0
			93	93		
4	C	116	Total	O	0	0
			116	116		
4	D	155	Total	O	0	0
			155	155		
4	E	138	Total	O	0	0
			138	138		

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.

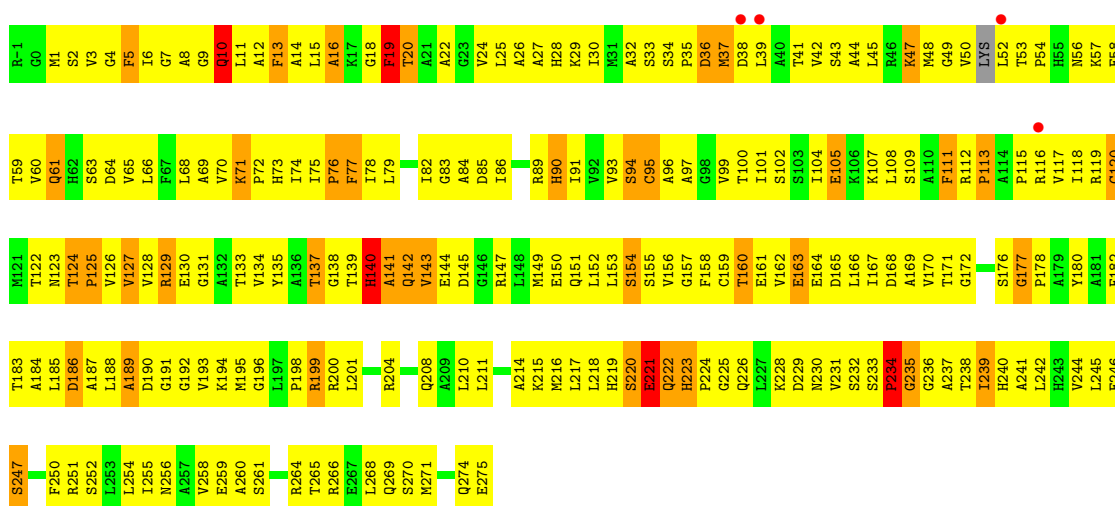
• Molecule 1: Pyrroline-5-carboxylatereductase 1

Chain A:



• Molecule 1: Pyrroline-5-carboxylatereductase 1

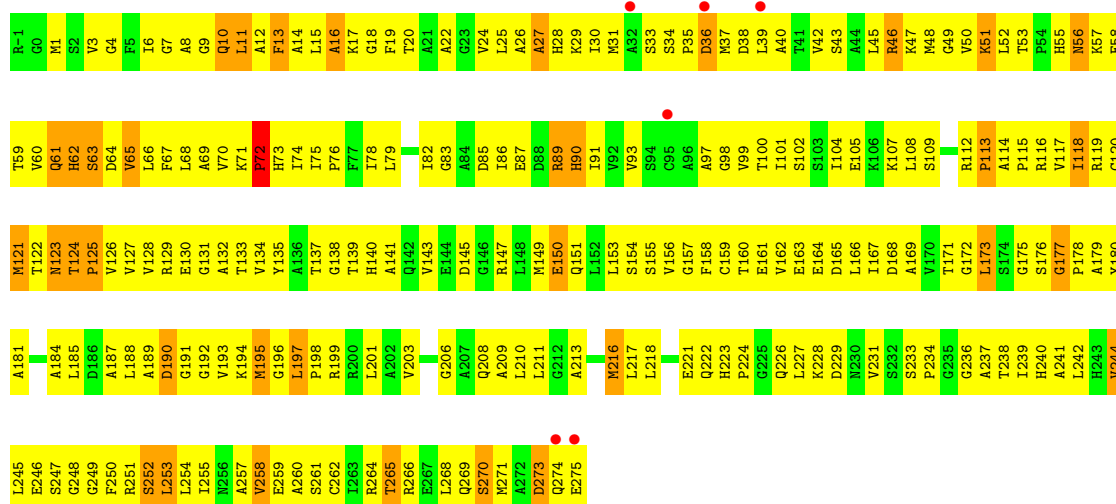
Chain B:



• Molecule 1: Pyrroline-5-carboxylatereductase 1

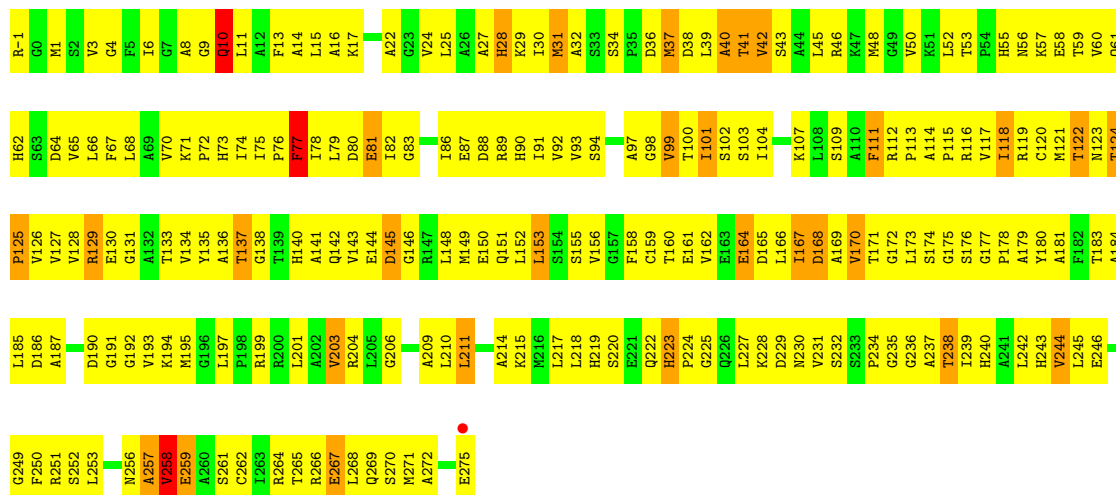
Chain C:





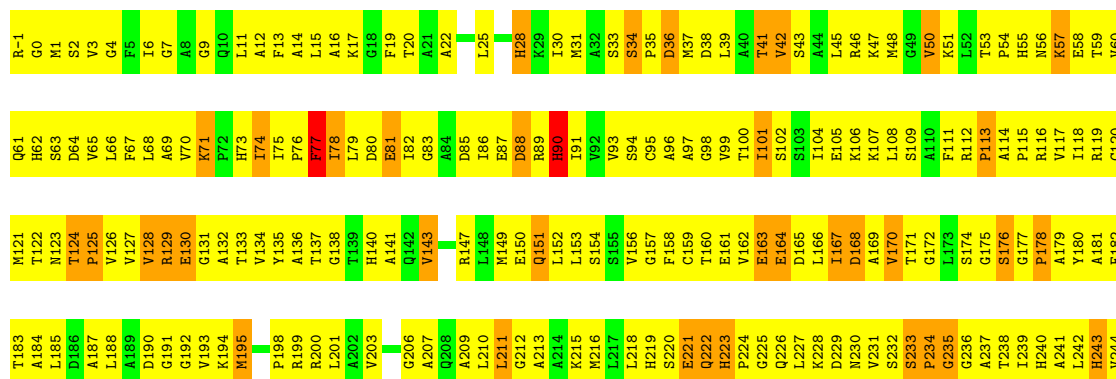
● Molecule 1: Pyrroline-5-carboxylatereductase 1

Chain D:



● Molecule 1: Pyrroline-5-carboxylatereductase 1

Chain E:



L245	F250	E259	A260	S261	C262	I263	R264	T265	R266	Q269	Q274	E275
E246	R251	A260	S261	C262	I263	R264	T265	R266	Q269	Q274	E275	
S247	S252	V258	E259	A260	S261	C262	I263	R264	T265	R266	Q269	E275
	L253	E259	A260	S261	C262	I263	R264	T265	R266	Q269	Q274	E275
	L254	E259	A260	S261	C262	I263	R264	T265	R266	Q269	Q274	E275
	I255	E259	A260	S261	C262	I263	R264	T265	R266	Q269	Q274	E275
	N256	E259	A260	S261	C262	I263	R264	T265	R266	Q269	Q274	E275
	A257	E259	A260	S261	C262	I263	R264	T265	R266	Q269	Q274	E275
	V258	E259	A260	S261	C262	I263	R264	T265	R266	Q269	Q274	E275

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	208.18Å 122.64Å 120.71Å 90.00° 122.03° 90.00°	Depositor
Resolution (Å)	50.00 – 3.10 28.96 – 2.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-3.10) 94.9 (28.96-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.71 (at 2.80Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.241 , 0.278 0.240 , 0.243	Depositor DCC
R_{free} test set	2279 reflections (5.01%)	DCC
Wilson B-factor (Å ²)	61.4	Xtriage
Anisotropy	0.443	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 67.1	EDS
Estimated twinning fraction	0.017 for $-1/2^*h+1/2^*k+l, 1/2^*h-1/2^*k+l, 1/2^*h+1/2^*k$ 0.026 for $-1/2^*h-1/2^*k+l, -1/2^*h-1/2^*k-l, 1/2^*h-1/2^*k$	Xtriage
L-test for twinning	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 62185 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	11077	wwPDB-VP
Average B, all atoms (Å ²)	97.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.17% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: NAI

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	0.41	0/2069	0.72	1/2800 (0.0%)
1	B	0.37	0/2053	0.71	1/2779 (0.0%)
1	C	0.38	0/2063	0.70	1/2793 (0.0%)
1	D	0.42	0/2069	0.69	0/2800
1	E	0.49	2/2069 (0.1%)	0.86	6/2800 (0.2%)
All	All	0.41	2/10323 (0.0%)	0.74	9/13972 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	129	ARG	C-N	11.03	1.59	1.34
1	E	128	VAL	C-N	-5.02	1.22	1.34

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	128	VAL	O-C-N	14.89	146.53	122.70
1	E	128	VAL	CA-C-N	-11.74	91.36	117.20
1	E	129	ARG	O-C-N	-10.77	105.48	122.70
1	E	128	VAL	C-N-CA	-8.96	99.30	121.70
1	E	129	ARG	CA-C-N	6.87	132.32	117.20

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens

added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2038	0	2084	489	6
1	B	2023	0	2059	491	5
1	C	2032	0	2072	530	2
1	D	2038	0	2084	436	2
1	E	2038	0	2084	492	1
2	A	43	0	23	26	0
2	B	43	0	24	67	5
2	C	43	0	23	39	4
2	D	43	0	24	40	0
2	E	43	0	21	32	1
3	A	10	0	5	8	0
3	B	10	0	5	17	0
3	C	10	0	5	12	0
3	D	10	0	5	21	0
3	E	10	0	5	11	0
4	A	141	0	0	262	6
4	B	93	0	0	169	3
4	C	116	0	0	256	4
4	D	155	0	0	247	2
4	E	138	0	0	298	1
All	All	11077	0	10523	2520	22

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 120.

The worst 5 of 2520 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:1300:NAI:C1D	2:A:1300:NAI:N1N	1.68	1.55
2:E:5300:NAI:O3	2:E:5300:NAI:PN	1.13	1.50
1:B:129:ARG:CZ	2:B:2300:NAI:H2N	1.48	1.40
2:E:5300:NAI:O5B	2:E:5300:NAI:C5B	1.71	1.36
2:D:4300:NAI:H1D	3:D:4301:GLU:N	1.41	1.36

The worst 5 of 22 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	Distance(Å)	Clash(Å)
1:B:200:ARG:NH1	2:B:2300:NAI:N7A[2_555]	1.66	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:204:ARG:CB	2:C:3300:NAI:C3B[2.555]	1.75	0.45
1:B:204:ARG:CB	2:B:2300:NAI:C3B[2.555]	1.76	0.44
2:B:2300:NAI:O5B	4:B:2359:HOH:O[2.555]	1.88	0.32
1:D:204:ARG:CB	2:E:5300:NAI:C2B[2.555]	1.94	0.26

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	275/277 (99%)	189 (69%)	54 (20%)	32 (12%)	1	4
1	B	272/277 (98%)	168 (62%)	62 (23%)	42 (15%)	0	1
1	C	275/277 (99%)	198 (72%)	49 (18%)	28 (10%)	1	6
1	D	275/277 (99%)	190 (69%)	64 (23%)	21 (8%)	2	11
1	E	275/277 (99%)	178 (65%)	64 (23%)	33 (12%)	1	4
All	All	1372/1385 (99%)	923 (67%)	293 (21%)	156 (11%)	1	4

5 of 156 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	8	ALA
1	A	36	ASP
1	A	39	LEU
1	A	107	LYS
1	A	129	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	215/215 (100%)	188 (87%)	27 (13%)	7	24
1	B	213/215 (99%)	197 (92%)	16 (8%)	19	58
1	C	214/215 (100%)	197 (92%)	17 (8%)	18	55
1	D	215/215 (100%)	195 (91%)	20 (9%)	13	44
1	E	215/215 (100%)	200 (93%)	15 (7%)	21	61
All	All	1072/1075 (100%)	977 (91%)	95 (9%)	14	47

5 of 95 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	265	THR
1	C	124	THR
1	E	160	THR
1	C	51	LYS
1	C	90	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	90	HIS
1	C	243	HIS
1	E	28	HIS
1	C	73	HIS
1	E	142	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

10 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	NAI	A	1300	-	45,47,48	5.92	31 (68%)	67,71,73	5.80	36 (53%)
3	GLU	A	1301	-	9,9,9	1.37	1 (11%)	11,11,11	5.48	1 (9%)
2	NAI	B	2300	-	45,47,48	5.49	26 (57%)	67,71,73	4.43	30 (44%)
3	GLU	B	2301	-	9,9,9	1.62	2 (22%)	11,11,11	5.57	2 (18%)
2	NAI	C	3300	-	45,47,48	5.49	26 (57%)	67,71,73	4.44	30 (44%)
3	GLU	C	3301	-	9,9,9	1.62	2 (22%)	11,11,11	5.57	2 (18%)
2	NAI	D	4300	-	45,47,48	5.50	27 (60%)	67,71,73	4.44	30 (44%)
3	GLU	D	4301	-	9,9,9	1.18	1 (11%)	11,11,11	1.78	2 (18%)
2	NAI	E	5300	-	45,47,48	7.28	32 (71%)	67,71,73	6.91	42 (62%)
3	GLU	E	5301	-	9,9,9	1.19	1 (11%)	11,11,11	1.50	2 (18%)

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	NAI	A	1300	-	2/2/13/16	0/30/72/72	0/3/5/5
3	GLU	A	1301	-	-	0/9/9/9	0/0/0/0
2	NAI	B	2300	-	1/1/13/16	0/30/72/72	0/3/5/5
3	GLU	B	2301	-	-	0/9/9/9	0/0/0/0
2	NAI	C	3300	-	1/1/13/16	0/30/72/72	0/3/5/5
3	GLU	C	3301	-	-	0/9/9/9	0/0/0/0
2	NAI	D	4300	-	1/1/13/16	0/30/72/72	0/3/5/5
3	GLU	D	4301	-	-	0/9/9/9	0/0/0/0
2	NAI	E	5300	-	3/3/13/16	1/30/72/72	0/3/5/5
3	GLU	E	5301	-	-	0/9/9/9	0/0/0/0

The worst 5 of 149 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	5300	NAI	PN-O3	-25.89	1.13	1.59
2	E	5300	NAI	C1D-N1N	15.97	1.81	1.46
2	C	3300	NAI	C8A-N7A	15.07	1.64	1.34
2	B	2300	NAI	C8A-N7A	15.06	1.64	1.34
2	D	4300	NAI	C8A-N7A	15.03	1.64	1.34

The worst 5 of 177 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	5300	NAI	O4B-C1B-N9A	26.52	133.11	108.44
2	A	1300	NAI	C1B-N9A-C4A	21.01	162.94	126.64
2	A	1300	NAI	C8A-N9A-C1B	-19.06	88.84	126.38
2	E	5300	NAI	C1D-N1N-C6N	-18.68	79.40	120.79
2	E	5300	NAI	C1D-N1N-C2N	18.18	151.99	121.02

5 of 8 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	1300	NAI	C1D
2	A	1300	NAI	C4D
2	D	4300	NAI	C4D
2	E	5300	NAI	C1D
2	E	5300	NAI	C4D

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	5300	NAI	PA-O5B-C5B-C4B

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	277/277 (100%)	-0.28	0 100 100	32, 82, 117, 153	0
1	B	276/277 (99%)	0.00	4 (1%) 72 17	39, 129, 183, 200	0
1	C	277/277 (100%)	0.01	6 (2%) 59 11	31, 125, 181, 195	0
1	D	277/277 (100%)	-0.30	1 (0%) 90 45	34, 76, 118, 191	0
1	E	277/277 (100%)	-0.29	0 100 100	24, 80, 128, 142	0
All	All	1384/1385 (99%)	-0.17	11 (0%) 72 28	24, 87, 168, 200	0

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	32	ALA	3.3
1	D	275	GLU	3.1
1	C	95	CYS	2.9
1	B	39	LEU	2.5
1	B	52	LEU	2.4

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	GLU	B	2301	10/10	0.89	32.11	192,200,200,200	0
3	GLU	E	5301	10/10	0.56	12.71	195,200,200,200	0
2	NAI	B	2300	43/44	0.72	9.62	192,195,195,195	0
3	GLU	C	3301	10/10	1.46	9.16	200,200,200,200	0
2	NAI	C	3300	43/44	0.93	8.54	189,195,195,195	0
2	NAI	D	4300	43/44	0.60	7.47	81,91,95,95	0
2	NAI	E	5300	43/44	0.54	6.06	69,94,95,95	0
2	NAI	A	1300	43/44	0.56	5.99	63,93,95,95	0
3	GLU	D	4301	10/10	0.62	-	182,193,196,198	0
3	GLU	A	1301	10/10	0.60	-	120,131,140,140	0

6.5 Other polymers ⓘ

There are no such residues in this entry.