



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:56 AM GMT

PDB ID : 2JGP  
Title : Structure of the TycC5-6 PCP-C bidomain of the tyrocidine synthetase TycC  
Authors : Samel, S.A.; Schoenafinger, G.; Knappe, T.A.; Marahiel, M.A.; Essen, L.-O.  
Deposited on : 2007-02-13  
Resolution : 1.85 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) 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 : trunk26765  
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

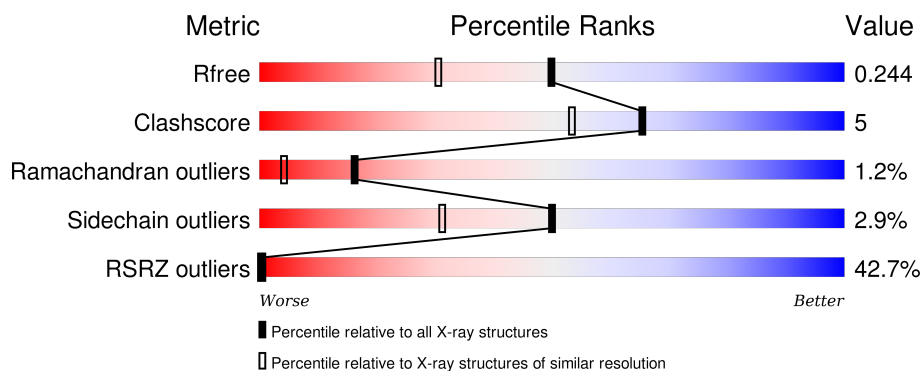
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.85 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	1745 (1.86-1.86)
Clashscore	102246	1898 (1.86-1.86)
Ramachandran outliers	100387	1875 (1.86-1.86)
Sidechain outliers	100360	1875 (1.86-1.86)
RSRZ outliers	91569	1747 (1.86-1.86)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	520	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	A	1523	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	A	1524	-	-	-	X
3	DIO	A	1526	-	-	-	X

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4477 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 TYROCIDINE SYNTHETASE 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	520	4161	2655	695	795	16	35	2	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	183	GLU	GLN	CONFLICT	UNP O30409

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	5	4	1	0	0
2	A	1	5	4	1	0	0

- Molecule 3 is 1,4-DIETHYLENE DIOXIDE (three-letter code: DIO) (formula: C<sub>4</sub>H<sub>8</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	4	2		
3	A	1	Total	C	O	0	0
			6	4	2		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Na	0	0
			1	1		

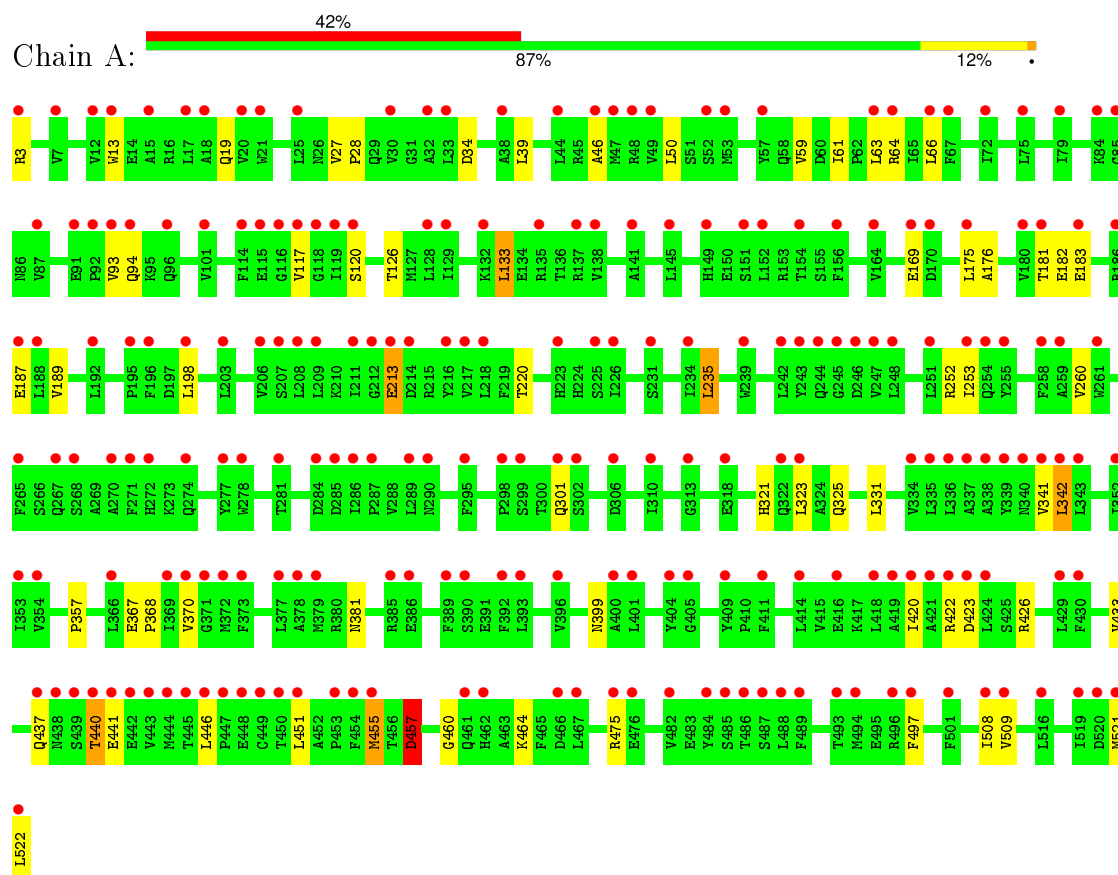
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	293	Total	O	0	0
			293	293		

### 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 ( $\text{RSRZ} > 2$ ). 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: TYROCIDINE SYNTHETASE 3



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	84.97Å 84.97Å 164.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.81 – 1.85 19.82 – 1.85	Depositor EDS
% Data completeness (in resolution range)	98.6 (19.81-1.85) 98.6 (19.82-1.85)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.12 (at 1.85Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.208 , 0.238 0.214 , 0.244	Depositor DCC
$R_{free}$ test set	1766 reflections (3.55%)	DCC
Wilson B-factor (Å <sup>2</sup> )	33.6	Xtriage
Anisotropy	0.131	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 53.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 51770 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	4477	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.38% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  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: NA, DIO, SO4

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	0.37	1/4259 (0.0%)	0.74	6/5783 (0.1%)

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	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	460	GLY	C-N	-7.94	1.15	1.34

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	457	ASP	CB-CG-OD2	-28.52	92.63	118.30
1	A	455	MET	O-C-N	-22.29	87.04	122.70
1	A	457	ASP	CB-CG-OD1	15.23	132.00	118.30
1	A	460	GLY	C-N-CA	6.67	138.37	121.70
1	A	455	MET	CA-C-N	5.61	129.54	117.20
1	A	460	GLY	O-C-N	-5.40	114.06	122.70

There are no chirality outliers.

All (2) planarity outliers are listed below:



Mol	Chain	Res	Type	Group
1	A	455	MET	Mainchain
1	A	457	ASP	Sidechain

## 5.2 Too-close contacts ⓘ

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	4161	0	4084	41	0
2	A	10	0	0	0	0
3	A	12	0	16	1	0
4	A	1	0	0	0	0
5	A	293	0	0	1	0
All	All	4477	0	4100	41	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 (41) 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:508:ILE:HD12	1:A:509:VAL:N	2.01	0.76
1:A:117:VAL:HG12	1:A:120:SER:HB3	1.72	0.71
1:A:117:VAL:CG1	1:A:120:SER:HB3	2.21	0.70
1:A:323:LEU:CD2	1:A:508:ILE:HD13	2.23	0.69
1:A:117:VAL:HG12	1:A:117:VAL:O	1.95	0.66
1:A:220:THR:HG21	3:A:1525:DIO:H22	1.82	0.61
1:A:252:ARG:NH1	1:A:253:ILE:HD11	2.15	0.61
1:A:420:ILE:HG23	1:A:422:ARG:HB2	1.83	0.60
1:A:175:LEU:C	1:A:175:LEU:HD23	2.24	0.57
1:A:521:MET:O	1:A:522:LEU:HB2	2.05	0.57
1:A:446:LEU:HD13	1:A:451:LEU:HD11	1.85	0.57
1:A:508:ILE:HD12	1:A:508:ILE:C	2.26	0.56
1:A:3:ARG:NH2	1:A:28:PRO:O	2.38	0.55
1:A:3:ARG:NH2	1:A:27:VAL:HG12	2.22	0.53
1:A:126:THR:HG21	1:A:189:VAL:HG11	1.90	0.53
1:A:175:LEU:HD23	1:A:176:ALA:N	2.25	0.52
1:A:19:GLN:NE2	5:A:2020:HOH:O	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:342:LEU:HD13	1:A:497:PHE:CZ	2.47	0.49
1:A:3:ARG:NH2	1:A:27:VAL:CG1	2.77	0.48
1:A:175:LEU:HD23	1:A:176:ALA:C	2.34	0.48
1:A:126:THR:HG21	1:A:189:VAL:CG1	2.44	0.47
1:A:321:HIS:CE1	1:A:331:LEU:HD22	2.49	0.47
1:A:13:TRP:CH2	1:A:59:VAL:HG21	2.50	0.47
1:A:50:LEU:HD22	1:A:61:ILE:O	2.14	0.47
1:A:381:ASN:ND2	1:A:399:ASN:HD22	2.14	0.45
1:A:117:VAL:O	1:A:117:VAL:CG1	2.63	0.45
1:A:446:LEU:CD1	1:A:451:LEU:HD11	2.46	0.45
1:A:50:LEU:HD11	1:A:63:LEU:HA	2.00	0.44
1:A:301:GLN:NE2	1:A:464:LYS:O	2.50	0.44
1:A:34:ASP:HB3	1:A:39:LEU:HD11	2.00	0.44
1:A:367:GLU:N	1:A:368:PRO:CD	2.82	0.43
1:A:323:LEU:HD22	1:A:508:ILE:HD13	2.00	0.42
1:A:181:THR:HG22	1:A:182:GLU:N	2.35	0.41
1:A:213:GLU:N	1:A:213:GLU:CD	2.73	0.41
1:A:175:LEU:C	1:A:175:LEU:CD2	2.88	0.41
1:A:46:ALA:HB1	1:A:66:LEU:HD23	2.02	0.41
1:A:440:THR:HG22	1:A:440:THR:O	2.20	0.41
1:A:181:THR:HG22	1:A:183:GLU:H	1.85	0.40
1:A:357:PRO:HD3	1:A:433:VAL:HG13	2.02	0.40
1:A:93:VAL:HG11	1:A:260:VAL:HB	2.04	0.40
1:A:235:LEU:CD1	1:A:370:VAL:HG21	2.50	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	520/520 (100%)	489 (94%)	25 (5%)	6 (1%)	<b>16</b> <b>4</b>

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	213	GLU
1	A	440	THR
1	A	441	GLU
1	A	133	LEU
1	A	475	ARG
1	A	423	ASP

### 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	452/450 (100%)	439 (97%)	13 (3%)	50 31

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	64	ARG
1	A	94	GLN
1	A	133	LEU
1	A	169	GLU
1	A	187	GLU
1	A	198	LEU
1	A	235	LEU
1	A	325	GLN
1	A	341	VAL
1	A	342	LEU
1	A	426	ARG
1	A	437	GLN
1	A	457	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	143	GLN

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Mol	Chain	Res	Type
1	A	267	GLN
1	A	280	GLN
1	A	325	GLN
1	A	381	ASN
1	A	427	ASN
1	A	500	HIS
1	A	510	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 for Mogul analysis.

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	SO4	A	1523	-	4,4,4	0.31	0	6,6,6	0.16	0
2	SO4	A	1524	-	4,4,4	0.31	0	6,6,6	0.15	0
3	DIO	A	1525	-	6,6,6	0.47	0	6,6,6	0.46	0
3	DIO	A	1526	-	6,6,6	0.48	0	6,6,6	0.51	0

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	SO4	A	1523	-	-	0/0/0/0	0/0/0/0
2	SO4	A	1524	-	-	0/0/0/0	0/0/0/0
3	DIO	A	1525	-	-	0/0/6/6	0/1/1/1
3	DIO	A	1526	-	-	0/0/6/6	0/1/1/1

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1525	DIO	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 ⓘ

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	515/520 (99%)	2.15	220 (42%) 0 0	43, 62, 75, 87	0

All (220) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	443	VAL	23.1
1	A	420	ILE	12.5
1	A	421	ALA	11.2
1	A	114	PHE	10.3
1	A	129	ILE	10.2
1	A	422	ARG	10.2
1	A	117	VAL	9.1
1	A	439	SER	8.4
1	A	440	THR	8.0
1	A	476	GLU	7.6
1	A	442	GLU	7.5
1	A	94	GLN	6.7
1	A	446	LEU	6.7
1	A	226	ILE	6.4
1	A	217	VAL	6.3
1	A	447	PRO	6.3
1	A	441	GLU	6.1
1	A	488	LEU	6.1
1	A	218	LEU	6.0
1	A	213	GLU	6.0
1	A	451	LEU	6.0
1	A	475	ARG	5.8
1	A	285	ASP	5.5
1	A	369	ILE	5.5
1	A	423	ASP	5.4
1	A	208	LEU	5.4
1	A	419	ALA	5.4

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Mol	Chain	Res	Type	RSRZ
1	A	489	PHE	5.3
1	A	418	LEU	5.3
1	A	209	LEU	5.2
1	A	520	ASP	5.2
1	A	467	LEU	5.1
1	A	370	VAL	5.1
1	A	516	LEU	5.1
1	A	438	ASN	5.1
1	A	247	VAL	4.9
1	A	444	MET	4.9
1	A	462	HIS	4.9
1	A	371	GLY	4.7
1	A	116	GLY	4.6
1	A	119	ILE	4.6
1	A	445	THR	4.5
1	A	286	ILE	4.4
1	A	66	LEU	4.4
1	A	32	ALA	4.4
1	A	72	ILE	4.4
1	A	487	SER	4.4
1	A	115	GLU	4.3
1	A	17	LEU	4.2
1	A	118	GLY	4.1
1	A	392	PHE	4.1
1	A	386	GLU	4.1
1	A	255	TYR	4.0
1	A	393	LEU	4.0
1	A	284	ASP	4.0
1	A	341	VAL	3.9
1	A	449	CYS	3.9
1	A	3	ARG	3.9
1	A	485	SER	3.9
1	A	343	LEU	3.9
1	A	522	LEU	3.8
1	A	93	VAL	3.8
1	A	267	GLN	3.8
1	A	187	GLU	3.8
1	A	30	VAL	3.8
1	A	484	TYR	3.8
1	A	454	PHE	3.8
1	A	245	GLY	3.8
1	A	353	ILE	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	519	ILE	3.7
1	A	248	LEU	3.7
1	A	21	TRP	3.7
1	A	352	ILE	3.7
1	A	225	SER	3.7
1	A	461	GLN	3.6
1	A	188	LEU	3.6
1	A	254[A]	GLN	3.6
1	A	482	VAL	3.6
1	A	25	LEU	3.6
1	A	152	LEU	3.5
1	A	203	LEU	3.5
1	A	13	TRP	3.5
1	A	508	ILE	3.5
1	A	270	ALA	3.5
1	A	339	TYR	3.4
1	A	91	GLU	3.4
1	A	214	ASP	3.4
1	A	92	PRO	3.4
1	A	175	LEU	3.3
1	A	141	ALA	3.3
1	A	138	VAL	3.3
1	A	289	LEU	3.3
1	A	258	PHE	3.3
1	A	378	ALA	3.3
1	A	57	TYR	3.3
1	A	299	SER	3.3
1	A	414	LEU	3.2
1	A	64	ARG	3.2
1	A	424	LEU	3.2
1	A	337	ALA	3.2
1	A	44	LEU	3.2
1	A	389	PHE	3.2
1	A	411	PHE	3.2
1	A	253	ILE	3.2
1	A	278	TRP	3.2
1	A	342	LEU	3.2
1	A	259	ALA	3.1
1	A	63	LEU	3.1
1	A	239	TRP	3.1
1	A	243	TYR	3.1
1	A	18	ALA	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	385	ARG	3.1
1	A	212	GLY	3.1
1	A	366	LEU	3.0
1	A	75	LEU	3.0
1	A	409	TYR	3.0
1	A	244	GLN	3.0
1	A	455	MET	3.0
1	A	334	VAL	3.0
1	A	453	PRO	3.0
1	A	379	MET	2.9
1	A	274	GLN	2.9
1	A	169	GLU	2.9
1	A	338	ALA	2.9
1	A	494	MET	2.8
1	A	132	LYS	2.8
1	A	196	PHE	2.8
1	A	145	LEU	2.8
1	A	335	LEU	2.8
1	A	135	ARG	2.8
1	A	295	PHE	2.8
1	A	416	GLU	2.8
1	A	128	LEU	2.8
1	A	242	LEU	2.8
1	A	46	ALA	2.8
1	A	271	PHE	2.8
1	A	313	GLY	2.8
1	A	466	ASP	2.7
1	A	234	ILE	2.7
1	A	154	THR	2.7
1	A	198	LEU	2.7
1	A	450	THR	2.7
1	A	486	THR	2.7
1	A	33	LEU	2.7
1	A	15	ALA	2.7
1	A	216	TYR	2.7
1	A	192	LEU	2.7
1	A	373	PHE	2.6
1	A	377	LEU	2.6
1	A	48	ARG	2.6
1	A	246	ASP	2.6
1	A	7	VAL	2.6
1	A	354	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	85	GLY	2.6
1	A	84[A]	LYS	2.6
1	A	272	HIS	2.6
1	A	156	PHE	2.6
1	A	404	TYR	2.6
1	A	521	MET	2.5
1	A	101	VAL	2.5
1	A	79	ILE	2.5
1	A	287	PRO	2.5
1	A	52	SER	2.5
1	A	151	SER	2.5
1	A	509	VAL	2.5
1	A	211	ILE	2.5
1	A	20	VAL	2.5
1	A	49	VAL	2.5
1	A	396	VAL	2.5
1	A	318	GLU	2.5
1	A	195	PRO	2.5
1	A	496	ARG	2.4
1	A	137	ARG	2.4
1	A	302	SER	2.4
1	A	170	ASP	2.4
1	A	183	GLU	2.4
1	A	277	TYR	2.4
1	A	501	PHE	2.4
1	A	207	SER	2.3
1	A	231	SER	2.3
1	A	429	LEU	2.3
1	A	372	MET	2.3
1	A	223	HIS	2.3
1	A	87	VAL	2.3
1	A	206	VAL	2.3
1	A	437	GLN	2.3
1	A	390	SER	2.3
1	A	400	ALA	2.3
1	A	265	PHE	2.3
1	A	181	THR	2.3
1	A	448	GLU	2.2
1	A	322	GLN	2.2
1	A	405	GLY	2.2
1	A	306	ASP	2.2
1	A	323	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	401	LEU	2.2
1	A	67	PHE	2.2
1	A	281	THR	2.2
1	A	53	MET	2.2
1	A	290	ASN	2.2
1	A	149	HIS	2.2
1	A	47	MET	2.2
1	A	340	ASN	2.1
1	A	261	TRP	2.1
1	A	430	PHE	2.1
1	A	251	LEU	2.1
1	A	12	VAL	2.1
1	A	164	VAL	2.1
1	A	301	GLN	2.1
1	A	186	ARG	2.1
1	A	336	LEU	2.1
1	A	310	ILE	2.1
1	A	96	GLN	2.1
1	A	268	SER	2.0
1	A	298	PRO	2.0
1	A	38	ALA	2.0
1	A	120	SER	2.0
1	A	497	PHE	2.0
1	A	493	THR	2.0
1	A	180	VAL	2.0

## 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 ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
2	SO4	A	1523	5/5	0.94	0.42	7.82	69,70,70,70	0
3	DIO	A	1526	6/6	0.63	0.29	4.95	79,79,79,79	0
2	SO4	A	1524	5/5	0.94	0.28	2.23	57,57,58,59	0
3	DIO	A	1525	6/6	0.87	0.22	0.46	55,56,56,56	0
4	NA	A	1527	1/1	0.76	0.42	-	69,69,69,69	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.