WORLDWIDE PDB

PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 02:54 AM GMT

PDB ID	:	2JAJ
Title	:	DDAH1 complexed with L-257
Authors	:	Murray-Rust, J.; O'Hara, B.P.; Rossiter, S.; Leiper, J.M.; Vallance, P.; Mc-Donald, N.Q.
Deposited on	:	2006-11-29
Resolution	:	2.00 Å(reported)

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

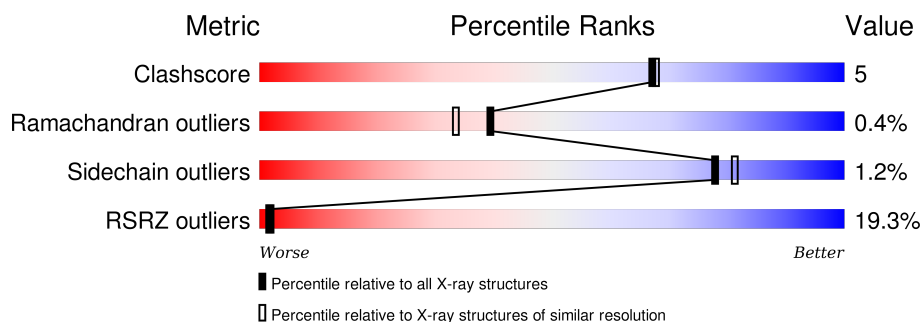|		
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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 2.00 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	Percentile Ranks	Value
Clashscore		5
Ramachandran outliers		0.4%
Sidechain outliers		1.2%
RSRZ outliers		19.3%

Worse   *Better*

■ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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 <=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	289	7% 88% 6% 6%
1	B	289	30% 80% 16% ··

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 4381 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 NG, NG-DIMETHYLARGININE DIMETHYLAMINOHYDR OLASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	272	Total 2054	C 1292	N 347	O 401	S 14	0	2	0
1	B	281	Total 2014	C 1270	N 344	O 387	S 13	0	0	0

- Molecule 2 is N 5 -{IMINO[(2-METHOXYETHYL)AMINO]METHYL}-L-ORNITHINE (three-letter code: D20) (formula: $C_9H_{20}N_4O_3$).
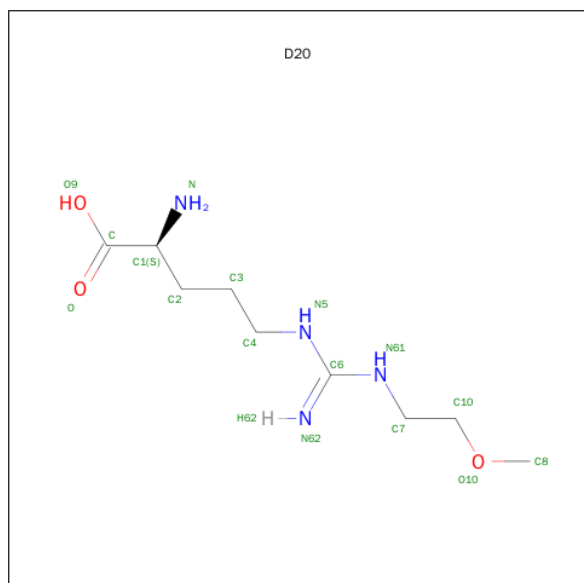
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total 16	C 9	N 4	O 3	0	0
2	B	1	Total 16	C 9	N 4	O 3	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	233	Total　O 233　　233	0	0
3	B	48	Total　O 48　　48	0	0

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: NG, NG-DIMETHYLARGININE DIMETHYLAMINOHYDROLASE 1
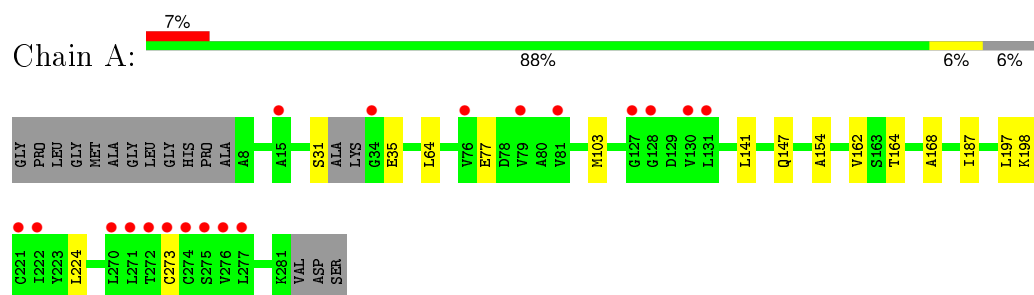
• Molecule 1: NG, NG-DIMETHYLARGININE DIMETHYLAMINOHYDROLASE 1
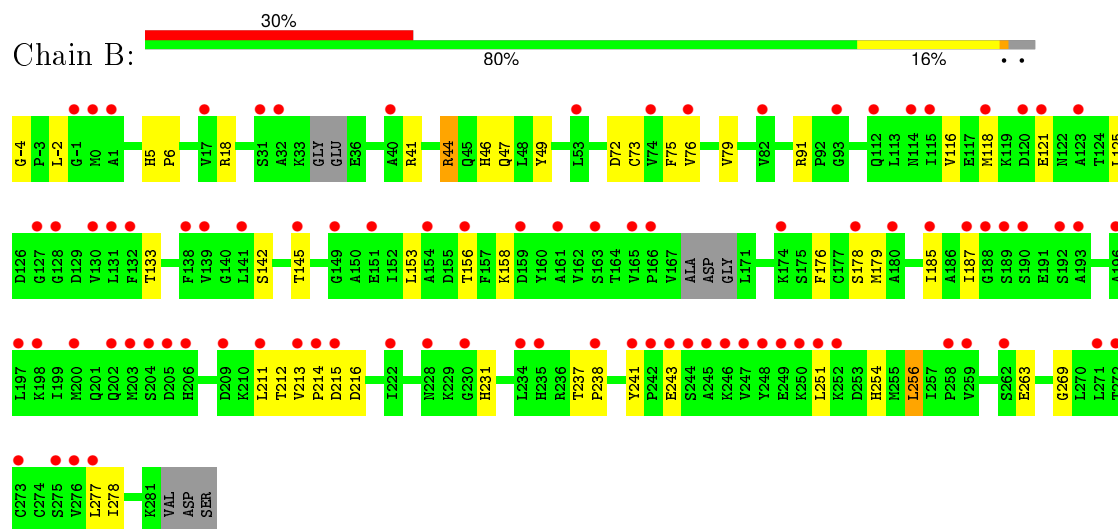
4   Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	44.85Å 46.91Å 147.61Å 90.00° 94.56° 90.00°	Depositor
Resolution (Å)	30.00 – 2.00 32.36 – 2.00	Depositor EDS
% Data completeness (in resolution range)	93.6 (30.00-2.00) 93.6 (32.36-2.00)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.19 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.211 , 0.263 0.213 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å^2)	24.2	Xtriage
Anisotropy	0.622	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 52.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< |L| > = 0.48, < L^2 > = 0.32$	Xtriage
Outliers	0 of 39147 reflections	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	4381	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 6.77% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: D20

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	0.95	0/2091	0.86	1/2835 (0.0%)
1	B	0.59	0/2047	0.73	0/2792
All	All	0.79	0/4138	0.80	1/5627 (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	A	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	203	MET	CG-SD-CE	6.14	110.02	100.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	168	ALA	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	2054	0	2025	9	0
1	B	2014	0	1902	31	0
2	A	16	0	19	0	0
2	B	16	0	18	1	0
3	A	233	0	0	2	0
3	B	48	0	0	1	0
All	All	4381	0	3964	39	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 5.

All (39) 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:B:116:VAL:HG11	1:B:156:THR:OG1	1.90	0.71
1:A:197:LEU:O	1:A:201:GLN:HG3	1.91	0.70
1:B:251:LEU:HB2	1:B:256:LEU:HD21	1.77	0.66
1:B:44:ARG:NH2	1:B:47:GLN:OE1	2.32	0.62
1:B:-4:GLY:N	3:B:2001:HOH:O	2.32	0.62
1:B:142:SER:OG	1:B:145:THR:N	2.30	0.60
1:A:224:LEU:HD23	3:A:2002:HOH:O	2.05	0.55
1:B:41:ARG:HB3	1:B:263:GLU:HG3	1.89	0.54
1:A:198:LYS:NZ	3:A:2173:HOH:O	2.43	0.52
1:B:46:HIS:O	1:B:49:TYR:HB3	2.09	0.52
1:B:251:LEU:HB3	1:B:254:HIS:HB2	1.91	0.51
1:B:75:PHE:CE2	1:B:269:GLY:HA3	2.45	0.51
1:B:215:ASP:CB	1:B:241:TYR:CD2	2.94	0.51
1:B:5:HIS:HB2	1:B:6:PRO:HD2	1.93	0.51
1:B:237:THR:HB	1:B:238:PRO:HD2	1.93	0.50
1:B:214:PRO:HG2	1:B:243:GLU:HB3	1.94	0.49
1:B:231:HIS:HB3	1:B:254:HIS:CD2	2.48	0.49
1:A:64:LEU:HD13	1:A:103:MET:HG2	1.94	0.48
1:B:215:ASP:CB	1:B:241:TYR:HD2	2.27	0.47
1:B:91:ARG:HB2	1:B:118:MET:HG2	1.97	0.47
1:B:176:PHE:HA	1:B:216:ASP:O	2.15	0.46
1:B:5:HIS:HB2	1:B:6:PRO:CD	2.46	0.46
1:A:187:ILE:HG12	1:A:197:LEU:HD22	1.99	0.45
1:B:18:ARG:HD3	1:B:73:CYS:HB2	1.97	0.45
1:B:153:LEU:O	1:B:156:THR:HB	2.16	0.45
1:B:215:ASP:HB3	1:B:241:TYR:CD2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:277:LEU:C	1:B:278:ILE:HG13	2.37	0.44
1:B:185:ILE:O	1:B:211:LEU:N	2.47	0.44
1:A:141:LEU:HG	1:A:164:THR:HB	2.00	0.43
1:B:76:VAL:O	1:B:79:VAL:HG22	2.19	0.43
1:A:147:GLN:HE22	1:B:-2:LEU:HD21	1.84	0.43
1:A:154:ALA:HA	1:A:162:VAL:HG21	2.02	0.42
1:B:178:SER:O	1:B:185:ILE:HG23	2.19	0.42
1:B:187:ILE:HG23	1:B:212:THR:HG23	2.01	0.42
1:B:125:LEU:HD12	1:B:145:THR:HG23	2.03	0.41
1:B:237:THR:HB	1:B:238:PRO:CD	2.50	0.41
1:B:133:THR:HA	1:B:179:MET:SD	2.60	0.41
1:B:72:ASP:OD1	2:B:500:D20:N	2.49	0.41
1:A:77:GLU:HB3	1:A:273:CYS:HA	2.02	0.40

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	270/289 (93%)	261 (97%)	8 (3%)	1 (0%)	39	33
1	B	275/289 (95%)	256 (93%)	18 (6%)	1 (0%)	39	33
All	All	545/578 (94%)	517 (95%)	26 (5%)	2 (0%)	39	33

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	35	GLU
1	B	121	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	220/241 (91%)	219 (100%)	1 (0%)	92	94
1	B	197/241 (82%)	193 (98%)	4 (2%)	63	65
All	All	417/482 (86%)	412 (99%)	5 (1%)	78	81

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	SER
1	B	44	ARG
1	B	158	LYS
1	B	213	VAL
1	B	256	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	202	GLN
1	B	206	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)

2 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	D20	A	500	-	12,15,15	1.15	1 (8%)	9,17,17	0.68	0
2	D20	B	500	-	12,15,15	1.01	0	9,17,17	0.89	1 (11%)

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	D20	A	500	-	-	0/12/16/16	0/0/0/0
2	D20	B	500	-	-	0/12/16/16	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	500	D20	C6-N62	2.65	1.36	1.29

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	500	D20	N61-C6-N5	2.16	121.75	119.28

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	500	D20	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(Å²)	Q<0.9
1	A	272/289 (94%)	0.43	19 (6%)	19	21	25, 31, 40, 52	0
1	B	281/289 (97%)	1.54	88 (31%)	1	1	29, 47, 70, 73	0
All	All	553/578 (95%)	0.99	107 (19%)	2	2	25, 37, 68, 73	0

All (107) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	213	VAL	8.2
1	B	189	SER	7.7
1	B	192	SER	6.6
1	B	200	MET	5.4
1	B	204	SER	5.2
1	B	242	PRO	5.0
1	B	165	VAL	4.9
1	B	238	PRO	4.6
1	B	209	ASP	4.5
1	A	34	GLY	4.5
1	B	163	SER	4.5
1	B	250	LYS	4.4
1	B	156	THR	4.4
1	B	241	TYR	4.4
1	B	205	ASP	4.2
1	B	114	ASN	4.1
1	B	115	ILE	4.0
1	B	188	GLY	4.0
1	B	246	LYS	4.0
1	B	76	VAL	3.9
1	B	252	LYS	3.8
1	A	272	THR	3.8
1	B	211	LEU	3.8
1	B	214	PRO	3.8

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Mol	Chain	Res	Type	RSRZ
1	B	202	GLN	3.7
1	B	-1	GLY	3.7
1	B	131	LEU	3.7
1	B	249	GLU	3.6
1	B	187	ILE	3.6
1	B	248	TYR	3.6
1	B	130	VAL	3.6
1	A	277	LEU	3.4
1	A	222	ILE	3.4
1	B	247	VAL	3.4
1	B	166	PRO	3.4
1	A	274	CYS	3.4
1	B	234	LEU	3.4
1	A	276	VAL	3.3
1	B	128	GLY	3.2
1	B	197	LEU	3.2
1	B	141	LEU	3.2
1	B	245	ALA	3.2
1	A	270	LEU	3.2
1	B	185	ILE	3.1
1	B	32	ALA	3.0
1	B	53	LEU	3.0
1	B	203	MET	3.0
1	A	271	LEU	3.0
1	A	76	VAL	2.9
1	A	81	VAL	2.9
1	B	138	PHE	2.9
1	A	130	VAL	2.9
1	B	259	VAL	2.9
1	B	0	MET	2.8
1	B	154	ALA	2.7
1	B	149	GLY	2.7
1	B	235	HIS	2.7
1	B	271	LEU	2.7
1	B	123	ALA	2.7
1	B	1	ALA	2.7
1	B	258	PRO	2.7
1	B	127	GLY	2.7
1	B	276	VAL	2.6
1	A	128	GLY	2.6
1	B	215	ASP	2.6
1	B	174	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	222	ILE	2.6
1	A	275	SER	2.5
1	B	198	LYS	2.5
1	B	151	GLU	2.5
1	B	251	LEU	2.5
1	A	79	VAL	2.4
1	B	228	ASN	2.4
1	B	272	THR	2.4
1	B	40	ALA	2.4
1	B	161	ALA	2.4
1	B	273	CYS	2.4
1	A	273	CYS	2.3
1	B	118	MET	2.3
1	B	159	ASP	2.3
1	A	131	LEU	2.3
1	B	196	ALA	2.3
1	B	132	PHE	2.3
1	B	230	GLY	2.3
1	B	17	VAL	2.3
1	B	93	GLY	2.2
1	A	221	CYS	2.2
1	B	275	SER	2.2
1	B	180	ALA	2.2
1	B	139	VAL	2.2
1	B	206	HIS	2.2
1	B	145	THR	2.2
1	B	178	SER	2.2
1	B	244	SER	2.2
1	B	190	SER	2.2
1	B	120	ASP	2.2
1	B	277	LEU	2.1
1	B	82	VAL	2.1
1	A	127	GLY	2.1
1	B	243	GLU	2.1
1	B	74	VAL	2.1
1	A	15	ALA	2.1
1	B	262	SER	2.0
1	B	121	GLU	2.0
1	B	112	GLN	2.0
1	B	31	SER	2.0
1	B	193	ALA	2.0

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
2	D20	A	500	16/16	0.91	0.17	-0.56	28,32,36,36	0
2	D20	B	500	16/16	0.86	0.14	-0.69	39,41,47,47	0

6.5 Other polymers (i)

There are no such residues in this entry.