

Full wwPDB X-ray Structure Validation Report (i)

Sep 26, 2023 – 10:49 AM EDT

PDB ID	:	$6\mathrm{CL5}$
Title	:	Structure of P. aeruginosa R1 pyocin fiber PALES_06171 comprising C-
		terminal residues 323-701
Authors	:	Buth, S.A.; Shneider, M.M.; Leiman, P.G.
Deposited on	:	2018-03-01
Resolution	:	2.32 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 (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 (1)) were used in the production of this report:

MolProbity	:	4.02b-467
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: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 2.32 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.



Motria	Whole archive	Similar resolution
wietric	$(\# { m Entries})$	$(\# { m Entries}, { m resolution} { m range}({ m \AA}))$
R_{free}	130704	5974(2.34-2.30)
Clashscore	141614	6604 (2.34-2.30)
Ramachandran outliers	138981	6523 (2.34-2.30)
Sidechain outliers	138945	6523 (2.34-2.30)
RSRZ outliers	127900	5855 (2.34-2.30)

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	Δ	38/	5%	
	11	004	9%	• •
1	В	384	95%	• •
1	С	384	92%	5% •
			3%	
1	D	384	95%	• •
1	E	384	93%	• •



Mol	Chain	Length	Quality of chain	
			5%	
1	F	384	94%	•••



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 35038 atoms, of which 16152 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.

Mol	Chain	Residues			Atom	IS			ZeroOcc	AltConf	Trace
1	Δ	274	Total	С	Η	Ν	0	S	0	0 0	0
	A	374	5500	1774	2692	491	533	10	0	0	0
1	В	374	Total	С	Н	Ν	0	S	0	0	0
1	D	574	5501	1774	2693	491	533	10	0	0	U
1	С	374	Total	С	Η	Ν	0	S	0	0	0
1		574	5499	1774	2691	491	533	10			0
1	Л	374	Total	С	Η	Ν	0	S	0	0	0
1	D		5500	1774	2692	491	533	10		0	U
1	F	374	Total	С	Η	Ν	0	S	0	0	0
1		374	5500	1774	2692	491	533	10	0	0	0
1	Б	274	Total	С	Н	Ν	0	S	0	0	0
	Г	0/4	5500	1774	2692	491	533	10		U	0

• Molecule 1 is a protein called Tail fiber protein.

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	318	SER	-	cloning artifact	UNP Q9KW03
А	319	GLY	-	cloning artifact	UNP Q9KW03
А	320	SER	-	cloning artifact	UNP Q9KW03
А	321	GLU	-	cloning artifact	UNP Q9KW03
А	322	PHE	-	cloning artifact	UNP Q9KW03
В	318	SER	-	cloning artifact	UNP Q9KW03
В	319	GLY	-	cloning artifact	UNP Q9KW03
В	320	SER	-	cloning artifact	UNP Q9KW03
В	321	GLU	-	cloning artifact	UNP Q9KW03
В	322	PHE	-	cloning artifact	UNP Q9KW03
С	318	SER	-	cloning artifact	UNP Q9KW03
С	319	GLY	-	cloning artifact	UNP Q9KW03
С	320	SER	-	cloning artifact	UNP Q9KW03
С	321	GLU	-	cloning artifact	UNP Q9KW03
С	322	PHE	-	cloning artifact	UNP Q9KW03
D	318	SER	-	cloning artifact	UNP Q9KW03
D	319	GLY	-	cloning artifact	UNP Q9KW03



Chain	Residue	Modelled	Actual Comment		Reference
D	320	SER	-	cloning artifact	UNP Q9KW03
D	321	GLU	-	cloning artifact	UNP Q9KW03
D	322	PHE	-	cloning artifact	UNP Q9KW03
Е	318	SER	-	cloning artifact	UNP Q9KW03
E	319	GLY	-	cloning artifact	UNP Q9KW03
E	320	SER	-	cloning artifact	UNP Q9KW03
Е	321	GLU	-	cloning artifact	UNP Q9KW03
E	322	PHE	-	cloning artifact	UNP Q9KW03
F	318	SER	-	cloning artifact	UNP Q9KW03
F	319	GLY	-	cloning artifact	UNP Q9KW03
F	320	SER	-	cloning artifact	UNP Q9KW03
F	321	GLU	-	cloning artifact	UNP Q9KW03
F	322	PHE	-	cloning artifact	UNP Q9KW03

• Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	Total Fe 1 1	0	0
2	D	1	Total Fe 1 1	0	0

• Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	Total Mg 1 1	0	0
3	D	1	Total Mg 1 1	0	0

• Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	1	Total Na 1 1	0	0
4	В	1	Total Na 1 1	0	0
4	С	1	Total Na 1 1	0	0
4	D	1	Total Na 1 1	0	0



Continued from previous page...

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	Е	1	Total Na 1 1	0	0
4	F	1	Total Na 1 1	0	0

• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	369	Total O 369 369	0	0
5	В	314	Total O 314 314	0	0
5	С	321	Total O 321 321	0	0
5	D	395	Total O 395 395	0	0
5	Е	305	Total O 305 305	0	0
5	F	324	Total O 324 324	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: Tail fiber protein

• Molecule 1: Tail fiber protein









4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	144.50Å 155.03Å 200.48Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
$Bosolution(\AA)$	47.69 - 2.32	Depositor
Resolution (A)	49.06 - 2.32	EDS
% Data completeness	99.1 (47.69-2.32)	Depositor
(in resolution range)	99.5(49.06-2.32)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.96 (at 2.32 \text{\AA})$	Xtriage
Refinement program	PHENIX (dev_3042: ???)	Depositor
P. P.	0.169 , 0.206	Depositor
n, n_{free}	0.169 , 0.207	DCC
R_{free} test set	9621 reflections (5.00%)	wwPDB-VP
Wilson B-factor $(Å^2)$	38.6	Xtriage
Anisotropy	0.893	Xtriage
Bulk solvent $k_{sol}(e/A^3), B_{sol}(A^2)$	$0.38 \;, 53.7$	EDS
L-test for $twinning^2$	$ < L >=0.48, < L^2>=0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	35038	wwPDB-VP
Average B, all atoms $(Å^2)$	66.0	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 31.60 % 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 1.0781e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

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.



¹Intensities estimated from amplitudes.

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: FE, MG, NA

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).

Mal	ol Chain Bond lengths		Bond angles		
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.28	0/2888	0.49	0/3959
1	В	0.27	0/2888	0.49	0/3959
1	С	0.27	0/2888	0.48	0/3959
1	D	0.28	0/2888	0.50	0/3959
1	Ε	0.27	0/2888	0.49	0/3959
1	F	0.27	0/2888	0.48	0/3959
All	All	0.27	0/17328	0.49	0/23754

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	А	2808	2692	2692	8	0
1	В	2808	2693	2692	7	0
1	С	2808	2691	2692	13	0
1	D	2808	2692	2692	7	0
1	Е	2808	2692	2692	10	0
1	F	2808	2692	2692	10	0
2	А	1	0	0	0	0



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	1	0	0	0	0
3	А	1	0	0	0	0
3	D	1	0	0	0	0
4	А	1	0	0	0	0
4	В	1	0	0	0	0
4	С	1	0	0	0	0
4	D	1	0	0	0	0
4	Е	1	0	0	0	0
4	F	1	0	0	0	0
5	А	369	0	0	1	5
5	В	314	0	0	0	3
5	С	321	0	0	0	1
5	D	395	0	0	1	2
5	Е	305	0	0	2	2
5	F	324	0	0	2	0
All	All	18886	16152	16152	46	7

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 1.

All (46) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:E:328:ALA:N	5:E:901:HOH:O	2.21	0.73
1:C:660:ALA:HB3	1:C:689:ALA:O	1.91	0.70
1:D:446:THR:OG1	5:D:901:HOH:O	2.13	0.67
1:F:525:ARG:NH1	5:F:903:HOH:O	2.30	0.65
1:C:615:LEU:HD12	1:C:700:GLY:O	1.99	0.62
1:A:615:LEU:HD12	1:A:700:GLY:O	2.00	0.61
1:F:615:LEU:HD12	1:F:700:GLY:O	2.04	0.57
1:E:626:ASP:OD1	1:E:627:HIS:N	2.38	0.55
1:C:626:ASP:OD1	1:C:627:HIS:N	2.40	0.54
1:D:685:TYR:OH	1:E:683:SER:OG	2.22	0.54
1:D:401:GLN:HG3	1:F:359:LEU:HD21	1.90	0.53
1:D:615:LEU:HD12	1:D:700:GLY:O	2.08	0.53
1:C:661:THR:HG22	1:C:662:SER:N	2.25	0.51
1:C:686:TYR:HE2	1:C:688:LEU:HD12	1.76	0.50
1:A:634:ARG:NH1	5:A:906:HOH:O	2.38	0.49
1:C:644:SER:O	1:C:675:ASN:ND2	2.45	0.49
1:C:615:LEU:HD11	1:C:699:ILE:CG2	2.44	0.48
1:F:626:ASP:OD1	1:F:627:HIS:N	2.46	0.48



		Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:B:626:ASP:OD1	1:B:627:HIS:N	2.47	0.47
1:F:563:HIS:ND1	1:F:567:GLN:OE1	2.48	0.46
1:E:661:THR:HB	1:E:688:LEU:HD12	1.97	0.46
1:B:530:ASP:OD1	1:C:525:ARG:HD3	2.17	0.44
1:A:401:GLN:HG3	1:C:359:LEU:HD21	1.99	0.44
1:B:440:ASP:HA	1:C:439:CYS:HA	1.99	0.44
1:E:440:ASP:HA	1:F:439:CYS:HA	2.00	0.43
1:B:423:SER:HB2	1:B:433:TRP:CD2	2.54	0.43
1:E:443:GLY:N	5:E:914:HOH:O	2.49	0.43
1:F:365:ASN:HA	1:F:378:LEU:O	2.18	0.43
1:D:365:ASN:HA	1:D:378:LEU:O	2.19	0.42
1:E:653:VAL:HG21	1:E:666:VAL:O	2.20	0.42
1:A:530:ASP:OD1	1:B:525:ARG:HD3	2.20	0.42
1:B:365:ASN:HA	1:B:378:LEU:O	2.19	0.42
1:C:365:ASN:HA	1:C:378:LEU:O	2.19	0.41
1:F:615:LEU:HD11	1:F:699:ILE:CG2	2.50	0.41
1:A:396:MET:O	1:A:405:ALA:HA	2.21	0.41
1:A:365:ASN:HA	1:A:378:LEU:O	2.21	0.41
1:D:467:TRP:HE3	1:D:489:LEU:HD11	1.86	0.41
1:E:359:LEU:HD21	1:F:401:GLN:HG3	2.02	0.41
1:E:396:MET:O	1:E:405:ALA:HA	2.20	0.41
1:A:459:ILE:O	1:A:459:ILE:HG22	2.19	0.40
1:A:563:HIS:ND1	1:A:567:GLN:OE1	2.47	0.40
1:B:697:MET:SD	1:C:697:MET:HE3	2.60	0.40
1:F:464:ASN:OD1	5:F:901:HOH:O	2.22	0.40
1:E:365:ASN:HA	1:E:378:LEU:O	2.22	0.40
1:C:686:TYR:CE2	1:C:688:LEU:HD12	2.56	0.40
1:D:596:VAL:HG22	1:D:612:ASP:OD1	2.21	0.40

All (7) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
5:D:1227:HOH:O	5:E:1162:HOH:O[4_465]	1.99	0.21
5:A:1173:HOH:O	5:B:1184:HOH:O[4_455]	2.00	0.20
5:A:1173:HOH:O	5:B:1176:HOH:O[4_455]	2.01	0.19
5:A:963:HOH:O	5:B:1032:HOH:O[4_455]	2.06	0.14
5:A:988:HOH:O	5:C:1160:HOH:O[4_455]	2.06	0.14
5:A:1012:HOH:O	5:A:1152:HOH:O[1_455]	2.18	0.02
5:D:1252:HOH:O	5:E:1162:HOH:O[4_465]	2.19	0.01



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	Perce	ntiles
1	А	372/384~(97%)	364~(98%)	8 (2%)	0	100	100
1	В	372/384~(97%)	365~(98%)	7 (2%)	0	100	100
1	С	372/384~(97%)	357~(96%)	15 (4%)	0	100	100
1	D	372/384~(97%)	366~(98%)	6(2%)	0	100	100
1	Е	372/384~(97%)	365~(98%)	7 (2%)	0	100	100
1	F	372/384~(97%)	359~(96%)	13 (4%)	0	100	100
All	All	2232/2304~(97%)	2176 (98%)	56 (2%)	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	Percen	tiles
1	А	291/298~(98%)	291 (100%)	0	100	100
1	В	291/298~(98%)	290 (100%)	1 (0%)	92	96
1	\mathbf{C}	291/298~(98%)	290 (100%)	1 (0%)	92	96
1	D	291/298~(98%)	291 (100%)	0	100	100
1	Ε	291/298~(98%)	289~(99%)	2(1%)	84	92
1	F	291/298~(98%)	291 (100%)	0	100	100
All	All	1746/1788~(98%)	1742 (100%)	4 (0%)	93	97



All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	364	SER
1	С	364	SER
1	Е	364	SER
1	Ε	525	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	С	526	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)

Of 10 ligands modelled in this entry, 10 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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, 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	А	374/384~(97%)	0.45	18 (4%) 30 38	37, 53, 97, 125	0
1	В	374/384~(97%)	0.64	35 (9%) 8 11	36, 55, 110, 125	0
1	С	374/384~(97%)	0.64	39 (10%) 6 9	34, 55, 109, 149	0
1	D	374/384~(97%)	0.37	12 (3%) 47 55	35, 52, 80, 100	0
1	Е	374/384~(97%)	0.46	23 (6%) 21 27	35, 56, 100, 129	0
1	F	374/384~(97%)	0.46	18 (4%) 30 38	35, 55, 97, 124	0
All	All	2244/2304~(97%)	0.50	145 (6%) 18 24	34, 54, 102, 149	0

All (145) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	568	ILE	8.6
1	С	580	LEU	8.4
1	А	575	LEU	7.2
1	С	575	LEU	6.3
1	В	580	LEU	5.9
1	С	592	ILE	5.8
1	С	568	ILE	5.6
1	С	645	ALA	5.6
1	D	592	ILE	5.2
1	В	571	GLY	5.2
1	В	701	TYR	4.6
1	С	585	ALA	4.6
1	В	586	ALA	4.6
1	Е	568	ILE	4.5
1	В	645	ALA	4.5
1	F	592	ILE	4.3
1	F	575	LEU	4.3
1	В	615	LEU	4.3
1	В	565	THR	4.2



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Mol	Chain	Res	Type	RSRZ	
1	А	568	ILE	4.1	
1	А	576	ALA	4.1	
1	А	563	HIS	4.1	
1	В	575	LEU	4.1	
1	В	570	SER	4.1	
1	F	645	ALA	4.1	
1	С	686	TYR	4.1	
1	С	573	LEU	4.0	
1	В	572	ILE	4.0	
1	Е	573	LEU	4.0	
1	В	608	TRP	3.9	
1	В	584	THR	3.9	
1	С	701	TYR	3.9	
1	А	579	GLY	3.9	
1	D	575	LEU	3.9	
1	С	588	ALA	3.8	
1	А	580	LEU	3.7	
1	А	592	ILE	3.6	
1	С	631	ILE	3.6	
1	С	642	PHE	3.5	
1	А	578	GLY	3.5	
1	F	568	ILE	3.5	
1	F	580	LEU	3.5	
1	А	574	PRO	3.4	
1	D	573	LEU	3.4	
1	Е	569	THR	3.4	
1	Е	570	SER	3.3	
1	Е	584	THR	3.3	
1	Е	329	LEU	3.3	
1	Ε	572	ILE	3.3	
1	В	644	SER	3.3	
1	В	567	GLN	3.2	
1	E	579	GLY	3.2	
1	В	616	ILE	3.1	
1	F	573	LEU	3.1	
1	A	566	SER	3.1	
1	С	577	ARG	3.1	
1	Е	585	ALA	3.1	
1	F	701	TYR	3.0	
1	C	687	GLY	3.0	
1	В	585	ALA	2.9	
1	F	576	ALA	2.9	



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 Mol
 Chain
 Res
 Type
 RSRZ
 Image: Continued from previous page...

1 F 574 PRO 2.9 1 D 564 ASP 2.9 1 B 642 PHE 2.9 1 A 593 GLY 2.9 1 C 700 GLY 2.9 1 C 574 PRO 2.9 1 C 594 ALA 2.8 1 C 594 ALA 2.8 1 C 569 THR 2.8 1 C 569 THR 2.8 1 C 569 THR 2.8 1 E 580 LEU 2.8 1 E 607 TRP 2.7 1 E 583 ASN 2.7 1 D 559 SER 2.7 1 D 574 PRO 2.6 1 F					
1 D 564 ASP 2.9 1 B 642 PHE 2.9 1 B 592 ILE 2.9 1 C 700 GLY 2.9 1 C 574 PRO 2.9 1 C 574 PRO 2.9 1 C 594 ALA 2.8 1 C 569 THR 2.8 1 C 572 ILE 2.8 1 E 580 LEU 2.8 1 E 580 ALA 2.7 1 E 583 ASN 2.7 1 D 574 PRO 2.6 1 D 574 PRO 2.6 1 F 642 PHE 2	1	F	574	PRO	2.9
1 B 642 PHE 2.9 1 A 593 GLY 2.9 1 C 700 GLY 2.9 1 C 574 PRO 2.9 1 C 574 PRO 2.9 1 C 594 ALA 2.8 1 C 569 THR 2.8 1 C 569 THR 2.8 1 C 572 ILE 2.8 1 E 580 LEU 2.8 1 E 607 TRP 2.7 1 E 607 TRP 2.7 1 E 583 ASN 2.7 1 E 583 ASN 2.7 1 D 574 PRO 2.6 1 F 642 PHE 2.6 1 F 642 PHE 2.6 1 F 643 PRO 2	1	D	564	ASP	2.9
1 A 593 GLY 2.9 1 B 592 ILE 2.9 1 C 700 GLY 2.9 1 C 574 PRO 2.9 1 C 594 ALA 2.8 1 C 569 THR 2.8 1 C 572 ILE 2.8 1 E 580 LEU 2.8 1 E 580 LEU 2.8 1 E 607 TRP 2.7 1 E 607 TRP 2.7 1 E 583 ASN 2.7 1 E 583 ASN 2.7 1 D 559 SER 2.7 1 D 574 PRO 2.6 1 F 642 PHE 2.6 1 F 642 PHE 2.6 1 A 564 ALA 2.6 1 F	1	В	642	PHE	2.9
1 B 592 ILE 2.9 1 C 700 GLY 2.9 1 C 574 PRO 2.9 1 C 594 ALA 2.8 1 C 688 LEU 2.8 1 C 569 THR 2.8 1 C 572 ILE 2.8 1 E 580 LEU 2.8 1 E 580 LEU 2.8 1 E 607 TRP 2.7 1 E 583 ASN 2.7 1 E 583 ASN 2.7 1 D 559 SER 2.7 1 D 574 PRO 2.6 1 F 642 PHE 2.6 1 F 642 PHE 2.6 1 A 564 ASP 2.6 1 A 565 THR 2.6 1 A	1	А	593	GLY	2.9
1 C 700 GLY 2.9 1 C 574 PRO 2.9 1 C 594 ALA 2.8 1 C 688 LEU 2.8 1 C 569 THR 2.8 1 C 572 ILE 2.8 1 E 580 LEU 2.8 1 E 580 LEU 2.8 1 E 607 TRP 2.7 1 E 607 TRP 2.7 1 E 583 ASN 2.7 1 E 583 ASN 2.7 1 D 559 SER 2.7 1 D 559 SER 2.7 1 D 574 PRO 2.6 1 F 642 PHE 2.6 1 F 643 PRO 2.6 1 A 565 THR 2.6 1 A	1	В	592	ILE	2.9
1 C 574 PRO 2.9 1 C 594 ALA 2.8 1 C 569 THR 2.8 1 C 572 ILE 2.8 1 E 580 LEU 2.8 1 E 572 ILE 2.8 1 E 579 GLY 2.7 1 E 607 TRP 2.7 1 E 583 ASN 2.7 1 E 583 ASN 2.7 1 E 583 ASN 2.7 1 D 559 SER 2.7 1 D 574 PRO 2.6 1 F 642 PHE 2.6 1 F 642 PHE 2.6 1 A 564 ASP 2.6 1 A 565 THR 2.6 1 A 565 THR 2	1	С	700	GLY	2.9
1 C 594 ALA 2.8 1 C 569 THR 2.8 1 C 572 ILE 2.8 1 E 580 LEU 2.8 1 E 580 LEU 2.8 1 B 579 GLY 2.7 1 E 607 TRP 2.7 1 F 328 ALA 2.7 1 E 583 ASN 2.7 1 E 583 ASN 2.7 1 D 559 SER 2.7 1 D 559 SER 2.7 1 D 574 PRO 2.6 1 F 642 PHE 2.6 1 E 582 ALA 2.6 1 A 564 ASP 2.6 1 A 565 THR 2.6 1 A 565 THR 2.6 1 A	1	С	574	PRO	2.9
1 C 688 LEU 2.8 1 C 572 ILE 2.8 1 E 580 LEU 2.8 1 E 579 GLY 2.7 1 E 607 TRP 2.7 1 E 607 TRP 2.7 1 E 583 ASN 2.7 1 E 583 ASN 2.7 1 E 583 ASN 2.7 1 D 559 SER 2.7 1 D 559 SER 2.7 1 D 574 PRO 2.6 1 F 642 PHE 2.6 1 E 582 ALA 2.6 1 A 564 ASP 2.6 1 A 565 THR 2.6 1 A 565 THR 2.6 1 A 565 THR 2	1	С	594	ALA	2.8
1 C 569 THR 2.8 1 C 572 ILE 2.8 1 E 580 LEU 2.8 1 B 579 GLY 2.7 1 E 607 TRP 2.7 1 F 328 ALA 2.7 1 F 328 ALA 2.7 1 C 328 ALA 2.7 1 C 328 ALA 2.7 1 D 559 SER 2.7 1 D 574 PRO 2.6 1 F 642 PHE 2.6 1 F 642 PHE 2.6 1 E 582 ALA 2.6 1 A 564 ASP 2.6 1 A 565 THR 2.6 1 A 565 THR 2.6 1 A 565 THR 2.6 1 A	1	С	688	LEU	2.8
1 C 572 ILE 2.8 1 E 580 LEU 2.8 1 B 579 GLY 2.7 1 E 607 TRP 2.7 1 F 328 ALA 2.7 1 E 583 ASN 2.7 1 E 583 ASN 2.7 1 C 328 ALA 2.7 1 D 559 SER 2.7 1 D 574 PRO 2.6 1 F 642 PHE 2.6 1 E 582 ALA 2.6 1 E 582 ALA 2.6 1 A 564 ASP 2.6 1 A 565 THR 2.6 1 A 562 ASN 2.6 1 A 563 HIS 2.5 1 B 574 PRO 2	1	С	569	THR	2.8
1 E 580 LEU 2.8 1 B 579 GLY 2.7 1 E 607 TRP 2.7 1 F 328 ALA 2.7 1 E 583 ASN 2.7 1 E 583 ASN 2.7 1 C 328 ALA 2.7 1 D 559 SER 2.7 1 D 574 PRO 2.6 1 F 642 PHE 2.6 1 C 586 ALA 2.6 1 E 582 ALA 2.6 1 E 582 ALA 2.6 1 A 564 ASP 2.6 1 B 596 VAL 2.6 1 A 565 THR 2.6 1 A 565 THR 2.6 1 B 574 PRO 2.5 1 B	1	С	572	ILE	2.8
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	Е	580	LEU	2.8
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	В	579	GLY	2.7
1F328ALA2.71E583ASN2.71C328ALA2.71D559SER2.71D574PRO2.61F642PHE2.61C586ALA2.61E582ALA2.61E582ALA2.61A564ASP2.61B596VAL2.61B596VAL2.61A565THR2.61A565THR2.61A562ASN2.61A562ASN2.61B574PRO2.51B574PRO2.51B574PRO2.51B647LEU2.51C579GLY2.51B546TRP2.51E554ALA2.51E554ALA2.51E571GLY2.41F632ILE2.41A594ALA2.41E556PHE2.4	1	Е	607	TRP	2.7
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	F	328	ALA	2.7
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	Е	583	ASN	2.7
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	С	328	ALA	2.7
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	D	559	SER	2.7
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	D	574	PRO	2.6
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	F	642	PHE	2.6
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	С	586	ALA	2.6
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	Е	582	ALA	2.6
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	А	564	ASP	2.6
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	В	596	VAL	2.6
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	F	643	PRO	2.6
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	А	565	THR	2.6
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	А	562	ASN	2.6
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	В	563	HIS	2.5
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	В	574	PRO	2.5
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	В	647	LEU	2.5
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	С	689	ALA	2.5
1 B 546 TRP 2.5 1 E 642 PHE 2.5 1 C 330 ALA 2.5 1 E 554 ALA 2.5 1 E 554 ALA 2.5 1 B 573 LEU 2.5 1 E 571 GLY 2.4 1 F 632 ILE 2.4 1 A 594 ALA 2.4 1 C 576 ALA 2.4 1 E 556 PHE 2.4	1	С	579	GLY	2.5
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	В	546	TRP	2.5
1 C 330 ALA 2.5 1 E 554 ALA 2.5 1 B 573 LEU 2.5 1 E 571 GLY 2.4 1 F 632 ILE 2.4 1 A 594 ALA 2.4 1 C 576 ALA 2.4 1 E 556 PHE 2.4	1	Е	642	PHE	2.5
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	С	330	ALA	2.5
1 B 573 LEU 2.5 1 E 571 GLY 2.4 1 F 632 ILE 2.4 1 A 594 ALA 2.4 1 C 576 ALA 2.4 1 E 556 PHE 2.4	1	Е	554	ALA	2.5
1 E 571 GLY 2.4 1 F 632 ILE 2.4 1 A 594 ALA 2.4 1 C 576 ALA 2.4 1 E 556 PHE 2.4	1	В	573	LEU	2.5
1 F 632 ILE 2.4 1 A 594 ALA 2.4 1 C 576 ALA 2.4 1 E 556 PHE 2.4	1	Е	571	GLY	2.4
1 A 594 ALA 2.4 1 C 576 ALA 2.4 1 E 556 PHE 2.4	1	F	632	ILE	2.4
1 C 576 ALA 2.4 1 E 556 PHE 2.4	1	А	594	ALA	2.4
1 E 556 PHE 2.4	1	С	576	ALA	2.4
	1	Е	556	PHE	2.4



Mol	Chain	Res	Type	RSRZ
1	А	567	GLN	2.4
1	С	630	GLY	2.4
1	С	616	ILE	2.4
1	В	576	ALA	2.4
1	А	661	THR	2.4
1	С	430	ILE	2.4
1	С	571	GLY	2.4
1	D	568	ILE	2.3
1	С	615	LEU	2.3
1	Е	575	LEU	2.3
1	D	594	ALA	2.3
1	С	578	GLY	2.3
1	С	581	GLY	2.3
1	F	628	PRO	2.3
1	F	631	ILE	2.3
1	С	692	TYR	2.2
1	Е	586	ALA	2.2
1	D	565	THR	2.2
1	В	582	ALA	2.2
1	В	564	ASP	2.2
1	D	580	LEU	2.2
1	С	584	THR	2.2
1	В	549	LEU	2.2
1	В	622	VAL	2.2
1	В	700	GLY	2.2
1	В	554	ALA	2.2
1	С	593	GLY	2.2
1	D	439	CYS	2.2
1	С	597	PRO	2.2
1	С	589	ARG	2.1
1	В	640	ILE	2.1
1	А	439	CYS	2.1
1	С	660	ALA	2.1
1	Е	596	VAL	2.1
1	Е	553	PRO	2.1
1	Е	592	ILE	2.1
1	D	576	ALA	2.0
1	F	430	ILE	2.0
1	Е	555	THR	2.0
1	F	700	GLY	2.0
1	F	330	ALA	2.0
1	В	646	CYS	2.0

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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, 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	$B-factors(Å^2)$	Q<0.9
4	NA	С	801	1/1	0.63	0.12	77,77,77,77	0
4	NA	D	803	1/1	0.69	0.18	84,84,84,84	0
3	MG	А	802	1/1	0.72	0.07	153,153,153,153	0
3	MG	D	802	1/1	0.88	0.18	89,89,89,89	0
4	NA	F	801	1/1	0.88	0.06	75,75,75,75	0
4	NA	Е	801	1/1	0.94	0.16	138,138,138,138	0
4	NA	В	801	1/1	0.96	0.12	75,75,75,75	0
4	NA	А	803	1/1	0.97	0.09	$65,\!65,\!65,\!65$	0
2	FE	А	801	1/1	0.98	0.05	80,80,80,80	0
2	FE	D	801	1/1	0.99	0.06	68,68,68,68	0

6.5 Other polymers (i)

There are no such residues in this entry.

