wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 04:42 AM GMT

PDB ID	:	2NV9
Title	:	The X-ray Crystal Structure of the Paramecium bursaria Chlorella virus arginine decarboxylase
Authors	:	Shah, R.H.; Akella, R.; Goldsmith, E.; Phillips, M.A.
Deposited on	:	2006-11-11
Resolution	:	1.95 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

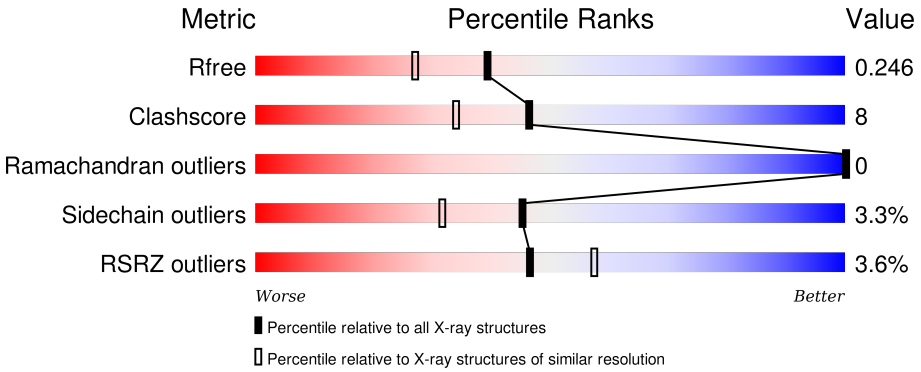
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	1833 (1.96-1.96)
Clashscore	102246	1953 (1.96-1.96)
Ramachandran outliers	100387	1936 (1.96-1.96)
Sidechain outliers	100360	1936 (1.96-1.96)
RSRZ outliers	91569	1835 (1.96-1.96)

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 <=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	372	4% 87% 12%
1	B	372	3% 87% 12%
1	C	372	6% 85% 12%
1	D	372	4% 83% 14%
1	E	372	% 85% 13%

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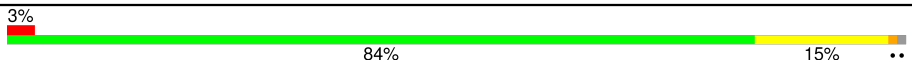
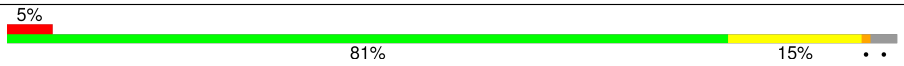
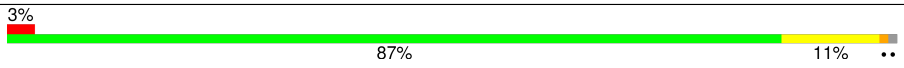
Mol	Chain	Length	Quality of chain
1	F	372	
1	G	372	
1	H	372	

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
2	PLP	A	2001	-	-	X	-
2	PLP	B	2002	-	-	X	-
2	PLP	C	2003	-	-	X	-
2	PLP	D	2004	-	-	X	-
2	PLP	E	2005	-	-	X	-
2	PLP	F	2006	-	-	X	-
2	PLP	G	2007	-	-	X	-
2	PLP	H	2008	-	-	X	-

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 24712 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.

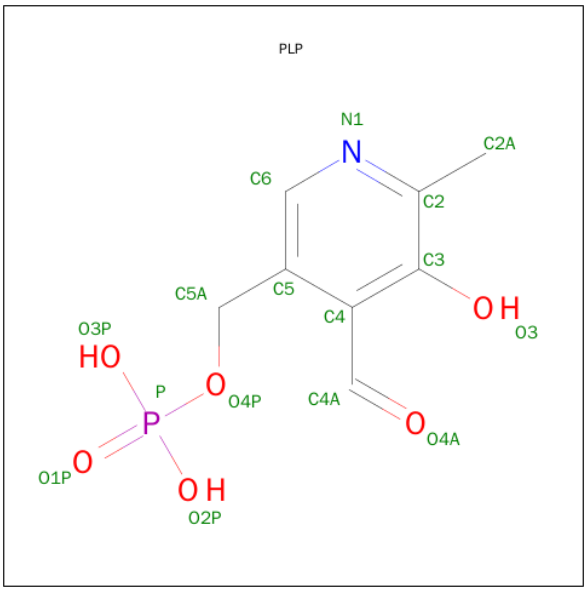
- Molecule 1 is a protein called A207R protein, arginine decarboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	371	Total	C	N	O	S	0	1	0
			2955	1890	482	570	13			
1	B	372	Total	C	N	O	S	0	1	0
			2962	1896	483	570	13			
1	C	367	Total	C	N	O	S	0	1	0
			2925	1874	478	560	13			
1	D	363	Total	C	N	O	S	0	1	0
			2890	1853	471	553	13			
1	E	370	Total	C	N	O	S	0	1	0
			2945	1884	479	569	13			
1	F	369	Total	C	N	O	S	0	1	0
			2936	1882	478	563	13			
1	G	362	Total	C	N	O	S	0	2	0
			2885	1848	468	556	13			
1	H	367	Total	C	N	O	S	0	1	0
			2915	1868	476	558	13			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	142	ALA	THR	ENGINEERED	UNP Q84527
B	142	ALA	THR	ENGINEERED	UNP Q84527
C	142	ALA	THR	ENGINEERED	UNP Q84527
D	142	ALA	THR	ENGINEERED	UNP Q84527
E	142	ALA	THR	ENGINEERED	UNP Q84527
F	142	ALA	THR	ENGINEERED	UNP Q84527
G	142	ALA	THR	ENGINEERED	UNP Q84527
H	142	ALA	THR	ENGINEERED	UNP Q84527

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: $C_8H_{10}NO_6P$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C N O P 16 8 1 6 1	0	0
2	B	1	Total C N O P 16 8 1 6 1	0	0
2	C	1	Total C N O P 16 8 1 6 1	0	0
2	D	1	Total C N O P 16 8 1 6 1	0	0
2	E	1	Total C N O P 16 8 1 6 1	0	0
2	F	1	Total C N O P 16 8 1 6 1	0	0
2	G	1	Total C N O P 16 8 1 6 1	0	0
2	H	1	Total C N O P 16 8 1 6 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	143	Total O 143 143	0	0
3	B	146	Total O 146 146	0	0
3	C	112	Total O 112 112	0	0
3	D	128	Total O 128 128	0	0

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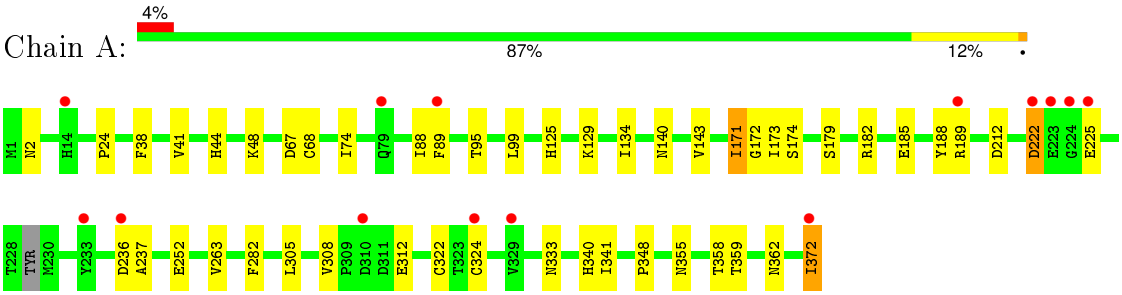
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	E	205	Total O 205 205	0	0
3	F	137	Total O 137 137	0	0
3	G	135	Total O 135 135	0	0
3	H	165	Total O 165 165	0	0

3 Residue-property plots (i)

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.

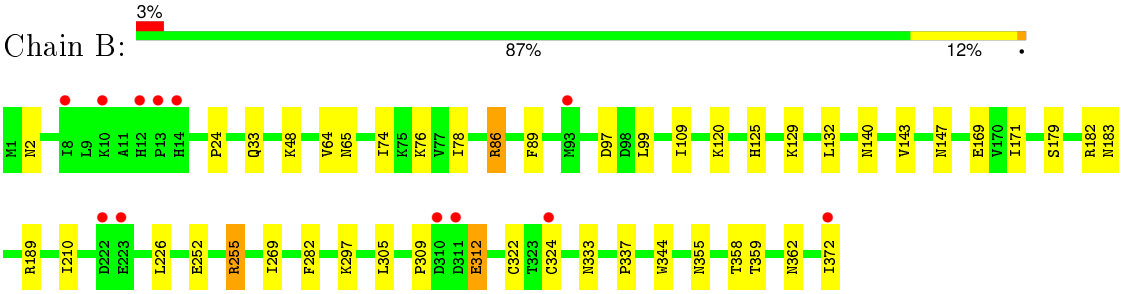
- Molecule 1: A207R protein, arginine decarboxylase

Chain A:



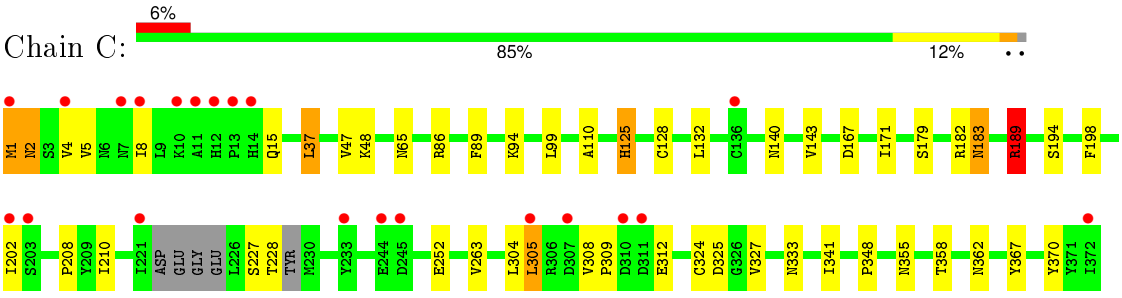
- Molecule 1: A207R protein, arginine decarboxylase

Chain B:



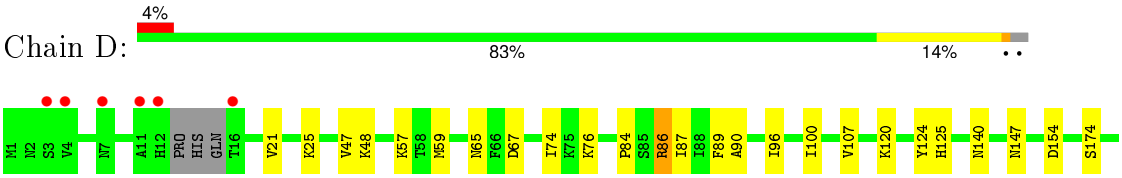
- Molecule 1: A207R protein, arginine decarboxylase

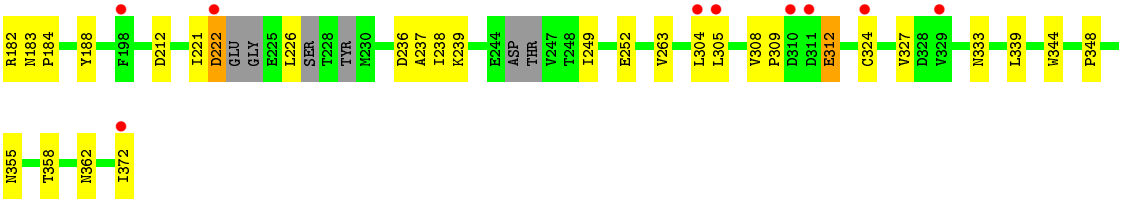
Chain C:



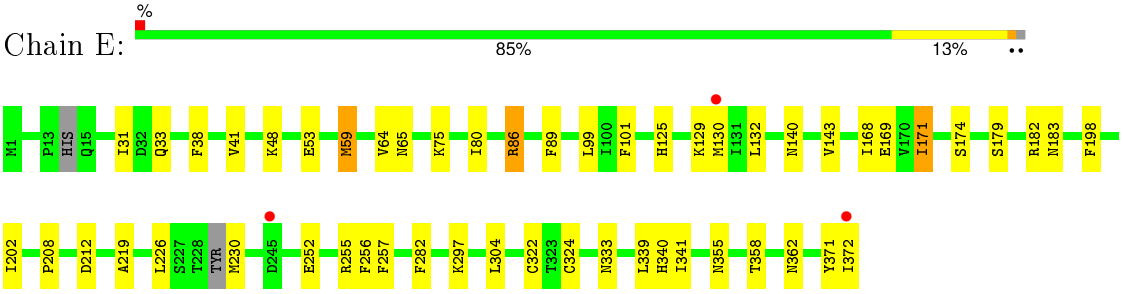
- Molecule 1: A207R protein, arginine decarboxylase

Chain D:

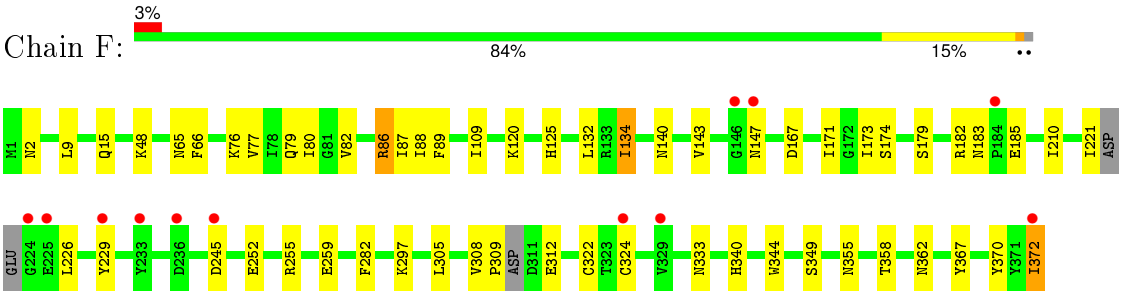




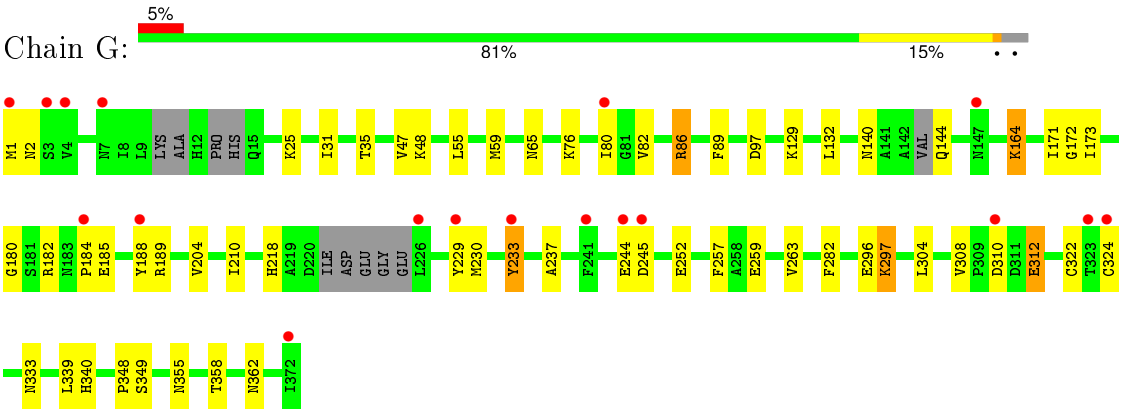
• Molecule 1: A207R protein, arginine decarboxylase



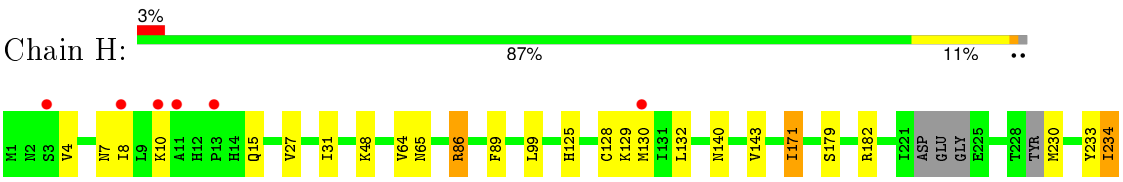
• Molecule 1: A207R protein, arginine decarboxylase

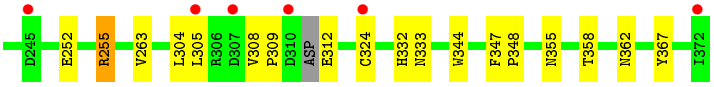


• Molecule 1: A207R protein, arginine decarboxylase



• Molecule 1: A207R protein, arginine decarboxylase




D245
E252
R255
V263
L304
L305
R306
D307
V308
P309
D310
ASP
E312
C324
H332
N333
W344
F347
P348
N355
T358
N362
Y367
I372

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	116.11Å 116.87Å 269.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.91 – 1.95 48.88 – 1.95	Depositor EDS
% Data completeness (in resolution range)	88.7 (48.91-1.95) 88.7 (48.88-1.95)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.43 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.211 , 0.242 0.225 , 0.246	Depositor DCC
R_{free} test set	1455 reflections (0.62%)	DCC
Wilson B-factor (Å^2)	15.5	Xtriage
Anisotropy	0.812	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 43.3	EDS
Estimated twinning fraction	0.000 for k,h,-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Outliers	6 of 235861 reflections (0.003%)	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	24712	wwPDB-VP
Average B, all atoms (Å^2)	12.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 43.16 % of the origin peak, indicating pseudo translational symmetry.The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.8352e-04.The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: PLP

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	0.81	0/3029	0.70	1/4115 (0.0%)
1	B	0.79	0/3038	0.71	3/4129 (0.1%)
1	C	0.75	0/2998	0.73	3/4072 (0.1%)
1	D	0.76	0/2958	0.73	2/4011 (0.0%)
1	E	0.80	0/3017	0.72	1/4097 (0.0%)
1	F	0.76	0/3009	0.71	3/4086 (0.1%)
1	G	0.78	0/2954	0.72	2/4008 (0.0%)
1	H	0.77	0/2986	0.72	4/4053 (0.1%)
All	All	0.78	0/23989	0.72	19/32571 (0.1%)

There are no bond length outliers.

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	189	ARG	NE-CZ-NH1	8.94	124.77	120.30
1	F	86	ARG	NE-CZ-NH2	-8.44	116.08	120.30
1	E	86	ARG	NE-CZ-NH2	-7.65	116.47	120.30
1	H	86	ARG	NE-CZ-NH2	-7.63	116.48	120.30
1	B	86	ARG	NE-CZ-NH2	-6.78	116.91	120.30

There are no chirality outliers.

There are no planarity outliers.

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	2955	0	2844	44	0
1	B	2962	0	2849	46	0
1	C	2925	0	2824	48	0
1	D	2890	0	2788	47	0
1	E	2945	0	2836	45	0
1	F	2936	0	2832	59	0
1	G	2885	0	2773	53	0
1	H	2915	0	2814	47	0
2	A	16	0	7	9	0
2	B	16	0	7	10	0
2	C	16	0	7	8	0
2	D	16	0	8	6	0
2	E	16	0	7	7	0
2	F	16	0	7	9	0
2	G	16	0	8	8	0
2	H	16	0	7	9	0
3	A	143	0	0	3	0
3	B	146	0	0	7	0
3	C	112	0	0	0	0
3	D	128	0	0	3	0
3	E	205	0	0	2	0
3	F	137	0	0	3	0
3	G	135	0	0	5	0
3	H	165	0	0	2	0
All	All	24712	0	22618	348	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.

The worst 5 of 348 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:F:48:LYS:NZ	2:F:2006:PLP:C4A	2.05	1.20
1:A:48:LYS:NZ	2:A:2001:PLP:C4A	2.11	1.14
1:C:48:LYS:NZ	2:C:2003:PLP:H4A	1.60	1.14
1:H:308:VAL:HB	1:H:312:GLU:HG3	1.29	1.12
1:A:308:VAL:HB	1:A:312:GLU:HG3	1.28	1.10

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	368/372 (99%)	354 (96%)	14 (4%)	0	100	100
1	B	371/372 (100%)	362 (98%)	9 (2%)	0	100	100
1	C	362/372 (97%)	351 (97%)	11 (3%)	0	100	100
1	D	353/372 (95%)	340 (96%)	13 (4%)	0	100	100
1	E	365/372 (98%)	355 (97%)	10 (3%)	0	100	100
1	F	364/372 (98%)	353 (97%)	11 (3%)	0	100	100
1	G	354/372 (95%)	344 (97%)	10 (3%)	0	100	100
1	H	360/372 (97%)	349 (97%)	11 (3%)	0	100	100
All	All	2897/2976 (97%)	2808 (97%)	89 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	328/328 (100%)	318 (97%)	10 (3%)	48	36
1	B	328/328 (100%)	319 (97%)	9 (3%)	52	41
1	C	325/328 (99%)	311 (96%)	14 (4%)	35	20
1	D	320/328 (98%)	309 (97%)	11 (3%)	44	30
1	E	327/328 (100%)	318 (97%)	9 (3%)	51	39
1	F	325/328 (99%)	313 (96%)	12 (4%)	41	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	G	320/328 (98%)	310 (97%)	10 (3%)	47 34
1	H	323/328 (98%)	313 (97%)	10 (3%)	47 34
All	All	2596/2624 (99%)	2511 (97%)	85 (3%)	45 32

5 of 85 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	125	HIS
1	E	125	HIS
1	H	89	PHE
1	D	147	ASN
1	D	312	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 62 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	333	ASN
1	E	144	GLN
1	H	218	HIS
1	E	7	ASN
1	E	218	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry (i)

8 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	PLP	A	2001	-	16,16,16	1.78	2 (12%)	21,23,23	1.17	2 (9%)
2	PLP	B	2002	1	16,16,16	1.72	3 (18%)	21,23,23	1.12	1 (4%)
2	PLP	C	2003	1	16,16,16	1.65	3 (18%)	21,23,23	1.05	0
2	PLP	D	2004	-	16,16,16	1.66	1 (6%)	21,23,23	1.22	2 (9%)
2	PLP	E	2005	-	16,16,16	1.64	1 (6%)	21,23,23	1.56	4 (19%)
2	PLP	F	2006	-	16,16,16	1.98	3 (18%)	21,23,23	0.94	1 (4%)
2	PLP	G	2007	-	16,16,16	1.56	2 (12%)	21,23,23	1.28	3 (14%)
2	PLP	H	2008	-	16,16,16	1.74	1 (6%)	21,23,23	1.01	1 (4%)

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	PLP	A	2001	-	-	0/8/8/8	0/1/1/1
2	PLP	B	2002	1	-	0/8/8/8	0/1/1/1
2	PLP	C	2003	1	-	0/8/8/8	0/1/1/1
2	PLP	D	2004	-	-	0/8/8/8	0/1/1/1
2	PLP	E	2005	-	-	0/8/8/8	0/1/1/1
2	PLP	F	2006	-	-	0/8/8/8	0/1/1/1
2	PLP	G	2007	-	-	0/8/8/8	0/1/1/1
2	PLP	H	2008	-	-	0/8/8/8	0/1/1/1

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	2006	PLP	C3-C2	-2.69	1.38	1.40
2	C	2003	PLP	C3-C2	-2.21	1.39	1.40
2	G	2007	PLP	C2A-C2	2.05	1.54	1.50
2	B	2002	PLP	P-O3P	2.28	1.62	1.54
2	F	2006	PLP	O4A-C4A	2.30	1.28	1.21

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	2005	PLP	C5A-C5-C6	-3.59	112.48	119.28
2	D	2004	PLP	C2A-C2-C3	-2.36	118.19	121.04
2	E	2005	PLP	C5-C6-N1	-2.32	119.83	123.86
2	A	2001	PLP	C5A-C5-C6	-2.26	115.00	119.28
2	G	2007	PLP	C5-C6-N1	-2.02	120.35	123.86

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 66 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	2001	PLP	9	0
2	B	2002	PLP	10	0
2	C	2003	PLP	8	0
2	D	2004	PLP	6	0
2	E	2005	PLP	7	0
2	F	2006	PLP	9	0
2	G	2007	PLP	8	0
2	H	2008	PLP	9	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, 95^{th} 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	371/372 (99%)	0.47	14 (3%)	44	56	9, 12, 16, 24	0
1	B	372/372 (100%)	0.42	12 (3%)	51	61	8, 12, 16, 23	0
1	C	367/372 (98%)	0.38	21 (5%)	27	37	7, 12, 17, 22	0
1	D	363/372 (97%)	0.33	15 (4%)	41	52	7, 12, 17, 24	0
1	E	370/372 (99%)	0.38	3 (0%)	87	92	9, 12, 16, 20	0
1	F	369/372 (99%)	0.38	12 (3%)	50	61	8, 12, 16, 21	0
1	G	362/372 (97%)	0.46	18 (4%)	32	44	7, 12, 16, 25	1 (0%)
1	H	367/372 (98%)	0.34	12 (3%)	50	61	9, 12, 16, 21	0
All	All	2941/2976 (98%)	0.40	107 (3%)	46	57	7, 12, 16, 25	1 (0%)

The worst 5 of 107 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	323[A]	THR	9.1
1	G	229	TYR	5.8
1	E	372	ILE	5.7
1	F	372	ILE	5.4
1	B	14	HIS	4.9

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, 95^{th} 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
2	PLP	F	2006	16/16	0.95	0.14	0.55	9,12,15,15	0
2	PLP	G	2007	16/16	0.96	0.13	0.36	10,13,14,16	0
2	PLP	C	2003	16/16	0.95	0.14	0.32	11,12,13,16	0
2	PLP	D	2004	16/16	0.97	0.11	-0.04	11,12,15,17	0
2	PLP	A	2001	16/16	0.95	0.14	-0.20	9,12,14,15	0
2	PLP	H	2008	16/16	0.95	0.13	-0.23	8,11,14,15	0
2	PLP	E	2005	16/16	0.96	0.14	-0.29	8,11,14,16	0
2	PLP	B	2002	16/16	0.96	0.12	-0.95	8,10,13,16	0

6.5 Other polymers

There are no such residues in this entry.