wwPDB X-ray Structure Validation Summary Report (i)

Sep 24, 2023 – 10:16 PM EDT

PDB ID	:	5UYY
Title	:	Crystal structure of prephenate dehydrogenase tyrA from Bacillus anthracis in complex with L-tyrosine
Authors	:	Shabalin, I.G.; Hou, J.; Cymborowski, M.T.; Kwon, K.; Christendat, D.; Gritsunov, A.O.; Anderson, W.F.; Minor, W.; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on	:	2017-02-24
Resolution	:	2.60 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:

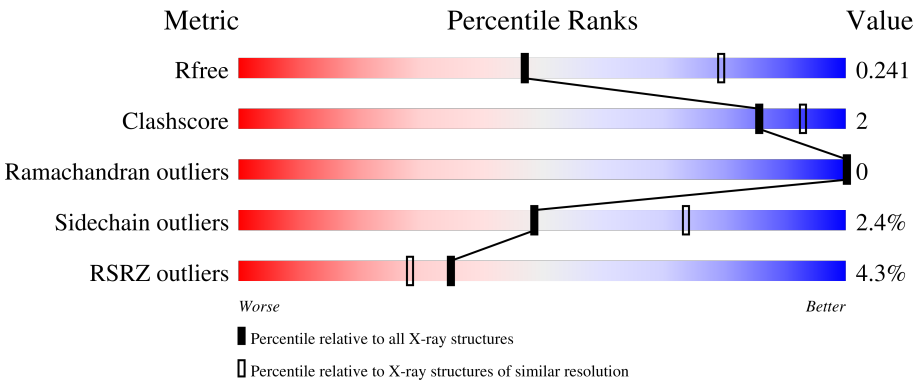
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

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

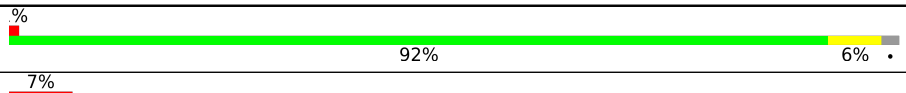
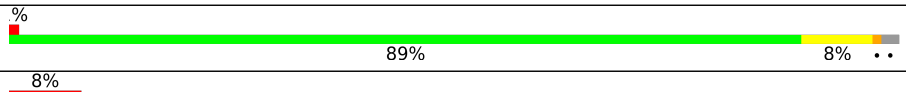
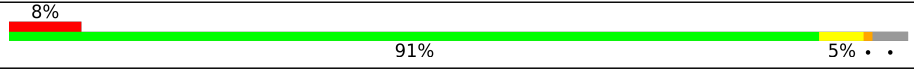
The reported resolution of this entry is 2.60 Å.

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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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	381	
1	B	381	
1	C	381	
1	D	381	

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 11890 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.

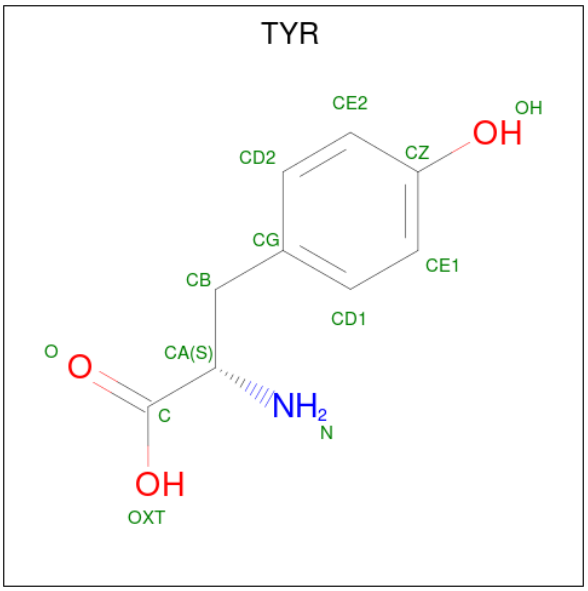
- Molecule 1 is a protein called Prephenate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	373	2881	1831	490	550	10	0	0	0
1	B	365	2792	1777	484	523	8	0	0	0
1	C	373	2876	1829	493	544	10	0	0	0
1	D	365	2783	1773	478	524	8	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP Q81P63
A	-1	ASN	-	expression tag	UNP Q81P63
A	0	ALA	-	expression tag	UNP Q81P63
B	-2	SER	-	expression tag	UNP Q81P63
B	-1	ASN	-	expression tag	UNP Q81P63
B	0	ALA	-	expression tag	UNP Q81P63
C	-2	SER	-	expression tag	UNP Q81P63
C	-1	ASN	-	expression tag	UNP Q81P63
C	0	ALA	-	expression tag	UNP Q81P63
D	-2	SER	-	expression tag	UNP Q81P63
D	-1	ASN	-	expression tag	UNP Q81P63
D	0	ALA	-	expression tag	UNP Q81P63

- Molecule 2 is TYROSINE (three-letter code: TYR) (formula: $C_9H_{11}NO_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C N O 13 9 1 3	0	0
2	B	1	Total C N O 13 9 1 3	0	0
2	C	1	Total C N O 13 9 1 3	0	0
2	D	1	Total C N O 13 9 1 3	0	0

- Molecule 3 is water.

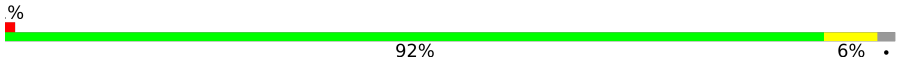
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	117	Total O 117 117	0	0
3	B	113	Total O 113 113	0	0
3	C	178	Total O 178 178	0	0
3	D	98	Total O 98 98	0	0

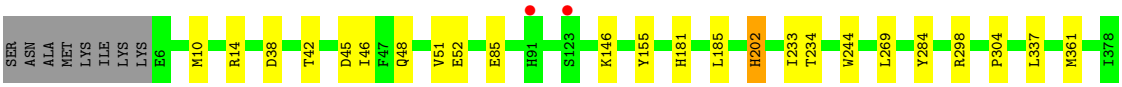
3 Residue-property plots (i)

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: Prephenate dehydrogenase

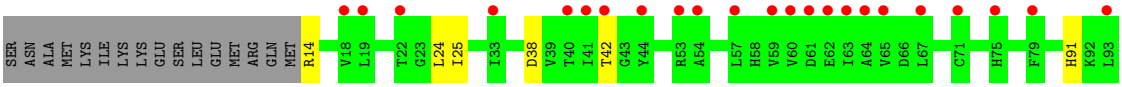
Chain A:

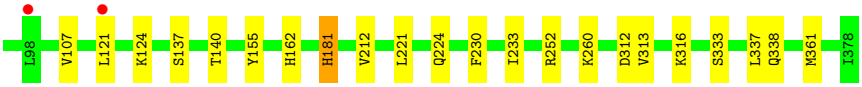




• Molecule 1: Prephenate dehydrogenase

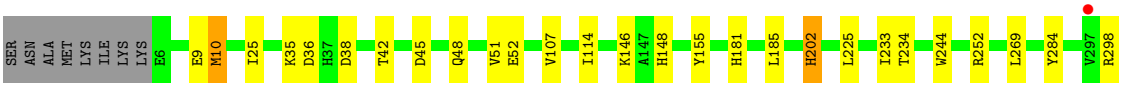
Chain B:





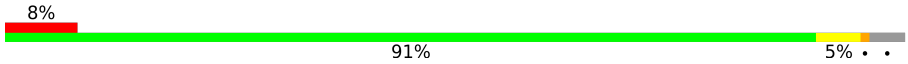
• Molecule 1: Prephenate dehydrogenase

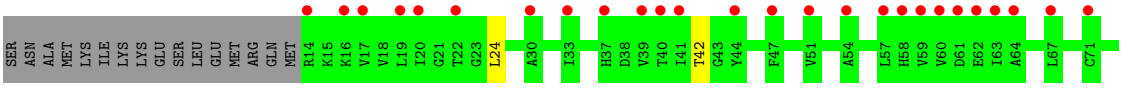
Chain C:

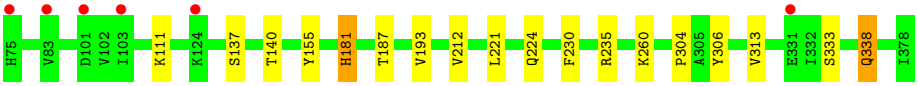


• Molecule 1: Prephenate dehydrogenase

Chain D:






H75
V83
D101
V102
I103
K111
K124
S137
T140
Y155
H181
T187
V193
V212
L221
Q224
F230
R235
K260
P304
A305
Y306
V313
E331
I332
S333
Q338
I378

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	84.68Å 105.59Å 179.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.60 44.80 – 2.59	Depositor EDS
% Data completeness (in resolution range)	99.9 (50.00-2.60) 99.5 (44.80-2.59)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	1.90 (at 2.58Å)	Xtriage
Refinement program	REFMAC 5.8.0107	Depositor
R, R_{free}	0.189 , 0.246 0.189 , 0.241	Depositor DCC
R_{free} test set	2490 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å^2)	61.9	Xtriage
Anisotropy	0.368	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 48.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	11890	wwPDB-VP
Average B, all atoms (Å^2)	76.0	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 35.78 % 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 5.5304e-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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

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	0.77	0/2937	0.89	1/3976 (0.0%)
1	B	0.79	0/2848	0.85	3/3860 (0.1%)
1	C	0.85	1/2933 (0.0%)	0.90	4/3970 (0.1%)
1	D	0.80	0/2839	0.88	1/3848 (0.0%)
All	All	0.80	1/11557 (0.0%)	0.88	9/15654 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	9	GLU	CD-OE2	6.76	1.33	1.25

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	252	ARG	NE-CZ-NH1	6.41	123.51	120.30
1	C	252	ARG	NE-CZ-NH2	-6.02	117.29	120.30
1	B	312	ASP	CB-CG-OD2	5.65	123.38	118.30
1	B	252	ARG	NE-CZ-NH1	5.55	123.07	120.30
1	B	181	HIS	N-CA-CB	5.42	120.36	110.60

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	2881	0	2808	14	0
1	B	2792	0	2726	14	0
1	C	2876	0	2808	19	0
1	D	2783	0	2692	13	0
2	A	13	0	8	1	0
2	B	13	0	8	0	0
2	C	13	0	8	1	0
2	D	13	0	8	0	0
3	A	117	0	0	0	0
3	B	113	0	0	0	0
3	C	178	0	0	3	0
3	D	98	0	0	2	0
All	All	11890	0	11066	50	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 2.

The worst 5 of 50 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:185:LEU:HD21	1:D:221:LEU:HD11	1.66	0.77
1:A:185:LEU:HD21	1:B:221:LEU:HD11	1.70	0.73
1:D:24:LEU:HD21	1:D:137:SER:HB3	1.81	0.61
1:B:25:ILE:HG21	1:B:107:VAL:HG11	1.83	0.60
1:B:24:LEU:HD21	1:B:137:SER:HB3	1.83	0.60

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	371/381 (97%)	367 (99%)	4 (1%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	363/381 (95%)	357 (98%)	6 (2%)	0	100	100
1	C	371/381 (97%)	366 (99%)	5 (1%)	0	100	100
1	D	363/381 (95%)	358 (99%)	5 (1%)	0	100	100
All	All	1468/1524 (96%)	1448 (99%)	20 (1%)	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	299/324 (92%)	293 (98%)	6 (2%)	55	78
1	B	286/324 (88%)	278 (97%)	8 (3%)	43	69
1	C	298/324 (92%)	292 (98%)	6 (2%)	55	78
1	D	281/324 (87%)	273 (97%)	8 (3%)	43	69
All	All	1164/1296 (90%)	1136 (98%)	28 (2%)	49	74

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	10	MET
1	D	338	GLN
1	C	202	HIS
1	D	224	GLN
1	C	155	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	181	HIS
1	B	202	HIS
1	B	250	GLN

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Mol	Chain	Res	Type
1	D	181	HIS
1	D	224	GLN

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 monosaccharides 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	TYR	D	401	-	12,13,13	0.71	0	16,17,17	1.14	2 (12%)
2	TYR	A	401	-	12,13,13	0.63	0	16,17,17	0.90	1 (6%)
2	TYR	C	401	-	12,13,13	0.62	0	16,17,17	0.65	0
2	TYR	B	401	-	12,13,13	0.83	0	16,17,17	0.85	1 (6%)

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	TYR	D	401	-	-	0/8/8/8	0/1/1/1
2	TYR	A	401	-	-	0/8/8/8	0/1/1/1
2	TYR	C	401	-	-	1/8/8/8	0/1/1/1
2	TYR	B	401	-	-	0/8/8/8	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	401	TYR	OXT-C-O	-3.08	117.09	124.09
2	D	401	TYR	OXT-C-CA	2.85	123.08	113.38
2	A	401	TYR	OXT-C-CA	2.66	122.43	113.38
2	B	401	TYR	OXT-C-CA	2.23	120.97	113.38

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	401	TYR	O-C-CA-N

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	TYR	1	0
2	C	401	TYR	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	373/381 (97%)	-0.18	2 (0%)	91	89	48, 76, 111, 131	0
1	B	365/381 (95%)	0.11	25 (6%)	17	12	42, 76, 126, 150	0
1	C	373/381 (97%)	-0.25	4 (1%)	80	78	41, 63, 112, 149	0
1	D	365/381 (95%)	0.17	32 (8%)	10	7	41, 78, 128, 168	0
All	All	1476/1524 (96%)	-0.04	63 (4%)	35	28	41, 72, 123, 168	0

The worst 5 of 63 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	60	VAL	5.1
1	D	64	ALA	4.2
1	D	14	ARG	4.1
1	B	65	VAL	4.0
1	D	33	ILE	3.5

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 monosaccharides 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. 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
2	TYR	B	401	13/13	0.96	0.14	36,39,45,46	0
2	TYR	A	401	13/13	0.98	0.12	45,57,65,65	0
2	TYR	C	401	13/13	0.98	0.10	44,54,62,62	0
2	TYR	D	401	13/13	0.98	0.13	34,36,43,44	0

6.5 Other polymers (i)

There are no such residues in this entry.