



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 1, 2023 – 05:28 PM EDT

PDB ID : 3S3F  
Title : Crystal Structure of the catalytic domain of PTP10D from *Drosophila melanogaster* with a small molecule inhibitor Vanadate  
Authors : Madan, L.L.; Gopal, B.  
Deposited on : 2011-05-18  
Resolution : 2.70 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>.

---

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
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) : 2.36

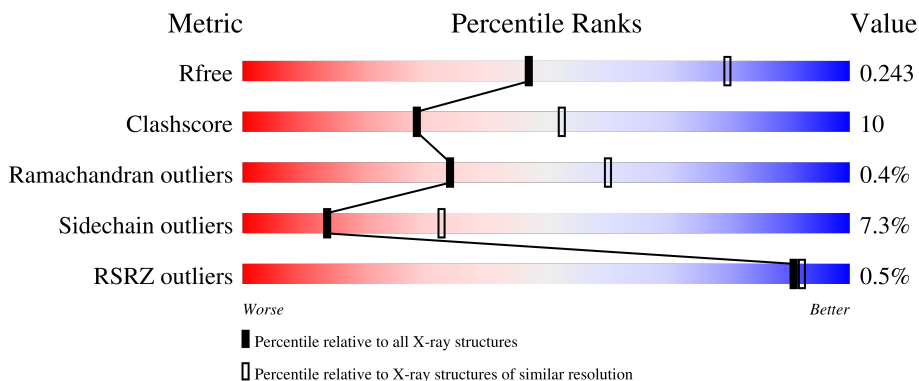
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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))
$R_{free}$	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	307	 77% 15% • 7%
1	B	307	 % 69% 21% •• 7%

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	VO4	B	308	-	-	-	X

## 2 Entry composition i

There are 6 unique types of molecules in this entry. The entry contains 4803 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 Tyrosine-protein phosphatase 10D.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	287	2350	1493	422	418	17	0	0	0
1	B	285	2334	1482	417	418	17	0	0	0

There are 46 discrepancies between the modelled and reference sequences:

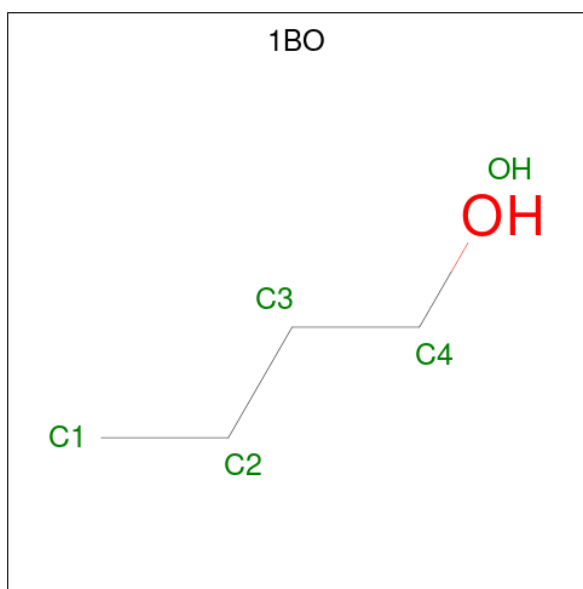
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP P35992
A	2	GLY	-	expression tag	UNP P35992
A	3	SER	-	expression tag	UNP P35992
A	4	SER	-	expression tag	UNP P35992
A	5	HIS	-	expression tag	UNP P35992
A	6	HIS	-	expression tag	UNP P35992
A	7	HIS	-	expression tag	UNP P35992
A	8	HIS	-	expression tag	UNP P35992
A	9	HIS	-	expression tag	UNP P35992
A	10	HIS	-	expression tag	UNP P35992
A	11	SER	-	expression tag	UNP P35992
A	12	SER	-	expression tag	UNP P35992
A	13	GLY	-	expression tag	UNP P35992
A	14	LEU	-	expression tag	UNP P35992
A	15	VAL	-	expression tag	UNP P35992
A	16	PRO	-	expression tag	UNP P35992
A	17	ARG	-	expression tag	UNP P35992
A	18	GLY	-	expression tag	UNP P35992
A	19	SER	-	expression tag	UNP P35992
A	20	HIS	-	expression tag	UNP P35992
A	21	MET	-	expression tag	UNP P35992
A	22	ALA	-	expression tag	UNP P35992
A	23	SER	-	expression tag	UNP P35992
B	1	MET	-	expression tag	UNP P35992
B	2	GLY	-	expression tag	UNP P35992

*Continued on next page...*

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	3	SER	-	expression tag	UNP P35992
B	4	SER	-	expression tag	UNP P35992
B	5	HIS	-	expression tag	UNP P35992
B	6	HIS	-	expression tag	UNP P35992
B	7	HIS	-	expression tag	UNP P35992
B	8	HIS	-	expression tag	UNP P35992
B	9	HIS	-	expression tag	UNP P35992
B	10	HIS	-	expression tag	UNP P35992
B	11	SER	-	expression tag	UNP P35992
B	12	SER	-	expression tag	UNP P35992
B	13	GLY	-	expression tag	UNP P35992
B	14	LEU	-	expression tag	UNP P35992
B	15	VAL	-	expression tag	UNP P35992
B	16	PRO	-	expression tag	UNP P35992
B	17	ARG	-	expression tag	UNP P35992
B	18	GLY	-	expression tag	UNP P35992
B	19	SER	-	expression tag	UNP P35992
B	20	HIS	-	expression tag	UNP P35992
B	21	MET	-	expression tag	UNP P35992
B	22	ALA	-	expression tag	UNP P35992
B	23	SER	-	expression tag	UNP P35992

- Molecule 2 is 1-BUTANOL (three-letter code: 1BO) (formula: C<sub>4</sub>H<sub>10</sub>O).



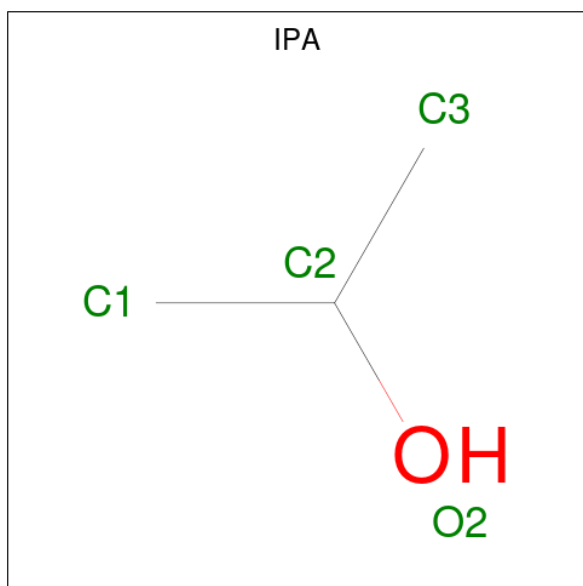
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	5	4	1	0	0

Continued on next page...

Continued from previous page...

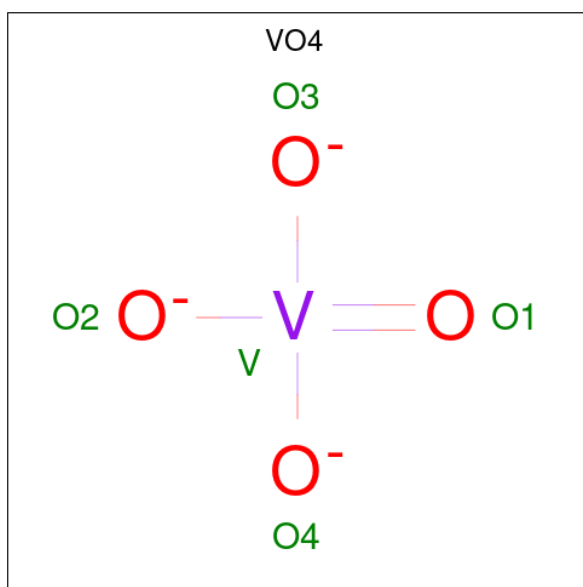
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	B	1	5	4	1	0	0

- Molecule 3 is ISOPROPYL ALCOHOL (three-letter code: IPA) (formula: C<sub>3</sub>H<sub>8</sub>O).



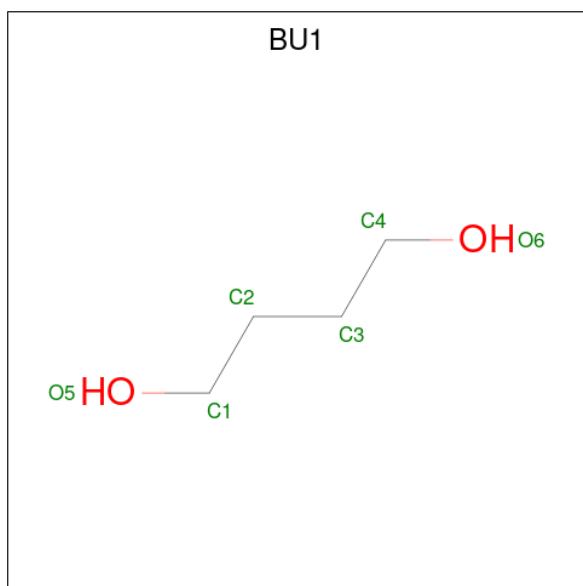
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	4	3	1	0	0
3	A	1	4	3	1	0	0

- Molecule 4 is VANADATE ION (three-letter code: VO<sub>4</sub>) (formula: O<sub>4</sub>V).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	V		
4	B	1	5	4	1	0	0

- Molecule 5 is 1,4-BUTANEDIOL (three-letter code: BU1) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
5	B	1	6	4	2	0	0

- Molecule 6 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
6	A	43	Total 43	O 43	0	0
6	B	47	Total 47	O 47	0	0

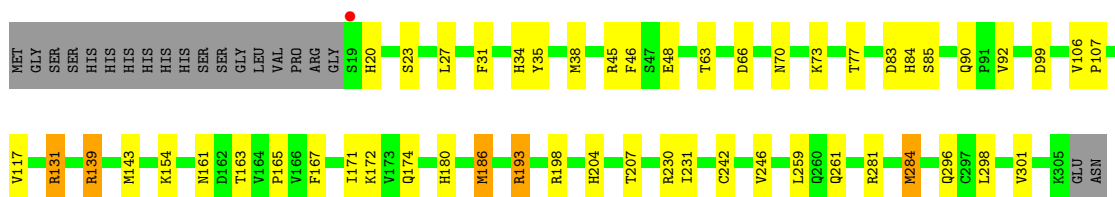


### 3 Residue-property plots [i](#)

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.

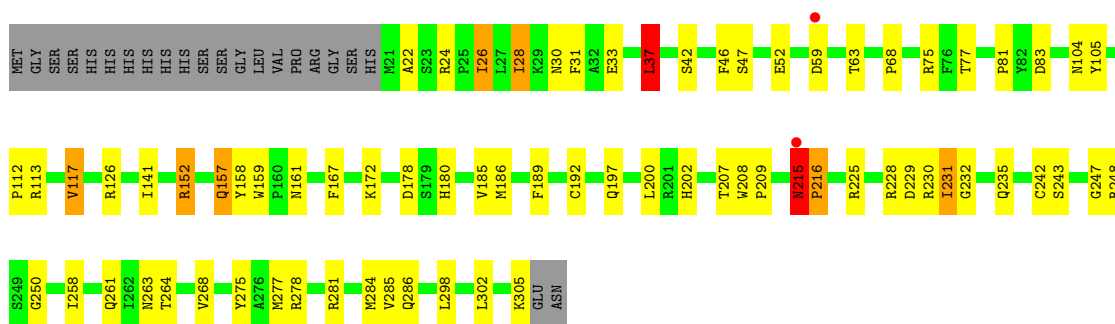
- Molecule 1: Tyrosine-protein phosphatase 10D

Chain A: 



- Molecule 1: Tyrosine-protein phosphatase 10D

Chain B: 



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	103.07Å 103.07Å 173.40Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	39.68 – 2.70 38.99 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.8 (39.68-2.70) 99.8 (38.99-2.70)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.27 (at 2.69Å)	Xtrriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.238 , 0.272 0.209 , 0.243	Depositor DCC
$R_{free}$ test set	1514 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	28.8	Xtrriage
Anisotropy	0.103	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 40.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.027 for -h,-k,l	Xtrriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	4803	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	37.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.36% 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: VO4, BU1, 1BO, IPA

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	0.59	0/2417	0.62	0/3276
1	B	0.58	1/2400 (0.0%)	0.64	1/3258 (0.0%)
All	All	0.59	1/4817 (0.0%)	0.63	1/6534 (0.0%)

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	B	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	242	CYS	CB-SG	-5.93	1.72	1.81

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	37	LEU	CA-CB-CG	5.40	127.72	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	215	ASN	Peptide

## 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	2350	0	2242	30	0
1	B	2334	0	2219	60	0
2	A	5	0	10	0	0
2	B	5	0	10	1	0
3	A	8	0	16	1	0
4	B	5	0	0	1	0
5	B	6	0	10	1	0
6	A	43	0	0	0	0
6	B	47	0	0	2	0
All	All	4803	0	4507	89	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 10.

All (89) 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:246:VAL:O	1:A:284:MET:O	1.53	1.25
1:A:246:VAL:HA	1:A:284:MET:CE	2.03	0.89
1:A:246:VAL:HA	1:A:284:MET:HE3	1.53	0.87
1:B:152:ARG:HH11	1:B:152:ARG:HG3	1.47	0.79
1:B:112:PRO:HD3	5:B:309:BU1:H12	1.64	0.78
1:B:104:ASN:HD22	1:B:281:ARG:HH11	1.32	0.77
1:A:284:MET:HE3	1:A:284:MET:HA	1.68	0.75
1:A:171:ILE:HD13	1:A:193:ARG:HG3	1.74	0.69
1:B:104:ASN:ND2	1:B:281:ARG:HH11	1.94	0.66
1:A:284:MET:CE	1:A:284:MET:HA	2.26	0.66
1:A:117:VAL:HG22	1:A:281:ARG:HD3	1.79	0.64
1:A:63:THR:HB	1:A:83:ASP:OD2	1.97	0.64
1:A:171:ILE:CD1	1:A:193:ARG:HG3	2.31	0.60
1:B:26:ILE:HD11	1:B:31:PHE:HA	1.86	0.57
1:B:225:ARG:HH21	1:B:305:LYS:NZ	2.00	0.57
1:B:126:ARG:HD3	1:B:158:TYR:HA	1.87	0.57
1:A:246:VAL:HA	1:A:284:MET:HE1	1.82	0.57
1:A:186:MET:HE1	1:A:230:ARG:HG2	1.87	0.56

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:152:ARG:HH11	1:B:152:ARG:CG	2.18	0.56
1:A:70:ASN:HA	1:A:73:LYS:HD2	1.86	0.56
1:B:28:ILE:HD13	1:B:302:LEU:HD22	1.88	0.56
1:B:243:SER:HB3	4:B:308:VO4:O4	2.06	0.56
1:A:180:HIS:H	3:A:310:IPA:H11	1.71	0.56
1:B:277:MET:CE	1:B:284:MET:HB3	2.36	0.55
1:B:250:GLY:HA2	1:B:277:MET:HE1	1.88	0.55
1:B:277:MET:HE3	1:B:284:MET:HB3	1.87	0.54
1:B:26:ILE:HD12	1:B:31:PHE:CD1	2.42	0.54
1:B:117:VAL:CG2	1:B:281:ARG:HD3	2.37	0.54
1:B:231:ILE:HG22	1:B:232:GLY:N	2.21	0.54
1:B:26:ILE:HD12	1:B:31:PHE:HD1	1.72	0.54
1:B:152:ARG:HG3	1:B:152:ARG:NH1	2.21	0.54
1:B:189:PHE:HE2	1:B:202:HIS:HB2	1.73	0.54
1:A:90:GLN:O	1:A:131:ARG:NH2	2.41	0.53
1:B:178:ASP:OD2	1:B:180:HIS:CE1	2.62	0.53
1:B:157:GLN:NE2	1:B:159:TRP:CE2	2.77	0.53
1:B:261:GLN:NE2	6:B:345:HOH:O	2.40	0.53
1:B:117:VAL:HG22	1:B:281:ARG:HD3	1.91	0.52
1:B:247:GLY:HA2	1:B:286:GLN:H	1.75	0.52
1:A:77:THR:HG23	1:B:68:PRO:HG3	1.92	0.51
1:A:31:PHE:CZ	1:A:298:LEU:HD23	2.45	0.51
1:A:84:HIS:CE1	1:A:85:SER:HB2	2.45	0.51
1:A:246:VAL:CA	1:A:284:MET:HE3	2.35	0.51
1:A:34:HIS:O	1:A:38:MET:HG2	2.12	0.50
1:B:225:ARG:HH21	1:B:305:LYS:HZ2	1.57	0.50
1:A:106:VAL:CG2	1:A:117:VAL:HG13	2.43	0.49
1:B:215:ASN:ND2	1:B:216:PRO:HD3	2.27	0.49
1:B:28:ILE:HD12	1:B:28:ILE:O	2.13	0.48
1:B:30:ASN:N	1:B:30:ASN:ND2	2.61	0.48
1:B:24:ARG:NH1	1:B:52:GLU:OE2	2.46	0.48
1:B:180:HIS:HD2	1:B:185:VAL:HG22	1.77	0.47
1:B:152:ARG:CG	1:B:152:ARG:NH1	2.76	0.47
1:B:81:PRO:HA	1:B:104:ASN:HD21	1.79	0.47
1:A:38:MET:HA	1:A:45:ARG:HB2	1.95	0.47
1:B:192:CYS:SG	1:B:197:GLN:HG2	2.54	0.47
1:B:250:GLY:HA2	1:B:284:MET:HE3	1.97	0.47
1:A:35:TYR:OH	1:A:296:GLN:HG3	2.16	0.46
1:A:259:LEU:HD21	1:A:301:VAL:HG21	1.97	0.46
1:B:247:GLY:N	1:B:284:MET:O	2.39	0.46
1:A:99:ASP:OD1	1:A:99:ASP:C	2.55	0.46

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:231:ILE:HD12	1:A:231:ILE:HA	1.83	0.45
1:B:278:ARG:NH2	1:B:285:VAL:O	2.45	0.45
1:B:30:ASN:N	1:B:30:ASN:HD22	2.13	0.45
1:B:172:LYS:HB3	1:B:192:CYS:HB2	1.99	0.45
1:B:26:ILE:C	1:B:26:ILE:HD13	2.36	0.45
1:B:141:ILE:HD12	1:B:200:LEU:HD21	1.98	0.45
1:B:180:HIS:CD2	1:B:185:VAL:HG22	2.52	0.44
1:B:105:TYR:HB3	1:B:113:ARG:HG2	2.00	0.44
1:B:63:THR:HB	1:B:83:ASP:OD2	2.18	0.44
1:A:139:ARG:CZ	1:A:198:ARG:HG2	2.49	0.43
1:A:143:MET:HG2	1:A:204:HIS:CD2	2.54	0.43
1:B:208:TRP:CZ2	1:B:248:ARG:HG2	2.53	0.43
1:B:228:ARG:HD3	1:B:228:ARG:HA	1.79	0.43
1:B:33:GLU:O	1:B:37:LEU:HD22	2.18	0.42
1:A:106:VAL:HG13	1:A:107:PRO:HD2	2.02	0.42
1:A:165:PRO:HB3	1:A:174:GLN:HB2	2.02	0.42
1:B:208:TRP:CD1	1:B:209:PRO:HD2	2.54	0.41
1:B:22:ALA:HA	1:B:275:TYR:CD1	2.55	0.41
1:B:189:PHE:HE2	1:B:202:HIS:CB	2.34	0.41
1:B:225:ARG:HE	1:B:305:LYS:NZ	2.17	0.41
1:B:263:ASN:HA	2:B:310:1BO:H22	2.01	0.41
1:B:250:GLY:CA	1:B:277:MET:HE1	2.50	0.41
1:B:231:ILE:HG23	1:B:235:GLN:HB3	2.02	0.41
1:B:258:ILE:HD12	1:B:298:LEU:HD22	2.02	0.41
1:B:261:GLN:NE2	6:B:344:HOH:O	2.52	0.41
1:B:178:ASP:OD2	1:B:180:HIS:HE1	2.03	0.41
1:B:75:ARG:HD2	1:B:243:SER:O	2.20	0.40
1:A:167:PHE:CZ	1:A:172:LYS:HD2	2.56	0.40
1:B:59:ASP:OD2	1:B:59:ASP:N	2.52	0.40
1:B:167:PHE:CE1	1:B:172:LYS:HB2	2.57	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	285/307 (93%)	276 (97%)	9 (3%)	0	100	100
1	B	283/307 (92%)	267 (94%)	14 (5%)	2 (1%)	22	46
All	All	568/614 (92%)	543 (96%)	23 (4%)	2 (0%)	34	60

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	216	PRO
1	B	215	ASN

### 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	Percentiles	
1	A	253/278 (91%)	235 (93%)	18 (7%)	14	34
1	B	252/278 (91%)	233 (92%)	19 (8%)	13	31
All	All	505/556 (91%)	468 (93%)	37 (7%)	14	33

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	HIS
1	A	23	SER
1	A	27	LEU
1	A	46	PHE
1	A	48	GLU
1	A	66	ASP
1	A	92	VAL
1	A	131	ARG
1	A	139	ARG
1	A	154	LYS
1	A	161	ASN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	163	THR
1	A	186	MET
1	A	193	ARG
1	A	207	THR
1	A	242	CYS
1	A	261	GLN
1	A	284	MET
1	B	26	ILE
1	B	28	ILE
1	B	37	LEU
1	B	42	SER
1	B	46	PHE
1	B	47	SER
1	B	77	THR
1	B	117	VAL
1	B	152	ARG
1	B	157	GLN
1	B	161	ASN
1	B	186	MET
1	B	207	THR
1	B	215	ASN
1	B	229	ASP
1	B	230	ARG
1	B	231	ILE
1	B	264	THR
1	B	268	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	109	HIS
1	A	261	GLN
1	A	263	ASN
1	B	30	ASN
1	B	104	ASN
1	B	161	ASN
1	B	180	HIS
1	B	215	ASN
1	B	261	GLN
1	B	263	ASN



### 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](#)

6 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	1BO	A	308	-	4,4,4	0.46	0	3,3,3	0.28	0
2	1BO	B	310	-	4,4,4	0.42	0	3,3,3	0.31	0
3	IPA	A	310	-	3,3,3	0.63	0	3,3,3	0.18	0
4	VO4	B	308	-	1,4,4	4.89	1 (100%)	-		
5	BU1	B	309	-	5,5,5	0.54	0	4,4,4	0.20	0
3	IPA	A	309	-	3,3,3	0.68	0	3,3,3	0.19	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	1BO	A	308	-	-	1/2/2/2	-
2	1BO	B	310	-	-	2/2/2/2	-
5	BU1	B	309	-	-	1/3/3/3	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	308	VO4	O1-V	4.89	1.91	1.63

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	308	1BO	C1-C2-C3-C4
2	B	310	1BO	C2-C3-C4-OH
2	B	310	1BO	C1-C2-C3-C4
5	B	309	BU1	O5-C1-C2-C3

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	310	1BO	1	0
3	A	310	IPA	1	0
4	B	308	VO4	1	0
5	B	309	BU1	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 [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<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	287/307 (93%)	-0.50	1 (0%) 94 95	17, 35, 59, 73	0
1	B	285/307 (92%)	-0.41	2 (0%) 87 89	17, 37, 68, 88	0
All	All	572/614 (93%)	-0.46	3 (0%) 91 92	17, 37, 63, 88	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	59	ASP	2.9
1	A	19	SER	2.5
1	B	215	ASN	2.4

### 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<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
4	VO4	B	308	5/5	0.60	0.41	125,125,125,125	0
2	1BO	B	310	5/5	0.69	0.26	69,69,69,70	0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	1BO	A	308	5/5	0.69	0.24	60,61,61,61	0
3	IPA	A	310	4/4	0.81	0.21	69,69,69,69	0
3	IPA	A	309	4/4	0.85	0.23	58,58,58,58	0
5	BU1	B	309	6/6	0.88	0.20	38,39,40,40	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.