



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:06 PM GMT

PDB ID : 4QXS  
Title : Crystal structure of human FPPS in complex with WC01088  
Authors : Park, J.; Zielinski, M.; Weiling, C.; Tsantrizos, Y.S.; Berghuis, A.M.  
Deposited on : 2014-07-21  
Resolution : 1.90 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 : rb-20026688  
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

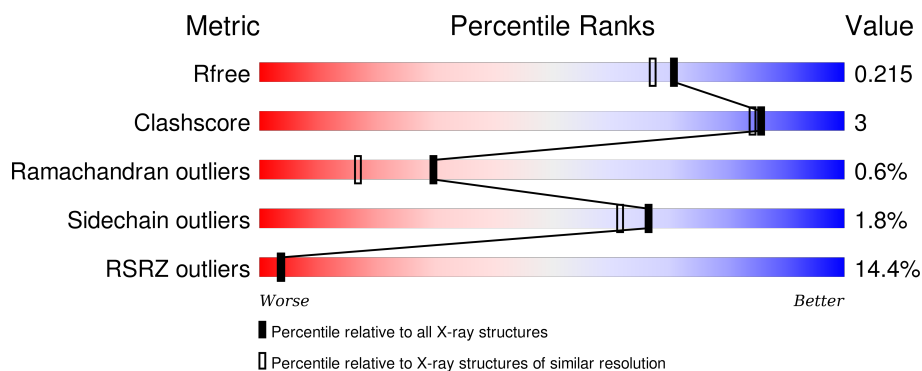
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*


The reported resolution of this entry is 1.90 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	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (1.90-1.90)

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	F	375	

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 2866 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 Farnesyl pyrophosphate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	F	341	Total	C	N	O	S	0	0	0
			2674	1729	435	499	11			

There are 22 discrepancies between the modelled and reference sequences:

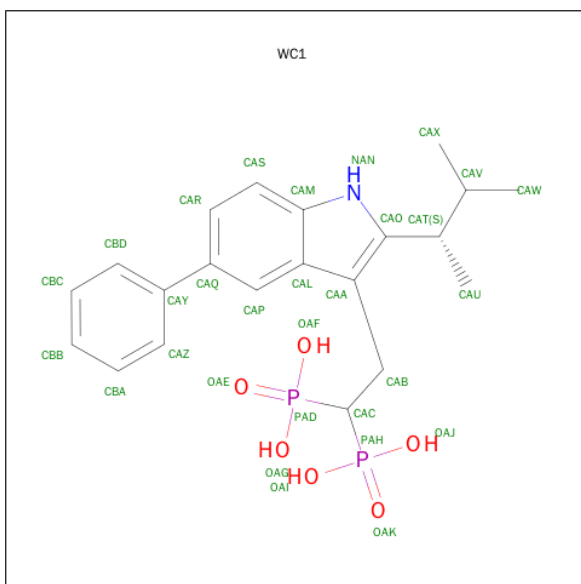
Chain	Residue	Modelled	Actual	Comment	Reference
F	-21	MET	-	EXPRESSION TAG	UNP P14324
F	-20	GLY	-	EXPRESSION TAG	UNP P14324
F	-19	SER	-	EXPRESSION TAG	UNP P14324
F	-18	SER	-	EXPRESSION TAG	UNP P14324
F	-17	HIS	-	EXPRESSION TAG	UNP P14324
F	-16	HIS	-	EXPRESSION TAG	UNP P14324
F	-15	HIS	-	EXPRESSION TAG	UNP P14324
F	-14	HIS	-	EXPRESSION TAG	UNP P14324
F	-13	HIS	-	EXPRESSION TAG	UNP P14324
F	-12	HIS	-	EXPRESSION TAG	UNP P14324
F	-11	SER	-	EXPRESSION TAG	UNP P14324
F	-10	SER	-	EXPRESSION TAG	UNP P14324
F	-9	GLY	-	EXPRESSION TAG	UNP P14324
F	-8	ARG	-	EXPRESSION TAG	UNP P14324
F	-7	GLU	-	EXPRESSION TAG	UNP P14324
F	-6	ASN	-	EXPRESSION TAG	UNP P14324
F	-5	LEU	-	EXPRESSION TAG	UNP P14324
F	-4	TYR	-	EXPRESSION TAG	UNP P14324
F	-3	PHE	-	EXPRESSION TAG	UNP P14324
F	-2	GLN	-	EXPRESSION TAG	UNP P14324
F	-1	GLY	-	EXPRESSION TAG	UNP P14324
F	0	HIS	-	EXPRESSION TAG	UNP P14324

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	F	1	Total	O	P	0	0
			5	4	1		
2	F	1	Total	O	P	0	0
			5	4	1		

- Molecule 3 is (2-{2-[(2S)-3-METHYLBUTAN-2-YL]-5-PHENYL-1H-INDOL-3-YL}ETHAN E-1,1-DIYL)BIS(PHOSPHONIC ACID) (three-letter code: WC1) (formula: C<sub>21</sub>H<sub>27</sub>NO<sub>6</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	F	1	Total	C	N	O	P	0
			30	21	1	6	2	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



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

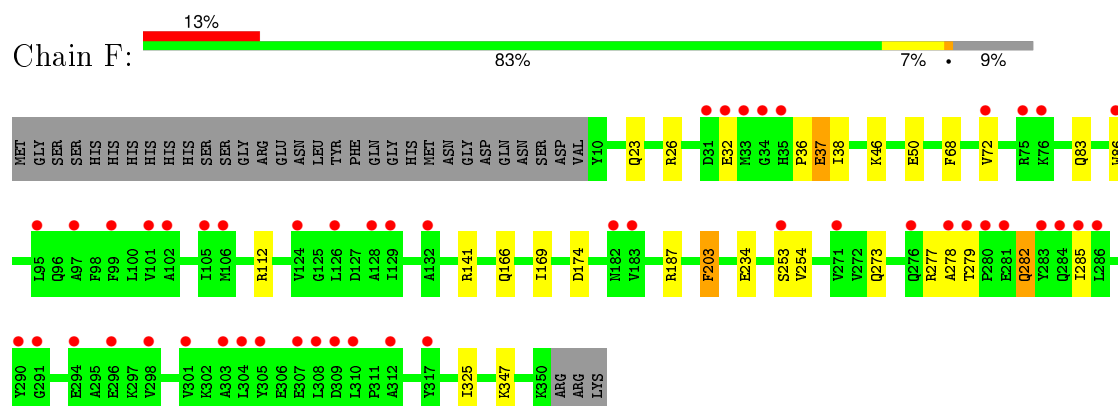
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	F	144	Total	O	0	2
			146	146		

### 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 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 ( $RSRZ > 2$ ). 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: Farnesyl pyrophosphate synthase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	110.65Å 110.65Å 77.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	55.21 – 1.90 55.21 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.3 (55.21-1.90) 99.3 (55.21-1.90)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.79 (at 1.90Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, $R_{free}$	0.170 , 0.206 0.178 , 0.215	Depositor DCC
$R_{free}$ test set	2023 reflections (5.56%)	DCC
Wilson B-factor (Å <sup>2</sup> )	40.8	Xtriage
Anisotropy	0.222	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 59.2	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 38378 reflections	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	2866	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.78% 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 ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: WC1, GOL, PO4

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	F	0.98	2/2732 (0.1%)	0.95	8/3715 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	203	PHE	CG-CD2	5.83	1.47	1.38
1	F	86	TRP	CB-CG	-5.65	1.40	1.50

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	141	ARG	NE-CZ-NH1	11.06	125.83	120.30
1	F	141	ARG	NE-CZ-NH2	-8.36	116.12	120.30
1	F	26	ARG	NE-CZ-NH2	7.77	124.19	120.30
1	F	112	ARG	NE-CZ-NH2	6.34	123.47	120.30
1	F	347	LYS	CD-CE-NZ	6.11	125.76	111.70
1	F	26	ARG	NE-CZ-NH1	-5.49	117.56	120.30
1	F	187	ARG	NE-CZ-NH2	5.33	122.97	120.30
1	F	174	ASP	CB-CG-OD1	5.15	122.93	118.30

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	F	2674	0	2592	13	0
2	F	10	0	0	1	0
3	F	30	0	26	1	0
4	F	6	0	8	0	0
5	F	146	0	0	1	0
All	All	2866	0	2626	15	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 3.

All (15) 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:F:68:PHE:CE1	1:F:72:VAL:HG21	2.30	0.66
1:F:273:GLN:OE1	1:F:277:ARG:NH1	2.33	0.60
1:F:278:ALA:HB1	1:F:282:GLN:HB2	1.86	0.56
1:F:282:GLN:HA	1:F:285:ILE:HD12	1.89	0.53
1:F:23:GLN:HE22	1:F:83:GLN:NE2	2.07	0.52
1:F:279:THR:H	1:F:282:GLN:HG3	1.76	0.49
2:F:401:PO4:O1	2:F:402:PO4:O2	2.33	0.46
1:F:23:GLN:HE22	1:F:83:GLN:HE21	1.63	0.46
1:F:166:GLN:NE2	1:F:203:PHE:CE1	2.84	0.45
1:F:37:GLU:HA	5:F:552:HOH:O	2.17	0.44
1:F:37:GLU:HG3	1:F:38:ILE:HG23	2.00	0.44
3:F:403:WC1:H17	3:F:403:WC1:H9	1.75	0.44
1:F:46:LYS:O	1:F:50:GLU:HG2	2.18	0.44
1:F:279:THR:OG1	1:F:282:GLN:HG2	2.19	0.42
1:F:234:GLU:HG3	1:F:325:ILE:HD11	2.04	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	F	339/375 (90%)	332 (98%)	5 (2%)	2 (1%)	30	17

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	37	GLU
1	F	36	PRO

### 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	F	272/322 (84%)	267 (98%)	5 (2%)	66	61

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	32	GLU
1	F	169	ILE
1	F	253	SER
1	F	254	VAL
1	F	282	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	F	19	GLN
1	F	83	GLN
1	F	166	GLN
1	F	282	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 ⓘ

4 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	$\# Z  > 2$
2	PO4	F	401	-	4,4,4	0.83	0	6,6,6	0.28	0
2	PO4	F	402	-	4,4,4	2.11	1 (25%)	6,6,6	0.31	0
3	WC1	F	403	-	31,32,32	2.85	16 (51%)	37,49,49	1.80	5 (13%)
4	GOL	F	404	-	5,5,5	0.32	0	5,5,5	1.29	1 (20%)

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	PO4	F	401	-	-	0/0/0/0	0/0/0/0
2	PO4	F	402	-	-	0/0/0/0	0/0/0/0
3	WC1	F	403	-	-	0/24/28/28	0/3/3/3
4	GOL	F	404	-	-	0/4/4/4	0/0/0/0

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	403	WC1	PAH-OAJ	-6.11	1.44	1.54
3	F	403	WC1	PAH-OAK	-4.56	1.41	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	403	WC1	CAP-CAL	-3.98	1.34	1.42
3	F	403	WC1	CAS-CAM	-3.89	1.34	1.41
3	F	403	WC1	CAT-CAV	-3.32	1.47	1.54
3	F	403	WC1	PAD-OAG	-2.92	1.50	1.54
3	F	403	WC1	CAQ-CAY	-2.47	1.42	1.49
3	F	403	WC1	PAD-OAF	-2.45	1.50	1.54
3	F	403	WC1	CAL-CAM	-2.37	1.36	1.42
3	F	403	WC1	CAA-CAO	-2.21	1.34	1.38
3	F	403	WC1	PAH-CAC	2.02	1.84	1.81
3	F	403	WC1	CAO-CAT	2.48	1.55	1.51
3	F	403	WC1	PAD-CAC	3.73	1.87	1.81
3	F	403	WC1	CAB-CAA	3.89	1.56	1.51
2	F	402	PO4	P-O2	4.00	1.67	1.53
3	F	403	WC1	PAD-OAE	5.04	1.59	1.49
3	F	403	WC1	PAH-OAI	6.32	1.65	1.54

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	403	WC1	CAP-CAL-CAM	-6.49	117.78	120.34
4	F	404	GOL	O2-C2-C1	-2.47	97.32	108.65
3	F	403	WC1	OAI-PAH-OAJ	-2.00	101.55	107.57
3	F	403	WC1	CBA-CAZ-CAY	2.19	123.45	120.56
3	F	403	WC1	OAF-PAD-OAG	4.42	120.88	107.57
3	F	403	WC1	OAJ-PAH-OAK	4.69	125.96	113.49

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	401	PO4	1	0
2	F	402	PO4	1	0
3	F	403	WC1	1	0

## 5.7 Other polymers [i](#)

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	F	341/375 (90%)	0.74	49 (14%) 3 4	31, 56, 106, 130	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	33	MET	6.2
1	F	301	VAL	5.7
1	F	298	VAL	5.4
1	F	283	TYR	4.5
1	F	285	ILE	4.5
1	F	31	ASP	4.1
1	F	278	ALA	4.1
1	F	253	SER	4.0
1	F	101	VAL	3.9
1	F	291	GLY	3.8
1	F	105	ILE	3.6
1	F	32	GLU	3.5
1	F	286	LEU	3.5
1	F	34	GLY	3.4
1	F	308	LEU	3.4
1	F	35	HIS	3.3
1	F	279	THR	3.3
1	F	182	ASN	3.3
1	F	86	TRP	3.3
1	F	126	LEU	3.2
1	F	309	ASP	3.1
1	F	72	VAL	3.1
1	F	129	ILE	3.1
1	F	290	TYR	3.1
1	F	284	GLN	3.1
1	F	303	ALA	3.0
1	F	102	ALA	3.0

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Mol	Chain	Res	Type	RSRZ
1	F	310	LEU	3.0
1	F	280	PRO	2.9
1	F	183	VAL	2.9
1	F	75	ARG	2.9
1	F	307	GLU	2.7
1	F	128	ALA	2.6
1	F	304	LEU	2.5
1	F	99	PHE	2.5
1	F	276	GLN	2.5
1	F	106	MET	2.5
1	F	296	GLU	2.3
1	F	312	ALA	2.2
1	F	97	ALA	2.2
1	F	317	TYR	2.2
1	F	76	LYS	2.2
1	F	95	LEU	2.1
1	F	294	GLU	2.1
1	F	305	TYR	2.1
1	F	132	ALA	2.1
1	F	271	VAL	2.0
1	F	281	GLU	2.0
1	F	124	VAL	2.0

## 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 carbohydrates 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. 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
4	GOL	F	404	6/6	0.94	0.15	1.77	51,59,65,68	0
3	WC1	F	403	30/30	0.98	0.08	-1.27	41,48,61,75	0
2	PO4	F	401	5/5	0.99	0.07	-1.82	48,50,51,54	0
2	PO4	F	402	5/5	0.95	0.10	-	49,60,63,67	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.