W O R L D W I D E
wwPDB
PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report (i)

Jan 31, 2016 – 08:43 PM GMT

PDB ID : 1LOS
Title : crystal structure of orotidine monophosphate decarboxylase mutant deltaR203A complexed with 6-azaUMP
Authors : Wu, N.; Pai, E.F.
Deposited on : 2002-05-06
Resolution : 1.90 Å(reported)

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 1.90 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.
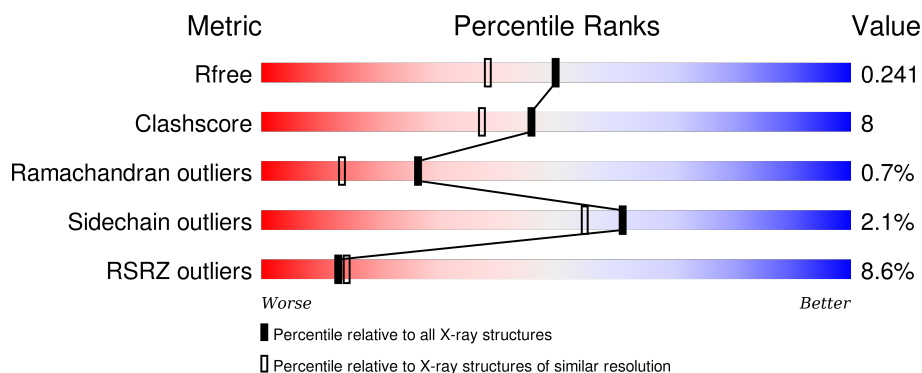
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R$_{free}$	91344	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (1.90-1.90)

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	224	
1	B	224	
1	C	224	
1	D	224	

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 6590 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 orotidine monophosphate decarboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	216	Total	C	N	O	S	0	0	0
			1643	1032	288	311	12			
1	B	206	Total	C	N	O	S	0	0	0
			1562	983	272	296	11			
1	C	191	Total	C	N	O	S	0	0	0
			1466	925	256	275	10			
1	D	214	Total	C	N	O	S	0	0	0
			1629	1023	286	308	12			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	LEU	MET	see remark 999	UNP O26232
A	101	PRO	ARG	see remark 999	UNP O26232
A	?	-	ALA	DELETION	UNP O26232
A	?	-	GLN	DELETION	UNP O26232
A	?	-	GLY	DELETION	UNP O26232
A	?	-	GLY	DELETION	UNP O26232
A	203	ALA	ARG	ENGINEERED	UNP O26232
B	1001	LEU	MET	see remark 999	UNP O26232
B	1101	PRO	ARG	see remark 999	UNP O26232
B	?	-	ALA	DELETION	UNP O26232
B	?	-	GLN	DELETION	UNP O26232
B	?	-	GLY	DELETION	UNP O26232
B	?	-	GLY	DELETION	UNP O26232
B	1203	ALA	ARG	ENGINEERED	UNP O26232
C	2001	LEU	MET	see remark 999	UNP O26232
C	2101	PRO	ARG	see remark 999	UNP O26232
C	?	-	ALA	DELETION	UNP O26232
C	?	-	GLN	DELETION	UNP O26232
C	?	-	GLY	DELETION	UNP O26232
C	?	-	GLY	DELETION	UNP O26232
C	2203	ALA	ARG	ENGINEERED	UNP O26232

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Chain	Residue	Modelled	Actual	Comment	Reference
D	3001	LEU	MET	see remark 999	UNP O26232
D	3101	PRO	ARG	see remark 999	UNP O26232
D	?	-	ALA	DELETION	UNP O26232
D	?	-	GLN	DELETION	UNP O26232
D	?	-	GLY	DELETION	UNP O26232
D	?	-	GLY	DELETION	UNP O26232
D	3203	ALA	ARG	ENGINEERED	UNP O26232

- Molecule 2 is 6-AZA URIDINE 5'-MONOPHOSPHATE (three-letter code: UP6) (formula: $C_8H_{12}N_3O_9P$).
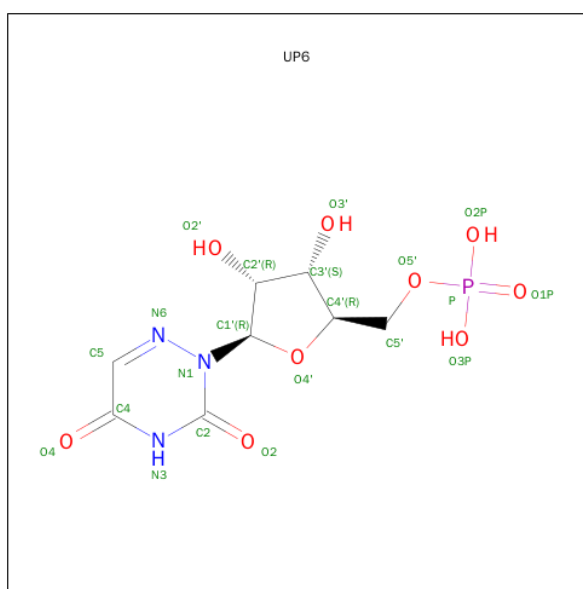
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 21	C 8	N 3	O 9	P 1	0	0
2	B	1	Total 21	C 8	N 3	O 9	P 1	0	0
2	C	1	Total 21	C 8	N 3	O 9	P 1	0	0
2	D	1	Total 21	C 8	N 3	O 9	P 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	86	Total 86	O 86	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	45	Total 45	O 45	0	0
3	C	28	Total 28	O 28	0	0
3	D	47	Total 47	O 47	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.

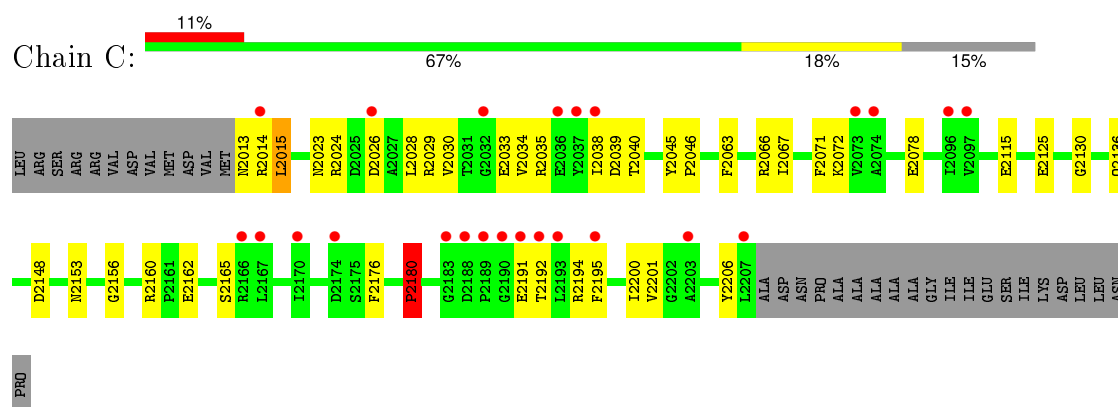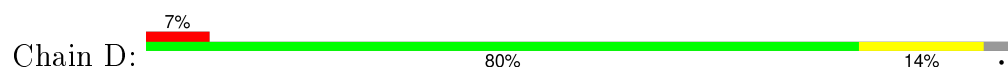• Molecule 1: orotidine monophosphate decarboxylase
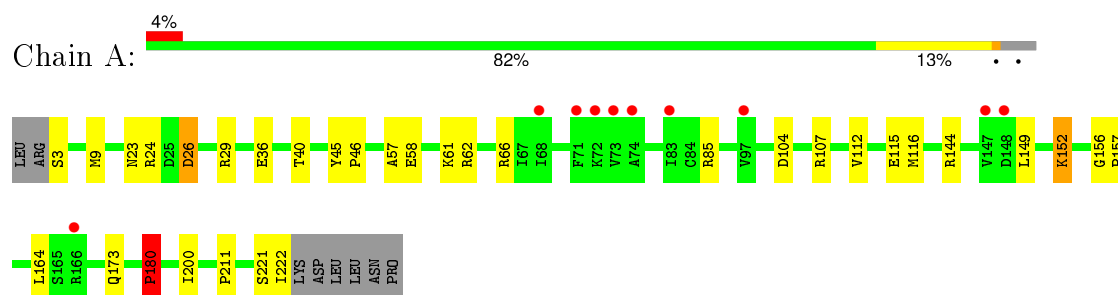
Chain A:

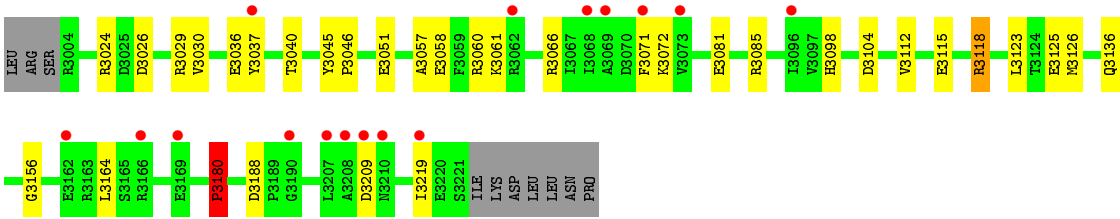• Molecule 1: orotidine monophosphate decarboxylase

Chain B:

• Molecule 1: orotidine monophosphate decarboxylase

Chain C:

• Molecule 1: orotidine monophosphate decarboxylase

Chain D:
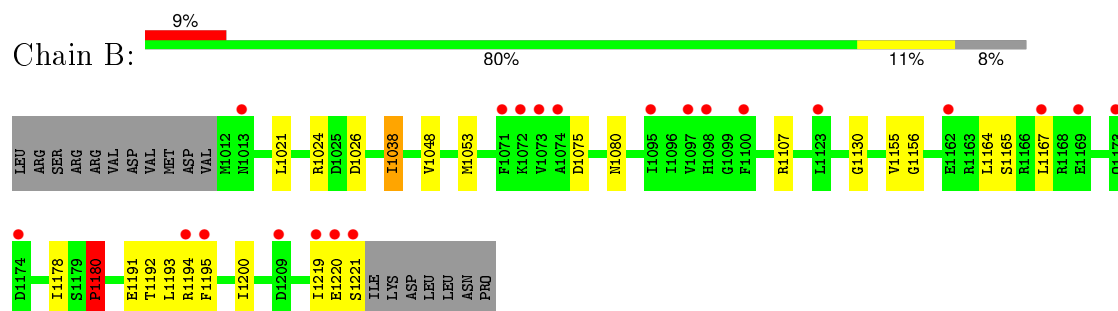
4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	52.49Å 56.15Å 73.87Å 82.76° 89.89° 76.91°	Depositor
Resolution (Å)	29.39 – 1.90 33.57 – 1.90	Depositor EDS
% Data completeness (in resolution range)	87.3 (29.39-1.90) 86.5 (33.57-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	2.38 (at 1.89Å)	Xtriage
Refinement program	CNS 0.9	Depositor
R, R_{free}	0.205 , 0.240 0.205 , 0.241	Depositor DCC
R_{free} test set	1792 reflections (3.19%)	DCC
Wilson B-factor (Å^2)	27.7	Xtriage
Anisotropy	0.392	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 59.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$<|L|> = 0.49, <L^2> = 0.33$	Xtriage
Outliers	0 of 58204 reflections	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	6590	wwPDB-VP
Average B, all atoms (Å^2)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.35% 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: UP6

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	0.48	0/1666	0.65	0/2249
1	B	0.46	0/1585	0.63	0/2140
1	C	0.41	0/1488	0.60	0/2007
1	D	0.43	0/1652	0.62	0/2230
All	All	0.45	0/6391	0.62	0/8626

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	1643	0	1658	26	0
1	B	1562	0	1572	18	0
1	C	1466	0	1480	37	0
1	D	1629	0	1642	21	0
2	A	21	0	10	0	0
2	B	21	0	10	0	0
2	C	21	0	10	0	0
2	D	21	0	10	1	0
3	A	86	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	45	0	0	1	0
3	C	28	0	0	0	0
3	D	47	0	0	1	0
All	All	6590	0	6392	98	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 98 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:107:ARG:HE	1:A:149:LEU:HD22	1.45	0.79
1:A:115:GLU:HG3	1:A:116:MET:HG3	1.65	0.77
1:D:3156:GLY:O	1:D:3180:PRO:HD2	1.87	0.74
1:C:2015:LEU:HD13	1:C:2038:ILE:HD11	1.71	0.73
1:A:29:ARG:HD3	3:A:4091:HOH:O	1.88	0.73

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	214/224 (96%)	206 (96%)	7 (3%)	1 (0%)	34	21
1	B	204/224 (91%)	194 (95%)	7 (3%)	3 (2%)	13	3
1	C	189/224 (84%)	178 (94%)	10 (5%)	1 (0%)	34	21
1	D	212/224 (95%)	203 (96%)	8 (4%)	1 (0%)	34	21
All	All	819/896 (91%)	781 (95%)	32 (4%)	6 (1%)	26	14

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1180	PRO
1	C	2180	PRO
1	A	180	PRO
1	D	3180	PRO
1	B	1193	LEU

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	172/180 (96%)	169 (98%)	3 (2%)	68	64
1	B	162/180 (90%)	159 (98%)	3 (2%)	65	59
1	C	154/180 (86%)	150 (97%)	4 (3%)	54	45
1	D	170/180 (94%)	166 (98%)	4 (2%)	57	49
All	All	658/720 (91%)	644 (98%)	14 (2%)	61	55

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	2015	LEU
1	C	2115	GLU
1	D	3180	PRO
1	B	1180	PRO
1	D	3118	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	2013	ASN
1	D	3136	GLN
1	C	2136	GLN
1	B	1080	ASN
1	C	2111	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)

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)

4 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	UP6	A	5001	-	17,22,22	1.77	3 (17%)	19,33,33	5.41	6 (31%)
2	UP6	B	5002	-	17,22,22	1.82	4 (23%)	19,33,33	5.44	5 (26%)
2	UP6	C	5003	-	17,22,22	1.74	3 (17%)	19,33,33	5.59	5 (26%)
2	UP6	D	5004	-	17,22,22	1.63	3 (17%)	19,33,33	5.44	5 (26%)

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	UP6	A	5001	-	-	0/6/26/26	0/2/2/2
2	UP6	B	5002	-	-	0/6/26/26	0/2/2/2
2	UP6	C	5003	-	-	0/6/26/26	0/2/2/2
2	UP6	D	5004	-	-	0/6/26/26	0/2/2/2

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The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	5002	UP6	P-O2P	-2.07	1.47	1.54
2	D	5004	UP6	C5-C4	2.77	1.43	1.39
2	D	5004	UP6	P-O3P	2.87	1.65	1.54
2	C	5003	UP6	C5-C4	2.93	1.43	1.39
2	A	5001	UP6	P-O3P	3.11	1.65	1.54

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	5003	UP6	C5-C4-N3	-18.84	114.09	123.17
2	A	5001	UP6	C5-C4-N3	-18.45	114.28	123.17
2	D	5004	UP6	C5-C4-N3	-18.40	114.31	123.17
2	B	5002	UP6	C5-C4-N3	-18.36	114.32	123.17
2	A	5001	UP6	O3P-P-O1P	2.13	117.43	110.58

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	D	5004	UP6	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(Å^2)	Q<0.9
1	A	216/224 (96%)	0.15	10 (4%)	36	39	21, 33, 48, 62	0
1	B	206/224 (91%)	0.41	21 (10%)	9	10	19, 35, 59, 77	0
1	C	191/224 (85%)	0.62	24 (12%)	5	5	24, 41, 69, 77	0
1	D	214/224 (95%)	0.36	16 (7%)	17	19	22, 37, 56, 71	0
All	All	827/896 (92%)	0.38	71 (8%)	13	14	19, 36, 60, 77	0

The worst 5 of 71 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	2037	TYR	8.6
1	C	2192	THR	5.1
1	B	1195	PHE	4.3
1	B	1013	ASN	4.3
1	C	2036	GLU	4.2

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	UP6	B	5002	21/21	0.95	0.11	-0.47	28,33,36,39	0
2	UP6	A	5001	21/21	0.96	0.10	-0.50	22,27,31,35	0
2	UP6	D	5004	21/21	0.96	0.10	-0.74	29,32,36,39	0
2	UP6	C	5003	21/21	0.92	0.10	-0.80	42,46,49,51	0

6.5 Other polymers (i)

There are no such residues in this entry.