Full wwPDB X-ray Structure Validation Report (i)

Oct 25, 2023 – 12:33 AM EDT

PDB ID	:	3DC8
Title	:	Crystal structure of dihydropyrimidinase from Sinorhizobium meliloti
Authors	:	Gavira, J.A.; Martinez-Rodriguez, S.
Deposited on	:	2008-06-03
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*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

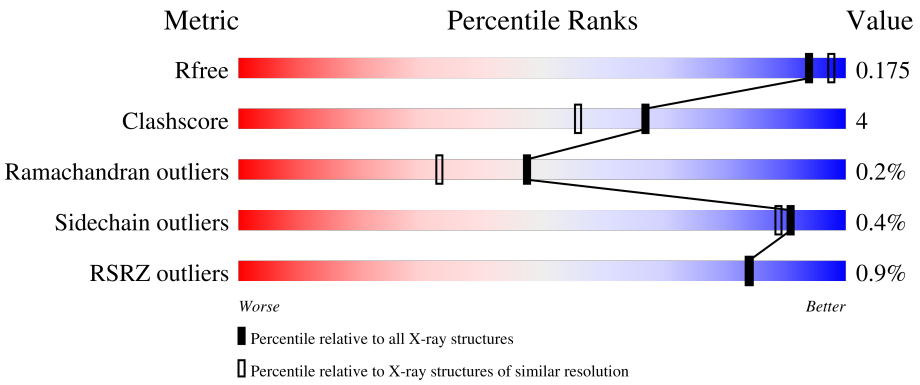
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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}	130704	2469 (1.86-1.86)
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)
RSRZ outliers	127900	2436 (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 of the lower bar indicate the fraction of residues that contain outliers for >=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 <=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	490	91% 8% •
1	B	490	?% 88% 8% •

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	GOL	A	505	-	X	-	-

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 8762 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 Dihydropyrimidinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	483	3708	2333	640	712	23	0	5	0
1	B	475	3680	2324	632	700	24	0	10	0

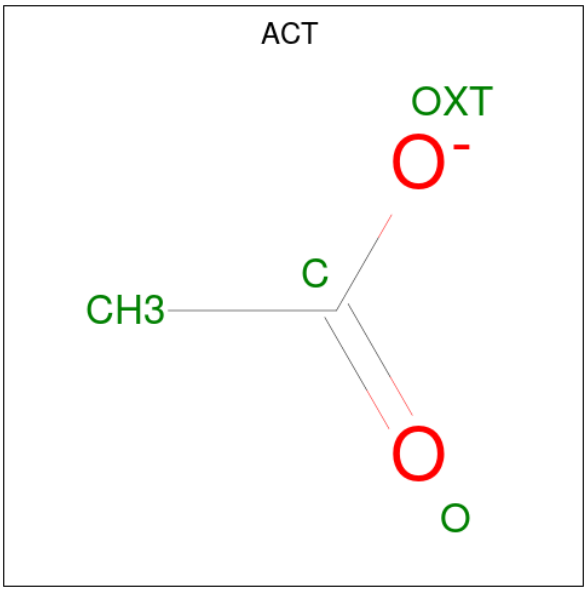
There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	485	HIS	-	expression tag	UNP Q0PQZ5
A	486	HIS	-	expression tag	UNP Q0PQZ5
A	487	HIS	-	expression tag	UNP Q0PQZ5
A	488	HIS	-	expression tag	UNP Q0PQZ5
A	489	HIS	-	expression tag	UNP Q0PQZ5
A	490	HIS	-	expression tag	UNP Q0PQZ5
B	485	HIS	-	expression tag	UNP Q0PQZ5
B	486	HIS	-	expression tag	UNP Q0PQZ5
B	487	HIS	-	expression tag	UNP Q0PQZ5
B	488	HIS	-	expression tag	UNP Q0PQZ5
B	489	HIS	-	expression tag	UNP Q0PQZ5
B	490	HIS	-	expression tag	UNP Q0PQZ5

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

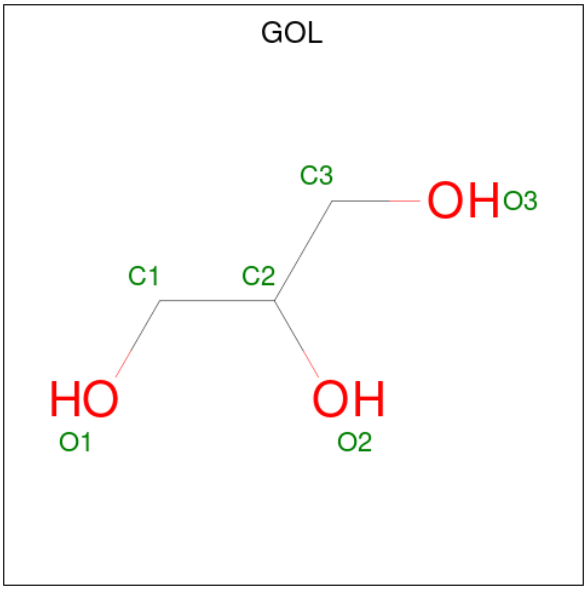
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
2	A	2	2	2	0	0
2	B	2	2	2	0	0

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



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

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



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

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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	669	669	669	0	0
			Total	O		
5	B	669	669	669	0	0

3 Residue-property plots (i)

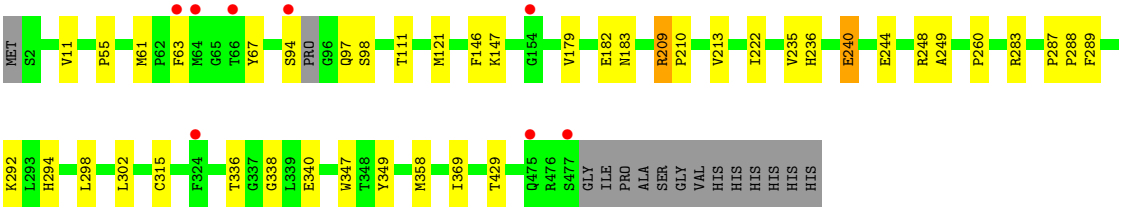
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Dihydropyrimidinase

Chain A:

• Molecule 1: Dihydropyrimidinase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	124.89Å 126.28Å 196.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.60 – 1.85 29.60 – 1.85	Depositor EDS
% Data completeness (in resolution range)	98.5 (29.60-1.85) 98.5 (29.60-1.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	2.92 (at 1.85Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.148 , 0.176 0.148 , 0.175	Depositor DCC
R_{free} test set	6524 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	13.6	Xtriage
Anisotropy	0.055	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 25.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.025 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	8762	wwPDB-VP
Average B, all atoms (Å^2)	5.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.55% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: ACT, GOL, KCX, ZN

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	1.33	9/3790 (0.2%)	0.87	4/5143 (0.1%)
1	B	1.35	10/3776 (0.3%)	0.89	3/5122 (0.1%)
All	All	1.34	19/7566 (0.3%)	0.88	7/10265 (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	1
1	B	0	1
All	All	0	2

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	209	ARG	CD-NE	-7.88	1.33	1.46
1	A	209	ARG	CD-NE	-7.31	1.34	1.46
1	B	240[A]	GLU	CG-CD	7.04	1.62	1.51
1	B	240[B]	GLU	CG-CD	7.04	1.62	1.51
1	A	320	GLU	CG-CD	6.68	1.61	1.51
1	A	212	GLU	CD-OE1	6.24	1.32	1.25
1	A	340	GLU	CD-OE1	6.16	1.32	1.25
1	B	248	ARG	CZ-NH1	5.87	1.40	1.33
1	B	336	THR	C-O	5.86	1.34	1.23
1	B	98	SER	CB-OG	-5.77	1.34	1.42
1	B	340	GLU	CD-OE1	5.63	1.31	1.25
1	A	244	GLU	CG-CD	5.52	1.60	1.51
1	A	212	GLU	CD-OE2	5.36	1.31	1.25
1	A	240[A]	GLU	CG-CD	5.23	1.59	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	240[B]	GLU	CG-CD	5.23	1.59	1.51
1	B	347	TRP	CE3-CZ3	5.23	1.47	1.38
1	A	349	TYR	CG-CD2	5.07	1.45	1.39
1	B	244	GLU	CG-CD	5.02	1.59	1.51
1	B	349	TYR	CE2-CZ	5.01	1.45	1.38

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	209	ARG	NE-CZ-NH1	18.15	129.38	120.30
1	B	209	ARG	NE-CZ-NH2	-17.01	111.80	120.30
1	A	209	ARG	NE-CZ-NH2	-16.69	111.95	120.30
1	A	209	ARG	NE-CZ-NH1	16.52	128.56	120.30
1	B	209	ARG	CD-NE-CZ	5.89	131.85	123.60
1	A	92	LEU	CA-CB-CG	5.73	128.48	115.30
1	A	209	ARG	CD-NE-CZ	5.49	131.28	123.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	93	PRO	Peptide
1	B	111	THR	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	3708	0	3626	19	0
1	B	3680	0	3619	36	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	4	0	3	0	0
3	B	4	0	3	0	0
4	A	18	0	22	3	0
4	B	6	0	8	0	0
5	A	669	0	0	1	2

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	669	0	0	2	2
All	All	8762	0	7281	58	2

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 4.

All (58) 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)
4:A:504:GOL:H32	4:A:505:GOL:H32	1.21	1.10
1:B:292:LYS:NZ	5:B:707:HOH:O	1.92	1.01
1:B:182:GLU:OE2	1:B:209:ARG:HD3	1.65	0.97
1:B:298:LEU:O	1:B:302[A]:LEU:HD13	1.65	0.95
1:A:182:GLU:OE2	1:A:209:ARG:HD3	1.74	0.87
4:A:504:GOL:H32	4:A:505:GOL:C3	2.06	0.82
1:B:61:MET:HE3	1:B:63:PHE:HB3	1.63	0.81
1:A:61:MET:HE2	1:A:315:CYS:SG	2.26	0.76
1:A:42:ASP:OD1	1:A:44[B]:THR:HG22	1.85	0.75
1:B:61:MET:HE3	1:B:63:PHE:CB	2.17	0.74
1:B:260:PRO:HG3	1:B:302[A]:LEU:HD11	1.76	0.67
1:A:61:MET:CE	1:A:315:CYS:SG	2.83	0.67
1:B:61:MET:HE2	1:B:315:CYS:SG	2.37	0.65
4:A:504:GOL:C3	4:A:505:GOL:H32	2.14	0.63
1:B:61:MET:CE	1:B:63:PHE:CB	2.78	0.62
1:B:260:PRO:HG3	1:B:302[B]:LEU:HD21	1.82	0.62
1:B:61:MET:O	1:B:67:TYR:HA	2.00	0.61
1:B:298:LEU:O	1:B:302[B]:LEU:CD2	2.48	0.61
1:A:94:SER:HA	1:A:97:GLN:HB3	1.82	0.61
1:B:240[B]:GLU:HG2	1:B:294:HIS:ND1	2.16	0.60
1:B:182:GLU:OE2	1:B:209:ARG:CD	2.46	0.59
1:B:298:LEU:O	1:B:302[A]:LEU:CD1	2.45	0.59
1:B:61:MET:CE	1:B:63:PHE:HB3	2.33	0.57
1:B:298:LEU:O	1:B:302[B]:LEU:HD22	2.03	0.57
1:B:97:GLN:O	5:B:668:HOH:O	2.18	0.55
1:B:222:ILE:HG21	1:B:249:ALA:HB2	1.90	0.54
1:B:61:MET:CE	1:B:315:CYS:SG	2.97	0.53
1:B:183:ASN:H	1:B:213[A]:VAL:HG12	1.75	0.51
1:A:94:SER:HG	1:A:96:GLY:N	2.08	0.51
1:B:61:MET:HE3	1:B:63:PHE:HB2	1.92	0.50
1:A:292:LYS:NZ	5:A:1048:HOH:O	2.44	0.50
1:A:182:GLU:OE2	1:A:209:ARG:CD	2.54	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:61:MET:CE	1:B:63:PHE:HB2	2.44	0.47
1:B:179:VAL:O	1:B:235:VAL:HG22	2.16	0.46
1:B:236:HIS:CE1	1:B:287:PRO:HD3	2.51	0.46
1:A:61:MET:HE1	1:A:315:CYS:SG	2.56	0.45
1:B:302[A]:LEU:CD1	1:B:302[A]:LEU:H	2.30	0.44
1:A:87:VAL:O	1:A:117:TYR:HA	2.18	0.44
1:A:55:PRO:HB3	1:A:369:ILE:HG12	1.99	0.44
1:B:11:VAL:HG11	1:B:358:MET:HB3	1.99	0.43
1:B:283:ARG:HG2	1:B:289:PHE:CE2	2.53	0.43
1:A:222:ILE:HG21	1:A:249:ALA:HB2	2.01	0.43
1:B:121:MET:O	1:B:146:PHE:HA	2.18	0.42
1:A:121:MET:O	1:A:146:PHE:HA	2.20	0.42
1:A:11:VAL:HG11	1:A:358:MET:HB3	2.02	0.41
1:A:214:GLU:HG2	1:A:242:ALA:HB2	2.01	0.41
1:B:61:MET:SD	1:B:63:PHE:HB2	2.60	0.41
1:B:55:PRO:HB3	1:B:369:ILE:HG12	2.01	0.41
1:A:209:ARG:HD2	1:A:288:PRO:HD3	2.02	0.41
1:B:209:ARG:HD2	1:B:288:PRO:HD3	2.03	0.41
1:A:11:VAL:HB	1:A:49:MET:HG2	2.03	0.41
1:A:56:HIS:CD2	1:A:313:ASP:HA	2.56	0.41
1:B:210:PRO:O	1:B:213[B]:VAL:HG22	2.21	0.41
1:B:94:SER:C	1:B:97:GLN:H	2.25	0.40
1:B:183:ASN:HB3	1:B:213[A]:VAL:HG13	2.03	0.40
1:A:484:VAL:O	1:A:484:VAL:HG23	2.22	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:548:HOH:O	5:B:973:HOH:O[4_555]	2.08	0.12
5:A:1153:HOH:O	5:B:626:HOH:O[5_445]	2.19	0.01

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	483/490 (99%)	466 (96%)	16 (3%)	1 (0%)	47	33
1	B	480/490 (98%)	466 (97%)	13 (3%)	1 (0%)	47	33
All	All	963/980 (98%)	932 (97%)	29 (3%)	2 (0%)	47	33

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	338	GLY
1	A	338	GLY

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	390/394 (99%)	388 (100%)	2 (0%)	88	86
1	B	388/394 (98%)	387 (100%)	1 (0%)	92	91
All	All	778/788 (99%)	775 (100%)	3 (0%)	91	89

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

Mol	Chain	Res	Type
1	A	15	LEU
1	A	429	THR
1	B	429	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	168	GLN
1	A	475	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

2 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	$\#\|Z\| > 2$
1	KCX	B	147	2,1	9,11,12	1.01	1 (11%)	5,12,14	1.68	1 (20%)
1	KCX	A	147	2,1	9,11,12	1.42	2 (22%)	5,12,14	1.62	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
1	KCX	B	147	2,1	-	0/9/10/12	-
1	KCX	A	147	2,1	-	0/9/10/12	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	147	KCX	OQ1-CX	2.29	1.25	1.21
1	A	147	KCX	CB-CA	2.28	1.56	1.53
1	B	147	KCX	OQ1-CX	2.01	1.25	1.21

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	147	KCX	OQ1-CX-NZ	-3.50	119.53	124.96
1	A	147	KCX	OQ1-CX-NZ	-3.03	120.25	124.96

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 10 ligands modelled in this entry, 4 are monoatomic - leaving 6 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	$\#\|Z\| > 2$
4	GOL	A	504	-	5,5,5	0.60	0	5,5,5	1.76	1 (20%)
3	ACT	B	503	-	3,3,3	1.56	1 (33%)	3,3,3	1.81	1 (33%)
4	GOL	A	506	-	5,5,5	0.87	0	5,5,5	0.49	0
4	GOL	B	504	-	5,5,5	0.79	0	5,5,5	1.56	1 (20%)
3	ACT	A	503	-	3,3,3	1.09	0	3,3,3	2.06	1 (33%)
4	GOL	A	505	-	5,5,5	1.36	1 (20%)	5,5,5	2.19	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
4	GOL	A	504	-	-	2/4/4/4	-
4	GOL	A	506	-	-	0/4/4/4	-
4	GOL	A	505	-	-	4/4/4/4	-
4	GOL	B	504	-	-	4/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	503	ACT	O-C	2.25	1.32	1.22
4	A	505	GOL	O3-C3	-2.23	1.33	1.42

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	505	GOL	C3-C2-C1	-4.33	94.88	111.70
4	A	504	GOL	C3-C2-C1	-3.12	99.59	111.70
3	A	503	ACT	OXT-C-CH3	2.82	126.82	115.18
4	B	504	GOL	C3-C2-C1	-2.61	101.54	111.70
3	B	503	ACT	OXT-C-O	-2.47	112.95	122.05

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	504	GOL	O1-C1-C2-C3
4	B	504	GOL	C1-C2-C3-O3
4	A	505	GOL	O2-C2-C3-O3
4	A	505	GOL	O1-C1-C2-C3
4	B	504	GOL	O1-C1-C2-C3
4	B	504	GOL	O2-C2-C3-O3
4	A	504	GOL	O1-C1-C2-O2
4	A	505	GOL	C1-C2-C3-O3
4	A	505	GOL	O1-C1-C2-O2
4	B	504	GOL	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	504	GOL	3	0
4	A	505	GOL	3	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, 95th 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^2)	Q<0.9
1	A	482/490 (98%)	-0.07	1 (0%)	95	94	2, 4, 8, 14	1 (0%)
1	B	474/490 (96%)	-0.13	8 (1%)	70	70	2, 4, 7, 11	1 (0%)
All	All	956/980 (97%)	-0.10	9 (0%)	84	84	2, 4, 7, 14	2 (0%)

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	94	SER	2.9
1	B	64	MET	2.8
1	B	477	SER	2.7
1	A	485	HIS	2.6
1	B	66	THR	2.2
1	B	324[A]	PHE	2.2
1	B	154	GLY	2.2
1	B	63	PHE	2.2
1	B	475	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, 95th 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^2)	Q<0.9
1	KCX	A	147	12/13	0.96	0.12	2,3,5,7	0
1	KCX	B	147	12/13	0.96	0.14	2,3,6,6	0

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, 95th 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^2)	Q<0.9
3	ACT	B	503	4/4	0.75	0.28	22,23,23,23	0
4	GOL	A	505	6/6	0.89	0.22	3,9,11,15	0
4	GOL	A	504	6/6	0.93	0.23	3,10,10,11	0
3	ACT	A	503	4/4	0.93	0.15	2,2,4,5	0
4	GOL	B	504	6/6	0.94	0.29	3,9,11,12	0
4	GOL	A	506	6/6	0.97	0.20	2,6,7,7	0
2	ZN	B	501	1/1	0.99	0.04	2,2,2,2	1
2	ZN	B	502	1/1	0.99	0.04	2,2,2,2	1
2	ZN	A	501	1/1	0.99	0.06	2,2,2,2	1
2	ZN	A	502	1/1	0.99	0.04	2,2,2,2	1

6.5 Other polymers (i)

There are no such residues in this entry.