



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 29, 2025 – 02:09 AM JST

PDB ID : 9V8D / pdb\_00009v8d  
Title : PPARgamma ligand-binding domain in complex with PG08  
Authors : Sigal, M.; Okada, C.; Katoh, T.; Suga, H.; Sengoku, T.  
Deposited on : 2025-05-29  
Resolution : 1.44 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

<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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
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) : 2.46

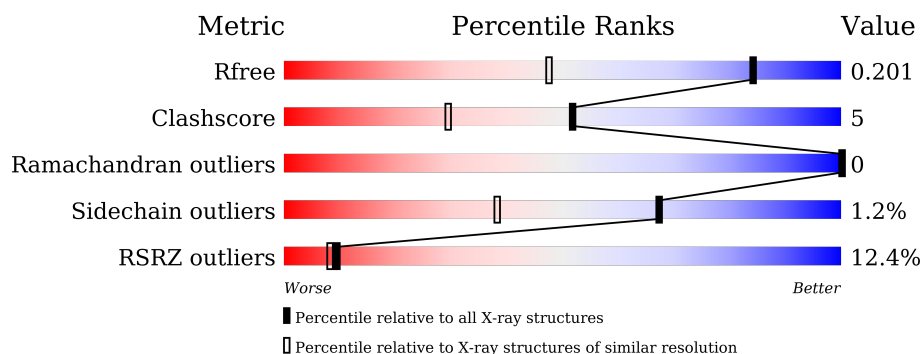
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.44 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))
$R_{free}$	164625	2809 (1.46-1.42)
Clashscore	180529	3008 (1.46-1.42)
Ramachandran outliers	177936	2971 (1.46-1.42)
Sidechain outliers	177891	2971 (1.46-1.42)
RSRZ outliers	164620	2809 (1.46-1.42)

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  $\geq 3$ , 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	275	<div> <div>12%</div> <div>86%</div> <div>8%</div> <div>5%</div> </div>
2	B	25	<div> <div>8%</div> <div>60%</div> <div>8%</div> <div>32%</div> </div>

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 2484 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.

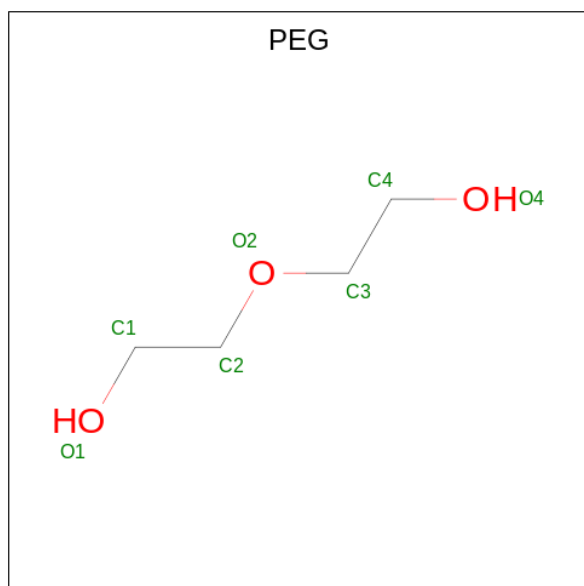
- Molecule 1 is a protein called Peroxisome proliferator-activated receptor gamma.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	261	Total	C	N	O	S	0	6	0
			2130	1370	347	403	10			

- Molecule 2 is a protein called PG08.

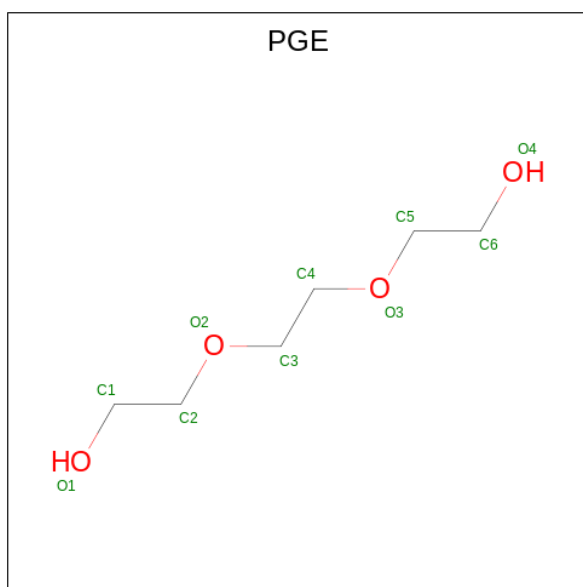
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	17	Total	C	N	O	0	0	0
			128	85	23	20			

- Molecule 3 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula:  $C_4H_{10}O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			7	4	3		

- Molecule 4 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula:  $C_6H_{14}O_4$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			10	6	4		

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula:  $C_2H_6O_2$ ).



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

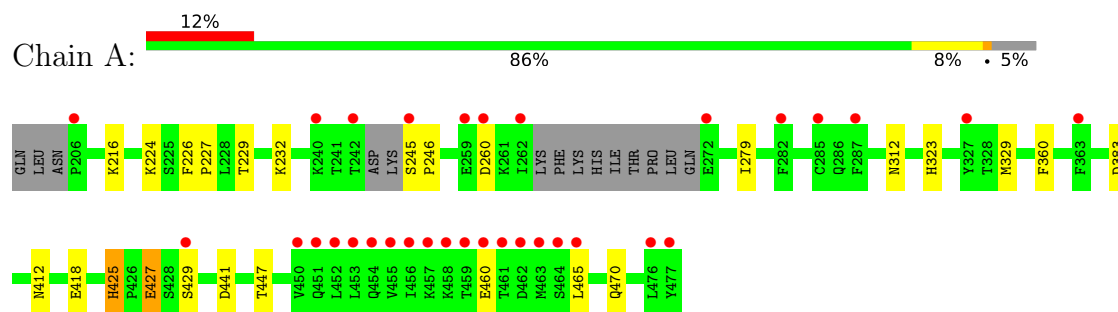
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	189	Total 189	O 189	0	0
6	B	16	Total 16	O 16	0	0

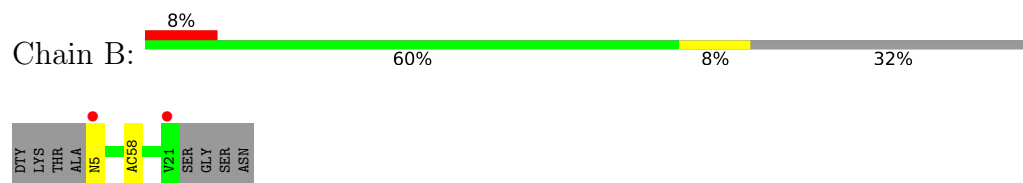
### 3 Residue-property plots [i](#)

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: Peroxisome proliferator-activated receptor gamma



- Molecule 2: PG08



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	43.62Å 53.46Å 66.91Å 90.00° 105.90° 90.00°	Depositor
Resolution (Å)	41.99 – 1.44 41.99 – 1.44	Depositor EDS
% Data completeness (in resolution range)	100.0 (41.99-1.44) 100.0 (41.99-1.44)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.34 (at 1.44Å)	Xtriage
Refinement program	REFMAC 5.8.0425	Depositor
R, $R_{free}$	0.172 , 0.201 0.171 , 0.201	Depositor DCC
$R_{free}$ test set	2002 reflections (3.73%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	14.0	Xtriage
Anisotropy	0.613	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 39.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	2484	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.64% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: EDO, PEG, AC5, PGE

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	0.67	0/2164	1.10	6/2914 (0.2%)
2	B	0.69	0/101	1.05	0/132
All	All	0.68	0/2265	1.09	6/3046 (0.2%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	425	HIS	CB-CG-CD2	-7.82	121.04	131.20
1	A	425	HIS	CB-CG-ND1	6.88	133.02	122.70
1	A	447	THR	CA-CB-OG1	-6.14	100.39	109.60
1	A	429	SER	N-CA-C	6.04	117.53	111.07
1	A	323	HIS	CA-CB-CG	-5.61	108.19	113.80
1	A	441	ASP	CA-CB-CG	5.13	117.73	112.60

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	2130	0	2171	21	0
2	B	128	0	140	5	0
3	A	7	0	10	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	10	0	14	4	0
5	A	4	0	6	0	0
6	A	189	0	0	6	0
6	B	16	0	0	0	0
All	All	2484	0	2341	23	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 (23) 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:383:ASP:OD2	1:A:425:HIS:HE1	1.71	0.73
1:A:227:PRO:O	1:A:232:LYS:NZ	2.21	0.72
1:A:224:LYS:NZ	4:A:502:PGE:H4	2.08	0.69
1:A:427:GLU:CD	1:A:427:GLU:H	2.01	0.69
1:A:425:HIS:HD2	6:A:611:HOH:O	1.78	0.66
1:A:312:ASN:HD21	2:B:5:ASN:CB	2.11	0.64
1:A:418:GLU:HG3	6:A:687:HOH:O	1.98	0.63
1:A:312:ASN:HD21	2:B:5:ASN:CG	2.09	0.61
3:A:501:PEG:H32	6:A:766:HOH:O	2.01	0.61
1:A:224:LYS:HZ2	4:A:502:PGE:H4	1.65	0.59
1:A:412[A]:ASN:HB2	6:A:712:HOH:O	2.08	0.53
1:A:229:THR:H	1:A:232:LYS:HE2	1.75	0.50
1:A:412[B]:ASN:HB3	6:A:712:HOH:O	2.13	0.49
1:A:224:LYS:HZ2	4:A:502:PGE:C4	2.27	0.48
1:A:224:LYS:HZ3	4:A:502:PGE:H2	1.80	0.46
1:A:226:PHE:CG	1:A:329:MET:HE1	2.54	0.43
1:A:312:ASN:ND2	2:B:5:ASN:CB	2.79	0.43
1:A:216[A]:LYS:NZ	6:A:607:HOH:O	2.49	0.42
2:B:5:ASN:HB2	2:B:8:AC5:HB12	2.02	0.41
1:A:245:SER:N	1:A:246:PRO:HD2	2.36	0.41
1:A:279:ILE:HD13	1:A:360:PHE:CZ	2.56	0.41
1:A:312:ASN:ND2	2:B:5:ASN:HB3	2.36	0.41
1:A:465:LEU:HD23	1:A:470:GLN:HG3	2.03	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	261/275 (95%)	257 (98%)	4 (2%)	0	100	100
2	B	12/25 (48%)	11 (92%)	1 (8%)	0	100	100
All	All	273/300 (91%)	268 (98%)	5 (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	239/248 (96%)	236 (99%)	3 (1%)	65	35
2	B	12/17 (71%)	12 (100%)	0	100	100
All	All	251/265 (95%)	248 (99%)	3 (1%)	67	38

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	260	ASP
1	A	427	GLU
1	A	460	GLU

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

Mol	Chain	Res	Type
1	A	294	GLN
1	A	312	ASN
1	A	425	HIS
1	A	430	GLN
1	A	470	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

3 non-standard protein/DNA/RNA residues 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	AC5	B	8	2	6,8,9	0.86	0	5,11,13	1.05	0
2	AC5	B	19	2	6,8,9	0.65	0	5,11,13	0.88	0
2	AC5	B	12	2	6,8,9	0.57	0	5,11,13	0.42	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	AC5	B	8	2	-	0/2/12/15	0/1/1/1
2	AC5	B	19	2	-	2/2/12/15	0/1/1/1
2	AC5	B	12	2	-	0/2/12/15	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	19	AC5	O-C-CA-CB1
2	B	19	AC5	O-C-CA-CB2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	8	AC5	1	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

3 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	$\# Z  > 2$
4	PGE	A	502	-	9,9,9	0.27	0	8,8,8	0.46	0
5	EDO	A	503	-	3,3,3	0.20	0	2,2,2	0.39	0
3	PEG	A	501	-	6,6,6	0.28	0	5,5,5	0.47	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
4	PGE	A	502	-	-	5/7/7/7	-
5	EDO	A	503	-	-	0/1/1/1	-
3	PEG	A	501	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	501	PEG	C1-C2-O2-C3
4	A	502	PGE	O2-C3-C4-O3
4	A	502	PGE	O3-C5-C6-O4
4	A	502	PGE	C4-C3-O2-C2
4	A	502	PGE	O1-C1-C2-O2
4	A	502	PGE	C3-C4-O3-C5
3	A	501	PEG	O2-C3-C4-O4

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	502	PGE	4	0
3	A	501	PEG	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	261/275 (94%)	0.42	32 (12%) <b>9</b> <b>8</b>	5, 19, 52, 94	6 (2%)
2	B	14/25 (56%)	0.61	2 (14%) <b>7</b> <b>6</b>	12, 18, 30, 39	0
All	All	275/300 (91%)	0.43	34 (12%) <b>9</b> <b>8</b>	5, 19, 52, 94	6 (2%)

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	477	TYR	5.4
1	A	363	PHE	5.3
1	A	455	VAL	4.8
1	A	461	THR	4.7
1	A	462	ASP	4.1
1	A	459	THR	4.0
1	A	456	ILE	3.6
1	A	242	THR	3.5
1	A	463	MET	3.4
1	A	262	ILE	3.4
1	A	260	ASP	3.4
2	B	5	ASN	3.3
1	A	287	PHE	3.3
1	A	452	LEU	3.1
1	A	458	LYS	3.0
1	A	429	SER	2.8
1	A	285	CYS	2.8
1	A	282	PHE	2.8
1	A	206	PRO	2.8
1	A	476	LEU	2.7
1	A	450	VAL	2.6
1	A	245	SER	2.6
1	A	272	GLU	2.6
2	B	21	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	457	LYS	2.5
1	A	460	GLU	2.5
1	A	464	SER	2.2
1	A	240	LYS	2.2
1	A	465	LEU	2.2
1	A	451	GLN	2.2
1	A	259	GLU	2.2
1	A	327	TYR	2.2
1	A	453	LEU	2.1
1	A	454	GLN	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [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<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	B-factors(Å <sup>2</sup> )	Q<0.9
2	AC5	B	8	8/9	0.97	0.06	17,18,19,20	0
2	AC5	B	12	8/9	0.98	0.07	15,16,19,20	0
2	AC5	B	19	8/9	0.98	0.05	12,13,14,15	0

## 6.3 Carbohydrates [i](#)

There are no oligosaccharides 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<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	B-factors(Å <sup>2</sup> )	Q<0.9
5	EDO	A	503	4/4	0.85	0.14	36,40,42,44	0
4	PGE	A	502	10/10	0.86	0.14	32,38,42,44	0
3	PEG	A	501	7/7	0.87	0.14	30,36,39,49	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.