



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 30, 2017 – 05:23 AM EDT

PDB ID : 5OSQ  
Title : ZP-N domain of mammalian sperm receptor ZP3 (crystal form II, processed in P21221)  
Authors : Jovine, L.; Monne, M.  
Deposited on : unknown  
Resolution : 2.05 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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20029824  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : rb-20029824

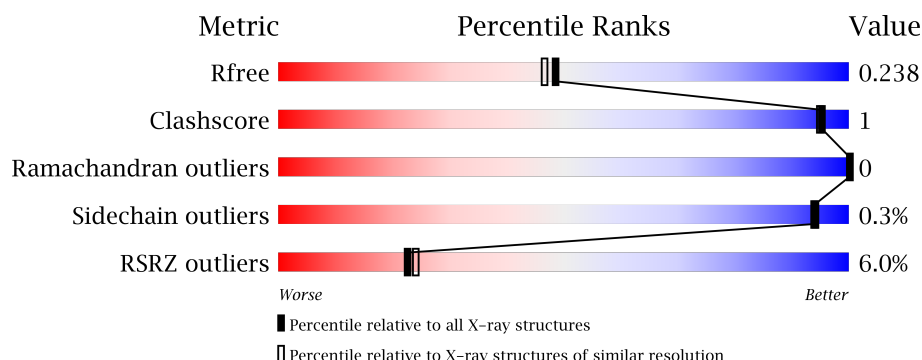
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.05 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))
$R_{free}$	100719	1316 (2.04-2.04)
Clashscore	112137	1394 (2.04-2.04)
Ramachandran outliers	110173	1383 (2.04-2.04)
Sidechain outliers	110143	1383 (2.04-2.04)
RSRZ outliers	101464	1319 (2.04-2.04)

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	481	<div> <div>7%</div> <div>95%</div> <div>••</div> </div>
1	B	481	<div> <div>5%</div> <div>94%</div> <div>••</div> </div>

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
4	PGE	B	505	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 15023 atoms, of which 7329 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 Maltose-binding periplasmic protein,Zona pellucida sperm-binding protein 3.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	472	Total	C	H	N	O	S	13	2	0
			7301	2341	3637	611	701	11			
1	B	472	Total	C	H	N	O	S	13	1	0
			7293	2337	3636	611	698	11			

There are 34 discrepancies between the modelled and reference sequences:

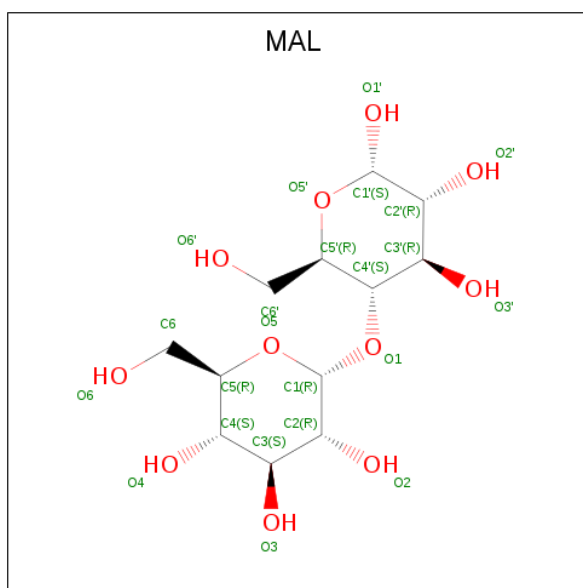
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP P0AEX9
A	3	THR	ILE	engineered mutation	UNP P0AEX9
A	360	ALA	GLU	engineered mutation	UNP P0AEX9
A	363	ALA	LYS	engineered mutation	UNP P0AEX9
A	364	ALA	ASP	engineered mutation	UNP P0AEX9
A	368	ASN	ARG	engineered mutation	UNP P0AEX9
A	369	ALA	-	linker	UNP P0AEX9
A	370	ALA	-	linker	UNP P0AEX9
A	371	ALA	-	linker	UNP P0AEX9
A	474	LEU	-	expression tag	UNP P10761
A	475	GLU	-	expression tag	UNP P10761
A	476	HIS	-	expression tag	UNP P10761
A	477	HIS	-	expression tag	UNP P10761
A	478	HIS	-	expression tag	UNP P10761
A	479	HIS	-	expression tag	UNP P10761
A	480	HIS	-	expression tag	UNP P10761
A	481	HIS	-	expression tag	UNP P10761
B	1	MET	-	initiating methionine	UNP P0AEX9
B	3	THR	ILE	engineered mutation	UNP P0AEX9
B	360	ALA	GLU	engineered mutation	UNP P0AEX9
B	363	ALA	LYS	engineered mutation	UNP P0AEX9
B	364	ALA	ASP	engineered mutation	UNP P0AEX9
B	368	ASN	ARG	engineered mutation	UNP P0AEX9
B	369	ALA	-	linker	UNP P0AEX9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	370	ALA	-	linker	UNP P0AEX9
B	371	ALA	-	linker	UNP P0AEX9
B	474	LEU	-	expression tag	UNP P10761
B	475	GLU	-	expression tag	UNP P10761
B	476	HIS	-	expression tag	UNP P10761
B	477	HIS	-	expression tag	UNP P10761
B	478	HIS	-	expression tag	UNP P10761
B	479	HIS	-	expression tag	UNP P10761
B	480	HIS	-	expression tag	UNP P10761
B	481	HIS	-	expression tag	UNP P10761

- Molecule 2 is MALTOSE (three-letter code: MAL) (formula:  $C_{12}H_{22}O_{11}$ ).

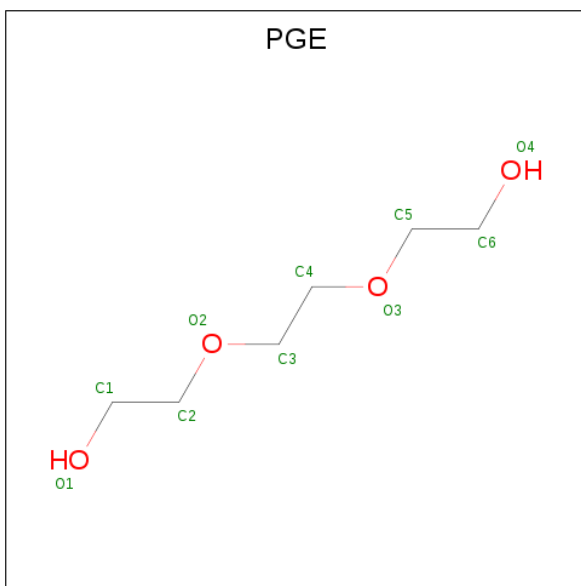


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			44	12	21	11		
2	B	1	Total	C	H	O	0	0
			44	12	21	11		

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	3	Total	Ca	0	0
			3	3		
3	A	3	Total	Ca	0	0
			3	3		

- Molecule 4 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula:  $C_6H_{14}O_4$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	H	O	0	0
			24	6	14	4		

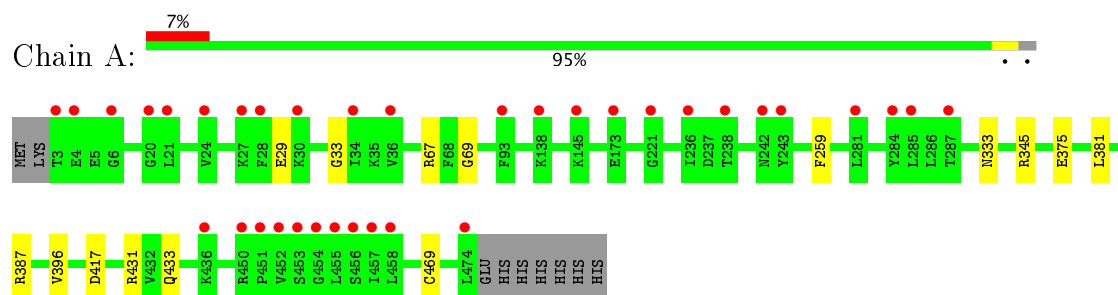
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	121	Total	O	0	1
			122	122		
5	B	188	Total	O	0	1
			189	189		

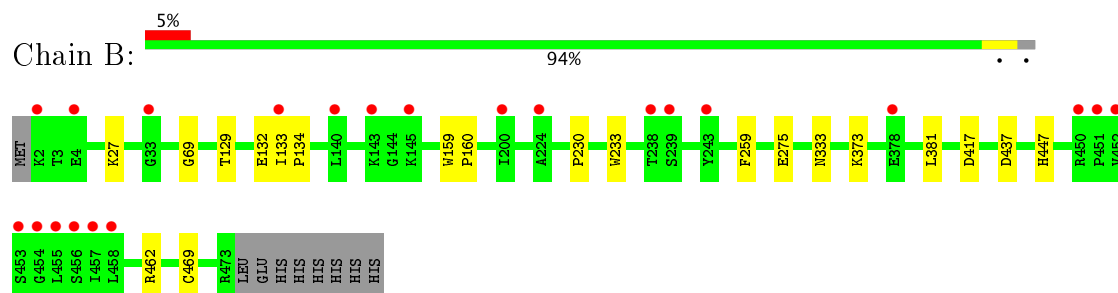
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Maltose-binding periplasmic protein,Zona pellucida sperm-binding protein 3



- Molecule 1: Maltose-binding periplasmic protein,Zona pellucida sperm-binding protein 3



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	91.34Å 92.16Å 140.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.90 – 2.05 47.73 – 2.05	Depositor EDS
% Data completeness (in resolution range)	99.8 (32.90-2.05) 87.7 (47.73-2.05)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.11	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.44 (at 2.05Å)	Xtriage
Refinement program	PHENIX 1.12-2829	Depositor
R, $R_{free}$	0.209 , 0.241 0.200 , 0.238	Depositor DCC
$R_{free}$ test set	1650 reflections (2.50%)	DCC
Wilson B-factor (Å <sup>2</sup> )	39.1	Xtriage
Anisotropy	0.090	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 49.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.002 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	15023	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	73.0	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 58.67 % 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 1.9751e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, PGE, MAL

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	0.34	0/3746	0.51	0/5091
1	B	0.36	0/3739	0.51	0/5080
All	All	0.35	0/7485	0.51	0/10171

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

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	3664	3637	3635	9	0
1	B	3657	3636	3635	12	0
2	A	23	21	22	0	0
2	B	23	21	22	0	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
4	B	10	14	14	1	0
5	A	122	0	0	3	0
5	B	189	0	0	3	0
All	All	7694	7329	7328	21	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 1.

All (21) 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:345[B]:ARG:NH2	5:A:604:HOH:O	2.30	0.64
1:A:375:GLU:OE1	5:A:601:HOH:O	2.16	0.60
1:B:437:ASP:OD2	5:B:601:HOH:O	2.18	0.57
1:B:69:GLY:HA3	1:B:333:ASN:O	2.07	0.54
1:A:431:ARG:NH1	1:A:433:GLN:OE1	2.45	0.49
1:A:381:LEU:HD13	1:A:469:CYS:SG	2.57	0.44
1:B:27:LYS:HD3	4:B:505:PGE:O2	2.17	0.44
1:B:129:THR:OG1	1:B:132:GLU:HG3	2.17	0.44
1:B:447:HIS:O	1:B:462:ARG:HA	2.17	0.44
1:B:230:PRO:HA	1:B:233:TRP:CE2	2.52	0.44
1:B:381:LEU:HD13	1:B:469:CYS:SG	2.59	0.42
1:A:69:GLY:HA3	1:A:333:ASN:O	2.20	0.42
1:A:417:ASP:N	1:A:417:ASP:OD1	2.52	0.42
1:B:133:ILE:N	1:B:134:PRO:CD	2.83	0.42
1:B:373:LYS:HG3	5:B:727:HOH:O	2.19	0.41
1:A:387:ARG:HA	1:A:396:VAL:HG22	2.02	0.41
1:B:159:TRP:N	1:B:160:PRO:CD	2.84	0.41
1:B:275:GLU:HG2	5:B:740:HOH:O	2.21	0.41
1:B:417:ASP:N	1:B:417:ASP:OD1	2.49	0.41
1:A:67:ARG:NH2	5:A:604:HOH:O	2.53	0.40
1:A:29:GLU:O	1:A:33:GLY:N	2.43	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	472/481 (98%)	462 (98%)	10 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	471/481 (98%)	463 (98%)	8 (2%)	0	100	100
All	All	943/962 (98%)	925 (98%)	18 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	386/393 (98%)	385 (100%)	1 (0%)	94	94
1	B	385/393 (98%)	384 (100%)	1 (0%)	94	94
All	All	771/786 (98%)	769 (100%)	2 (0%)	94	94

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

Mol	Chain	Res	Type
1	A	259	PHE
1	B	259	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 9 ligands modelled in this entry, 6 are monoatomic - leaving 3 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	MAL	A	501	-	24,24,24	0.61	0	35,35,35	0.89	2 (5%)
2	MAL	B	501	-	24,24,24	0.62	0	35,35,35	0.89	1 (2%)
4	PGE	B	505	-	9,9,9	0.34	0	8,8,8	0.31	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	MAL	A	501	-	-	0/8/48/48	0/2/2/2
2	MAL	B	501	-	-	0/8/48/48	0/2/2/2
4	PGE	B	505	-	-	0/7/7/7	0/0/0/0

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	MAL	C4-C3-C2	-2.37	106.66	110.84
2	A	501	MAL	C6-C5-C4	-2.34	107.53	113.00
2	B	501	MAL	C4-C3-C2	-2.10	107.13	110.84

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
4	B	505	PGE	1	0

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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	472/481 (98%)	0.61	35 (7%) 15 17	35, 68, 114, 148	0
1	B	472/481 (98%)	0.44	22 (4%) 32 35	30, 56, 103, 189	0
All	All	944/962 (98%)	0.53	57 (6%) 23 24	30, 62, 110, 189	0

All (57) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	454	GLY	10.5
1	B	456	SER	8.8
1	B	458	LEU	7.9
1	B	455	LEU	5.9
1	B	453	SER	5.6
1	A	474	LEU	5.4
1	A	93	PHE	4.8
1	A	454	GLY	4.7
1	B	2	LYS	4.6
1	A	3	THR	4.6
1	B	452	VAL	4.4
1	A	455	LEU	4.0
1	A	4	GLU	3.9
1	A	456	SER	3.8
1	B	140	LEU	3.8
1	A	457	ILE	3.6
1	A	28	PHE	3.5
1	A	34	ILE	3.4
1	A	221	GLY	3.4
1	A	451	PRO	3.3
1	A	145	LYS	3.2
1	A	236	ILE	3.2
1	A	281	LEU	3.2
1	A	452	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	451	PRO	3.0
1	A	453	SER	2.9
1	B	457	ILE	2.8
1	A	20	GLY	2.8
1	A	243	TYR	2.8
1	B	4	GLU	2.7
1	B	378	GLU	2.7
1	A	27	LYS	2.7
1	B	239	SER	2.6
1	B	133	ILE	2.6
1	A	285	LEU	2.5
1	A	30	LYS	2.5
1	A	242	ASN	2.5
1	A	287	THR	2.4
1	A	458	LEU	2.4
1	B	450	ARG	2.4
1	B	143	LYS	2.4
1	B	243	TYR	2.4
1	A	238	THR	2.3
1	B	238	THR	2.3
1	A	284	TYR	2.3
1	A	436	LYS	2.3
1	B	33	GLY	2.3
1	A	450	ARG	2.2
1	A	21	LEU	2.2
1	B	145	LYS	2.2
1	B	224	ALA	2.2
1	A	6	GLY	2.1
1	A	173	GLU	2.0
1	A	24	VAL	2.0
1	A	36	VAL	2.0
1	B	200	ILE	2.0
1	A	138	LYS	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(Å <sup>2</sup> )	Q<0.9
4	PGE	B	505	10/10	0.72	0.31	3.06	72,87,93,96	24
2	MAL	B	501	23/23	0.98	0.12	-0.64	29,38,48,58	0
3	CA	A	503	1/1	0.98	0.10	-0.87	65,65,65,65	0
2	MAL	A	501	23/23	0.97	0.11	-0.94	37,48,59,69	0
3	CA	B	503	1/1	0.94	0.07	-1.67	103,103,103,103	0
3	CA	A	504	1/1	0.77	0.07	-	109,109,109,109	0
3	CA	A	502	1/1	0.77	0.13	-	84,84,84,84	0
3	CA	B	504	1/1	0.94	0.07	-	83,83,83,83	0
3	CA	B	502	1/1	0.92	0.15	-	77,77,77,77	0

## 6.5 Other polymers

There are no such residues in this entry.