



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:54 PM UTC

PDB ID : 6ETA / pdb_00006eta
Title : Crystal Structure of Human Gamma-D crystallin Mutant P23T+R36S at Room Temperature
Authors : James, S.; McManus, J.; Khan, A.R.
Deposited on : 2017-10-25
Resolution : 2.20 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

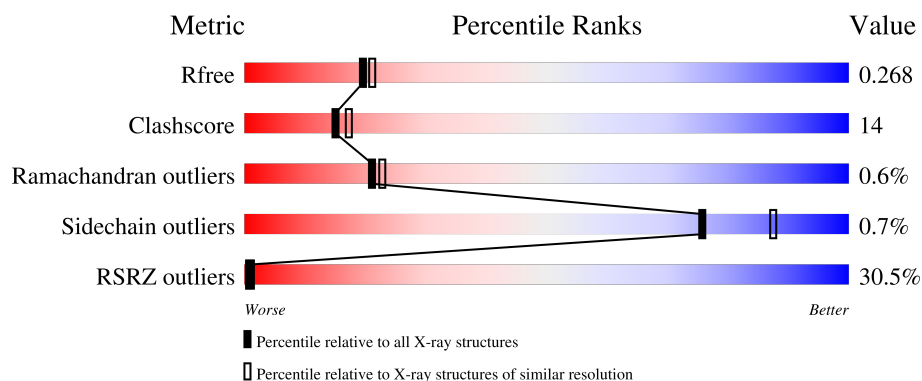
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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 $\leq 5\%$. 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	174	6% 84% 14% ..
1	B	174	54% 67% 29% ..

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2888 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 Gamma-crystallin D.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	171	Total	C	N	O	S	0	0	0
			1395	866	257	262	10			
1	B	170	Total	C	N	O	S	0	0	0
			1381	859	253	259	10			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	23	THR	PRO	engineered mutation	UNP P07320
A	36	SER	ARG	engineered mutation	UNP P07320
B	23	THR	PRO	engineered mutation	UNP P07320
B	36	SER	ARG	engineered mutation	UNP P07320

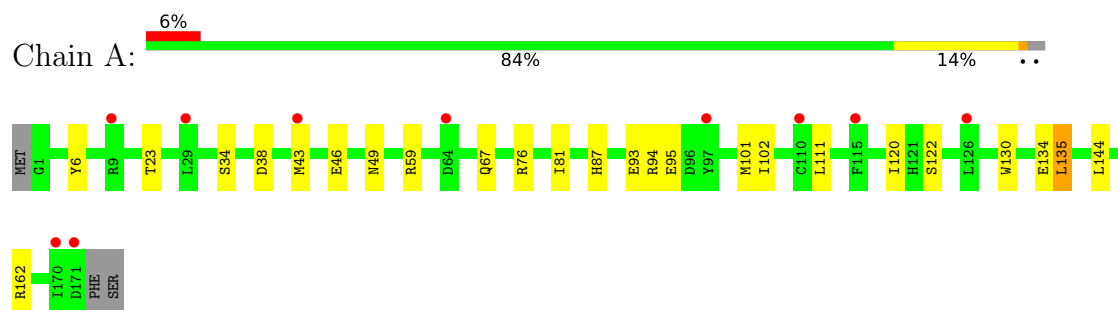
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	73	Total	O	0	0
			73	73		
2	B	39	Total	O	0	0
			39	39		

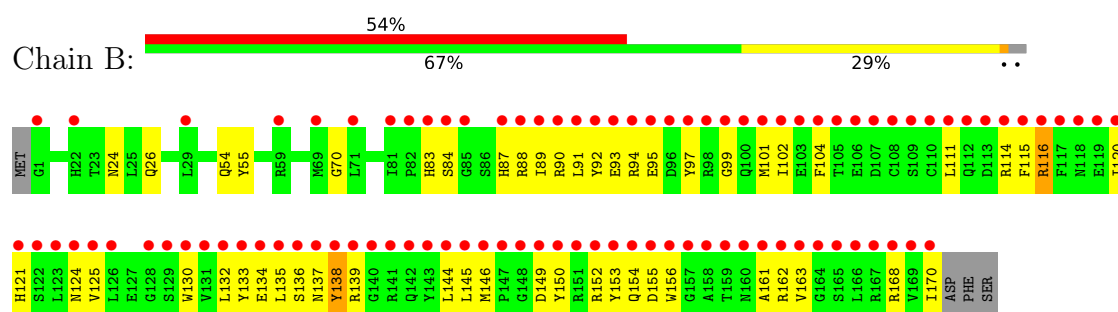
3 Residue-property plots [i](#)

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: Gamma-crystallin D



• Molecule 1: Gamma-crystallin D



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	54.04Å 82.10Å 106.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.16 – 2.20 48.16 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.6 (48.16-2.20) 99.6 (48.16-2.20)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.29 (at 2.20Å)	Xtriage
Refinement program	PHENIX (1.11.1 _2575: ???)	Depositor
R, R_{free}	0.233 , 0.265 0.235 , 0.268	Depositor DCC
R_{free} test set	1233 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	38.7	Xtriage
Anisotropy	0.541	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 43.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	2888	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.34% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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	0.12	0/1430	0.35	0/1931
1	B	0.21	0/1416	0.48	0/1913
All	All	0.17	0/2846	0.42	0/3844

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	1395	0	1282	14	0
1	B	1381	0	1267	59	0
2	A	73	0	0	1	0
2	B	39	0	0	1	0
All	All	2888	0	2549	73	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 14.

All (73) 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:89:ILE:HD11	1:B:130:TRP:CH2	2.07	0.89

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:89:ILE:HD11	1:B:130:TRP:CZ2	2.11	0.85
1:B:104:PHE:HZ	1:B:111:LEU:HD21	1.41	0.83
1:B:87:HIS:HB3	1:B:130:TRP:CZ2	2.20	0.77
1:B:104:PHE:CZ	1:B:111:LEU:HD21	2.20	0.77
1:B:87:HIS:ND1	1:B:168:ARG:HG2	2.07	0.68
1:B:94:ARG:NH1	1:B:95:GLU:OE1	2.27	0.68
1:B:152:ARG:HD2	1:B:153:TYR:H	1.58	0.67
1:B:111:LEU:HD23	1:B:114:ARG:HB2	1.77	0.67
1:B:89:ILE:HD11	1:B:130:TRP:CZ3	2.31	0.65
1:B:132:LEU:HD21	1:B:163:VAL:HG22	1.79	0.64
1:B:24:ASN:HD21	1:B:26:GLN:HE21	1.45	0.63
1:B:92:TYR:CG	1:B:97:TYR:HA	2.35	0.62
1:B:89:ILE:HD11	1:B:130:TRP:CE2	2.35	0.61
1:A:134:GLU:HG2	1:A:135:LEU:HD13	1.83	0.61
1:B:134:GLU:HG2	1:B:135:LEU:HD13	1.82	0.60
1:B:89:ILE:HG22	1:B:90:ARG:N	2.19	0.58
1:B:130:TRP:CZ3	1:B:168:ARG:HG3	2.38	0.58
1:B:89:ILE:CD1	1:B:130:TRP:CZ2	2.87	0.56
1:B:153:TYR:CE1	1:B:154:GLN:HG2	2.40	0.56
1:A:43:MET:HE3	1:A:144:LEU:HD13	1.88	0.55
1:B:93:GLU:HG2	1:B:99:GLY:HA3	1.88	0.55
1:B:24:ASN:ND2	1:B:26:GLN:HE21	2.04	0.54
1:B:136:SER:O	1:B:139:ARG:HG2	2.07	0.54
1:B:134:GLU:HG2	1:B:135:LEU:CD1	2.38	0.54
1:B:88:ARG:HH11	1:B:88:ARG:HG3	1.72	0.53
1:B:135:LEU:HD23	1:B:139:ARG:NE	2.24	0.53
1:B:111:LEU:CD2	1:B:114:ARG:HB2	2.39	0.53
1:A:43:MET:HE2	1:A:81:ILE:HD11	1.91	0.52
1:B:90:ARG:N	1:B:124:ASN:O	2.39	0.52
1:B:135:LEU:HD23	1:B:139:ARG:HE	1.74	0.52
1:B:115:PHE:O	1:B:116:ARG:HB3	2.11	0.51
1:A:87:HIS:HB3	1:A:130:TRP:CZ2	2.46	0.51
1:B:54:GLN:HE22	1:B:144:LEU:H	1.58	0.51
1:B:136:SER:O	1:B:139:ARG:NH1	2.43	0.51
1:B:102:ILE:HD11	1:B:115:PHE:CG	2.46	0.50
1:B:91:LEU:HB3	1:B:120:ILE:HD12	1.94	0.50
1:A:38:ASP:O	1:A:59:ARG:NH1	2.44	0.50
1:B:83:HIS:ND1	1:B:170:ILE:O	2.41	0.49
1:A:67:GLN:NE2	2:A:206:HOH:O	2.45	0.49
1:B:89:ILE:CD1	1:B:130:TRP:CH2	2.91	0.48
1:B:125:VAL:O	1:B:125:VAL:HG13	2.12	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:46:GLU:O	1:A:76:ARG:HG3	2.14	0.48
1:B:137:ASN:OD1	2:B:201:HOH:O	2.20	0.48
1:B:150:TYR:HB3	1:B:155:ASP:HB3	1.96	0.48
1:B:120:ILE:HB	1:B:163:VAL:HG21	1.96	0.47
1:B:87:HIS:HB3	1:B:130:TRP:HZ2	1.76	0.47
1:B:93:GLU:HG3	1:B:94:ARG:HG2	1.95	0.47
1:B:89:ILE:HD13	1:B:104:PHE:HB2	1.96	0.47
1:B:134:GLU:HG3	1:B:162:ARG:HB3	1.97	0.47
1:B:149:ASP:N	1:B:149:ASP:OD1	2.48	0.47
1:B:121:HIS:CD2	1:B:161:ALA:CB	2.99	0.45
1:B:88:ARG:HG3	1:B:88:ARG:NH1	2.31	0.45
1:B:135:LEU:HB2	1:B:139:ARG:HG3	1.99	0.44
1:B:102:ILE:HD11	1:B:115:PHE:CD2	2.52	0.44
1:A:23:THR:OG1	1:A:49:ASN:HA	2.17	0.44
1:B:121:HIS:HD2	1:B:161:ALA:CB	2.30	0.44
1:A:95:GLU:HA	1:A:122:SER:HB3	2.00	0.43
1:A:101:MET:HE2	1:A:102:ILE:C	2.44	0.43
1:A:6:TYR:HB2	1:A:34:SER:OG	2.20	0.42
1:B:135:LEU:CB	1:B:139:ARG:HG3	2.49	0.42
1:A:134:GLU:OE2	1:A:162:ARG:NH1	2.52	0.42
1:B:146:MET:HE3	1:B:146:MET:HB2	1.80	0.42
1:B:55:TYR:CZ	1:B:70:GLY:HA2	2.55	0.42
1:A:111:LEU:HD21	1:A:120:ILE:HD11	2.02	0.41
1:B:135:LEU:HB3	1:B:139:ARG:CZ	2.51	0.41
1:A:93:GLU:HG2	1:A:94:ARG:HG3	2.01	0.41
1:B:121:HIS:CD2	1:B:161:ALA:HB2	2.56	0.41
1:B:101:MET:HG2	1:B:102:ILE:N	2.36	0.41
1:B:111:LEU:HD23	1:B:111:LEU:HA	1.69	0.40
1:B:132:LEU:HB2	1:B:145:LEU:HD11	2.04	0.40
1:B:133:TYR:CD2	1:B:138:TYR:HB2	2.56	0.40
1:B:153:TYR:HA	1:B:156:TRP:CZ2	2.57	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	169/174 (97%)	166 (98%)	3 (2%)	0	100	100
1	B	168/174 (97%)	159 (95%)	7 (4%)	2 (1%)	10	8
All	All	337/348 (97%)	325 (96%)	10 (3%)	2 (1%)	21	23

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	116	ARG
1	B	138	TYR

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	146/156 (94%)	145 (99%)	1 (1%)	76	87
1	B	144/156 (92%)	143 (99%)	1 (1%)	76	87
All	All	290/312 (93%)	288 (99%)	2 (1%)	76	87

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	135	LEU
1	B	84	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	24	ASN
1	B	49	ASN
1	B	54	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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, 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	171/174 (98%)	0.46	10 (5%)	29 25	27, 38, 57, 114	0
1	B	170/174 (97%)	2.70	94 (55%)	0 0	30, 72, 130, 146	0
All	All	341/348 (97%)	1.57	104 (30%)	1 1	27, 47, 120, 146	0

All (104) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	163	VAL	9.4
1	B	170	ILE	7.9
1	B	124	ASN	7.5
1	B	138	TYR	7.5
1	B	109	SER	7.3
1	B	111	LEU	7.3
1	B	91	LEU	7.3
1	B	100	GLN	7.3
1	B	105	THR	6.9
1	B	115	PHE	6.9
1	B	137	ASN	6.5
1	B	120	ILE	6.4
1	B	117	PHE	6.4
1	B	104	PHE	6.1
1	B	125	VAL	5.9
1	B	133	TYR	5.8
1	B	89	ILE	5.7
1	A	171	ASP	5.7
1	B	101	MET	5.6
1	B	147	PRO	5.5
1	B	130	TRP	5.5
1	B	112	GLN	5.4
1	B	97	TYR	5.3
1	B	156	TRP	5.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	164	GLY	5.3
1	B	102	ILE	5.2
1	B	92	TYR	5.2
1	B	132	LEU	5.1
1	B	110	CYS	5.0
1	B	169	VAL	4.9
1	B	116	ARG	4.9
1	B	99	GLY	4.8
1	B	161	ALA	4.7
1	B	166	LEU	4.7
1	A	115	PHE	4.6
1	B	94	ARG	4.6
1	B	159	THR	4.6
1	B	140	GLY	4.4
1	B	131	VAL	4.3
1	B	149	ASP	4.3
1	B	121	HIS	4.2
1	B	103	GLU	4.2
1	B	123	LEU	4.2
1	B	165	SER	4.1
1	B	158	ALA	4.1
1	B	126	LEU	4.1
1	B	160	ASN	4.1
1	B	108	CYS	4.1
1	B	153	TYR	4.0
1	B	118	ASN	3.9
1	B	148	GLY	3.8
1	B	93	GLU	3.8
1	B	150	TYR	3.7
1	B	155	ASP	3.7
1	B	106	GLU	3.6
1	B	144	LEU	3.6
1	B	145	LEU	3.6
1	B	69	MET	3.5
1	B	135	LEU	3.5
1	B	168	ARG	3.4
1	B	90	ARG	3.4
1	B	162	ARG	3.4
1	B	119	GLU	3.4
1	B	83	HIS	3.3
1	B	151	ARG	3.3
1	B	167	ARG	3.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	85	GLY	3.3
1	B	139	ARG	3.3
1	B	157	GLY	3.3
1	A	110	CYS	3.2
1	B	122	SER	3.2
1	B	128	GLY	3.2
1	B	107	ASP	3.2
1	B	87	HIS	3.2
1	B	98	ARG	3.2
1	B	143	TYR	3.2
1	B	134	GLU	3.2
1	B	129	SER	3.1
1	B	113	ASP	3.1
1	B	146	MET	3.1
1	B	81	ILE	3.0
1	B	96	ASP	3.0
1	B	22	HIS	3.0
1	B	84	SER	2.9
1	B	1	GLY	2.8
1	A	29	LEU	2.8
1	B	152	ARG	2.8
1	B	136	SER	2.7
1	B	114	ARG	2.7
1	A	170	ILE	2.7
1	B	142	GLN	2.6
1	B	154	GLN	2.6
1	B	95	GLU	2.6
1	B	71	LEU	2.5
1	A	9	ARG	2.5
1	B	59	ARG	2.5
1	B	29	LEU	2.5
1	B	82	PRO	2.4
1	A	64	ASP	2.4
1	A	126	LEU	2.3
1	B	88	ARG	2.3
1	A	43	MET	2.3
1	B	141	ARG	2.2
1	A	97	TYR	2.1

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 [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.