



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 13, 2017 – 05:50 AM EST

PDB ID : 3VU9  
Title : Crystal Structure of Psy3-Csm2 complex  
Authors : Tawaramoto, M.; Sasanuma, H.; Hosaka, H.; Lao, J.P.; Sanda, E.; Suzuki, M.; Yamashita, E.; Hunter, N.; Shinohara, M.; Nakagawa, A.; Shinohara, A.  
Deposited on : unknown  
Resolution : 1.75 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-20030345  
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-20030345

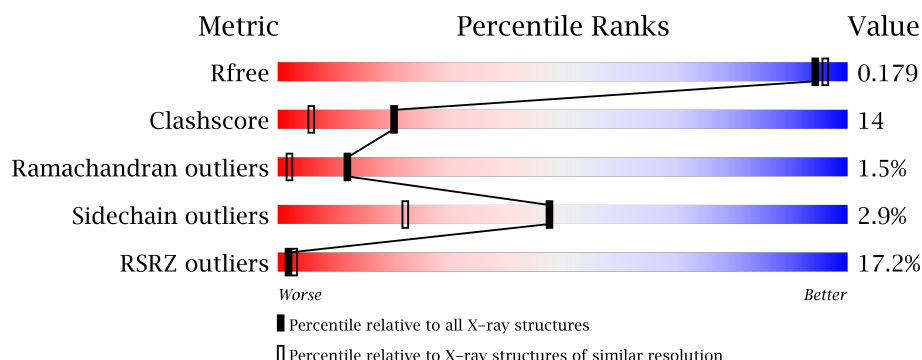
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.75 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	1762 (1.76-1.76)
Clashscore	112137	1889 (1.76-1.76)
Ramachandran outliers	110173	1868 (1.76-1.76)
Sidechain outliers	110143	1868 (1.76-1.76)
RSRZ outliers	101464	1770 (1.76-1.76)

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	245	<div> <div>20%</div> <div> <div></div> <div>63%</div> <div>22%</div> <div>•</div> <div>12%</div> </div> </div>
2	B	213	<div> <div>9%</div> <div> <div></div> <div>67%</div> <div>20%</div> <div>•</div> <div>10%</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
3	EDO	B	301	-	-	X	-

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3651 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 Platinum sensitivity protein 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	215	Total	C	N	O	S	0	5	0
			1784	1159	301	317	7			

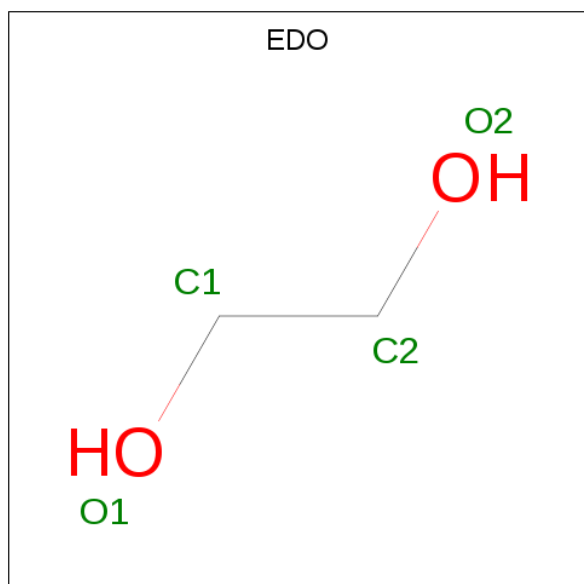
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	EXPRESSION TAG	UNP Q12318
A	-1	SER	-	EXPRESSION TAG	UNP Q12318
A	0	HIS	-	EXPRESSION TAG	UNP Q12318

- Molecule 2 is a protein called Chromosome segregation in meiosis protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	191	Total	C	N	O	S	0	2	0
			1592	1027	261	299	5			

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



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

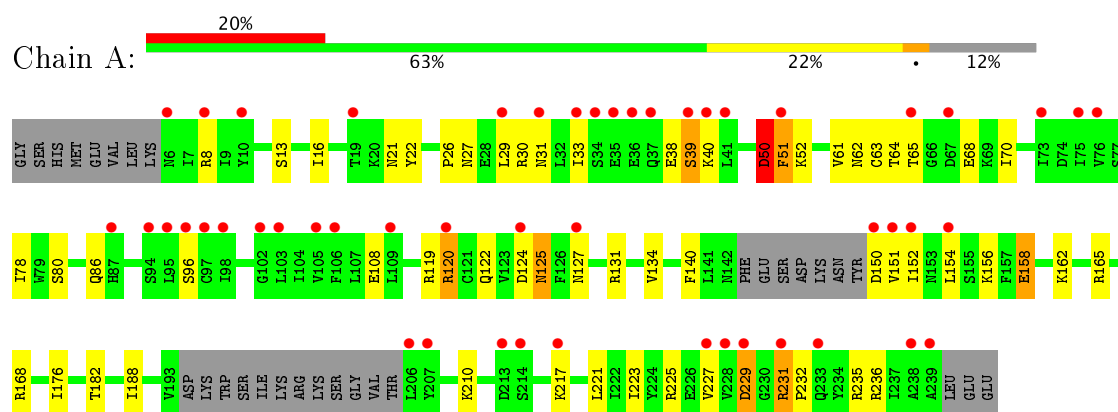
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	118	Total 118	O 118	0	0
4	B	149	Total 149	O 149	0	0

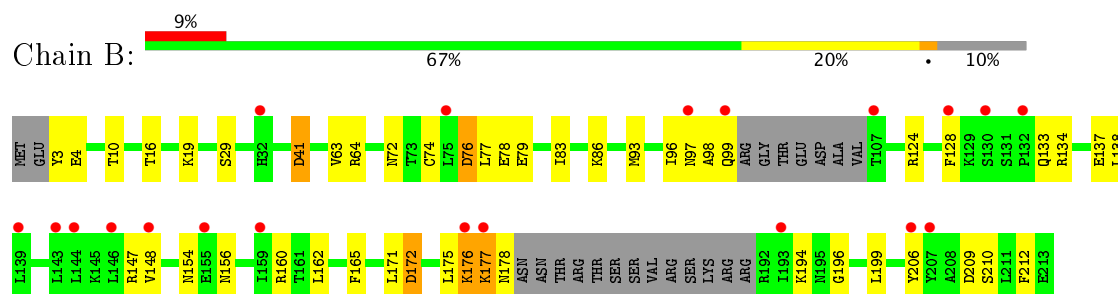
### 3 Residue-property plots [i](#)

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: Platinum sensitivity protein 3



#### • Molecule 2: Chromosome segregation in meiosis protein 2



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	134.56Å 50.40Å 76.35Å 90.00° 102.92° 90.00°	Depositor
Resolution (Å)	36.00 – 1.75 36.00 – 1.75	Depositor EDS
% Data completeness (in resolution range)	89.6 (36.00-1.75) 89.7 (36.00-1.75)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.93 (at 1.75Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, $R_{free}$	0.182 , 0.231 0.182 , 0.179	Depositor DCC
$R_{free}$ test set	2250 reflections (5.22%)	DCC
Wilson B-factor (Å <sup>2</sup> )	33.1	Xtriage
Anisotropy	0.425	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 59.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	3651	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.57% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: EDO

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	1.14	4/1820 (0.2%)	1.18	7/2457 (0.3%)
2	B	1.15	4/1624 (0.2%)	1.16	12/2193 (0.5%)
All	All	1.14	8/3444 (0.2%)	1.17	19/4650 (0.4%)

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

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	165	PHE	CE1-CZ	6.57	1.49	1.37
2	B	206	TYR	CE1-CZ	6.15	1.46	1.38
1	A	140	PHE	CD2-CE2	6.05	1.51	1.39
1	A	168	ARG	CZ-NH2	5.72	1.40	1.33
2	B	147	ARG	N-CA	5.26	1.56	1.46
1	A	80	SER	CB-OG	5.25	1.49	1.42
2	B	148	VAL	CB-CG2	5.11	1.63	1.52
1	A	96	SER	CA-CB	5.09	1.60	1.52

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	147	ARG	NE-CZ-NH2	-10.07	115.27	120.30
1	A	140	PHE	CB-CG-CD2	8.28	126.60	120.80
1	A	120[A]	ARG	NE-CZ-NH2	-7.56	116.52	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	120[B]	ARG	NE-CZ-NH2	-7.56	116.52	120.30
1	A	140	PHE	CB-CG-CD1	-7.10	115.83	120.80
2	B	76	ASP	CB-CG-OD1	6.46	124.11	118.30
2	B	138	LEU	CB-CG-CD2	-5.97	100.86	111.00
2	B	160	ARG	NE-CZ-NH2	-5.91	117.35	120.30
2	B	3	TYR	N-CA-C	-5.63	95.79	111.00
2	B	41	ASP	N-CA-CB	-5.63	100.46	110.60
1	A	120[A]	ARG	NE-CZ-NH1	5.60	123.10	120.30
1	A	120[B]	ARG	NE-CZ-NH1	5.60	123.10	120.30
2	B	78	GLU	OE1-CD-OE2	-5.42	116.79	123.30
2	B	172	ASP	CB-CG-OD2	-5.42	113.42	118.30
2	B	160	ARG	NE-CZ-NH1	5.38	122.99	120.30
2	B	209	ASP	CB-CG-OD2	-5.30	113.53	118.30
2	B	76	ASP	CB-CG-OD2	-5.29	113.54	118.30
1	A	108	GLU	OE1-CD-OE2	-5.28	116.96	123.30
2	B	77	LEU	CB-CG-CD1	-5.11	102.31	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	50[B]	ASP	Peptide

## 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	1784	0	1817	53	0
2	B	1592	0	1619	41	0
3	B	8	0	12	9	0
4	A	118	0	0	11	0
4	B	149	0	0	10	0
All	All	3651	0	3448	96	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 14.

All (96) 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)
2:B:83:ILE:HG13	4:B:545:HOH:O	1.34	1.24
1:A:64:THR:HA	4:A:388:HOH:O	1.75	0.85
1:A:51[A]:PHE:CD2	1:A:52:LYS:HD3	2.15	0.80
1:A:156:LYS:HG2	4:A:367:HOH:O	1.82	0.79
1:A:154:LEU:O	1:A:158:GLU:HG2	1.82	0.79
1:A:162:LYS:HG2	1:A:165:ARG:HH21	1.49	0.77
1:A:29:LEU:HD13	1:A:223:ILE:HD11	1.69	0.75
2:B:93:MET:HE2	2:B:96:ILE:HD12	1.70	0.74
1:A:63:CYS:CB	4:A:351:HOH:O	2.37	0.72
1:A:120[B]:ARG:HG3	4:A:400:HOH:O	1.91	0.71
2:B:10:THR:HB	2:B:162:LEU:HD23	1.75	0.69
1:A:13:SER:HA	1:A:16:ILE:HG12	1.75	0.67
2:B:212:PHE:HA	3:B:301:EDO:H12	1.76	0.67
3:B:302:EDO:H12	4:B:542:HOH:O	1.93	0.66
2:B:210:SER:OG	3:B:301:EDO:H22	1.95	0.66
2:B:134:ARG:NH1	2:B:137:GLU:OE1	2.29	0.65
2:B:194:LYS:HE3	2:B:196:GLY:O	1.97	0.65
2:B:154:ASN:ND2	2:B:156:ASN:H	1.95	0.63
1:A:29:LEU:HD13	1:A:223:ILE:CD1	2.29	0.63
2:B:63:VAL:HG23	2:B:64:ARG:N	2.14	0.63
1:A:119:ARG:HD2	4:A:344:HOH:O	1.98	0.62
3:B:301:EDO:C1	4:B:526:HOH:O	2.47	0.62
2:B:154:ASN:HD21	2:B:156:ASN:HB2	1.65	0.61
1:A:33:ILE:CG2	1:A:236:ARG:HH11	2.13	0.60
1:A:68:GLU:CB	4:A:385:HOH:O	2.49	0.60
3:B:301:EDO:H11	4:B:526:HOH:O	2.02	0.58
1:A:33:ILE:CG2	1:A:236:ARG:NH1	2.67	0.57
1:A:22:TYR:CD1	1:A:40:LYS:HA	2.39	0.57
1:A:64:THR:CA	4:A:388:HOH:O	2.43	0.57
2:B:93:MET:HE2	2:B:93:MET:HA	1.86	0.56
2:B:41:ASP:OD1	4:B:484:HOH:O	2.18	0.56
2:B:210:SER:OG	3:B:301:EDO:C2	2.54	0.55
1:A:162:LYS:HG2	1:A:165:ARG:NH2	2.21	0.54
2:B:76:ASP:OD1	2:B:79[A]:GLU:HG3	2.07	0.54
2:B:177:LYS:HG2	2:B:177:LYS:O	2.07	0.54
1:A:29:LEU:HD22	1:A:223:ILE:HD13	1.89	0.53
1:A:51[A]:PHE:HD2	1:A:52:LYS:CE	2.21	0.53
2:B:210:SER:CB	3:B:301:EDO:H22	2.37	0.53
1:A:38:GLU:C	1:A:40:LYS:N	2.62	0.53
2:B:124[A]:ARG:O	2:B:128:PHE:HD2	1.91	0.53
2:B:4:GLU:HA	4:B:527:HOH:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:GLN:HG3	4:B:476:HOH:O	2.08	0.52
1:A:51[A]:PHE:HD2	1:A:52:LYS:HD3	1.72	0.52
1:A:27:ASN:HA	1:A:30:ARG:HG2	1.91	0.52
2:B:63:VAL:HG23	2:B:64:ARG:H	1.75	0.51
1:A:182:THR:HG23	1:A:210:LYS:HE3	1.93	0.51
2:B:93:MET:CE	2:B:96:ILE:HD12	2.40	0.50
1:A:227:VAL:HG12	1:A:229:ASP:O	2.11	0.50
1:A:50[A]:ASP:HB3	1:A:52:LYS:O	2.12	0.50
2:B:97:ASN:O	2:B:99:GLN:N	2.45	0.50
1:A:38:GLU:C	1:A:40:LYS:H	2.16	0.50
1:A:33:ILE:HG22	1:A:236:ARG:NH1	2.27	0.49
2:B:72:ASN:OD1	2:B:74:CYS:HB2	2.13	0.49
2:B:133:GLN:OE1	2:B:133:GLN:N	2.33	0.49
1:A:62:ASN:CB	4:A:375:HOH:O	2.61	0.49
1:A:150:ASP:CG	1:A:151:VAL:H	2.16	0.49
1:A:38:GLU:O	1:A:40:LYS:N	2.45	0.48
1:A:120[B]:ARG:CG	4:A:400:HOH:O	2.58	0.48
2:B:93:MET:HE2	2:B:96:ILE:CD1	2.43	0.47
1:A:51[A]:PHE:HD2	1:A:52:LYS:HE2	1.78	0.47
2:B:93:MET:CE	2:B:96:ILE:CD1	2.92	0.47
2:B:171:LEU:O	2:B:175:LEU:HG	2.15	0.47
1:A:221:LEU:HD13	1:A:236:ARG:NH1	2.30	0.46
2:B:16:THR:OG1	2:B:19:LYS:HG2	2.15	0.46
2:B:74:CYS:SG	4:B:545:HOH:O	2.61	0.45
1:A:70[B]:ILE:HD11	4:A:351:HOH:O	2.16	0.45
2:B:63:VAL:CG2	2:B:64:ARG:N	2.79	0.45
2:B:176:LYS:O	2:B:178:ASN:N	2.47	0.44
1:A:26:PRO:HD2	1:A:29:LEU:HD12	1.99	0.44
1:A:231:ARG:HH11	1:A:232:PRO:HD2	1.83	0.44
1:A:124:ASP:N	4:A:346:HOH:O	2.51	0.43
2:B:172:ASP:O	2:B:176:LYS:HB2	2.19	0.43
2:B:212:PHE:CA	3:B:301:EDO:H12	2.47	0.43
1:A:152:ILE:HG13	1:A:156:LYS:HE2	2.00	0.43
1:A:51[A]:PHE:CD2	1:A:52:LYS:CD	2.95	0.43
1:A:51[A]:PHE:CZ	1:A:78:ILE:HD11	2.53	0.43
1:A:51[A]:PHE:HD2	1:A:52:LYS:CD	2.31	0.43
1:A:21:ASN:ND2	1:A:131:ARG:HD3	2.33	0.43
2:B:97:ASN:C	2:B:99:GLN:H	2.22	0.43
2:B:29:SER:HA	2:B:64:ARG:HH12	1.84	0.43
1:A:221:LEU:HD13	1:A:236:ARG:HH11	1.85	0.42
1:A:134:VAL:HA	1:A:176:ILE:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:231:ARG:HA	1:A:231:ARG:HD2	1.81	0.42
1:A:61:VAL:O	1:A:70[B]:ILE:CD1	2.68	0.42
2:B:154:ASN:HD22	2:B:156:ASN:H	1.65	0.42
1:A:33:ILE:HG21	1:A:236:ARG:NH1	2.35	0.41
1:A:225:ARG:HD3	1:A:225:ARG:HH11	1.72	0.41
1:A:188:ILE:HG12	2:B:199:LEU:HA	2.01	0.41
2:B:4:GLU:CA	4:B:527:HOH:O	2.67	0.41
1:A:21:ASN:HD21	1:A:131:ARG:HH11	1.68	0.41
2:B:172:ASP:OD2	2:B:194:LYS:NZ	2.54	0.41
1:A:125:ASN:OD1	1:A:127:ASN:HB2	2.20	0.41
2:B:171:LEU:HA	2:B:171:LEU:HD23	1.91	0.41
1:A:30:ARG:O	1:A:31:ASN:HB2	2.21	0.41
2:B:210:SER:HB2	3:B:301:EDO:H22	2.02	0.40
2:B:86:LYS:HE3	4:B:530:HOH:O	2.21	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	214/245 (87%)	194 (91%)	14 (6%)	6 (3%)	6	0
2	B	187/213 (88%)	179 (96%)	6 (3%)	2 (1%)	17	4
All	All	401/458 (88%)	373 (93%)	20 (5%)	8 (2%)	12	1

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	51[A]	PHE
1	A	51[B]	PHE
2	B	98	ALA
2	B	177	LYS

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Mol	Chain	Res	Type
1	A	39	SER
1	A	65	THR
1	A	50[A]	ASP
1	A	50[B]	ASP

### 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	199/229 (87%)	188 (94%)	11 (6%)	25	6
2	B	183/202 (91%)	182 (100%)	1 (0%)	91	86
All	All	382/431 (89%)	370 (97%)	12 (3%)	48	20

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	ARG
1	A	39	SER
1	A	50[A]	ASP
1	A	50[B]	ASP
1	A	86	GLN
1	A	125	ASN
1	A	158	GLU
1	A	217	LYS
1	A	229	ASP
1	A	231	ARG
1	A	235	ARG
2	B	176	LYS

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

Mol	Chain	Res	Type
1	A	21	ASN
2	B	27	ASN

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Mol	Chain	Res	Type
2	B	125	ASN
2	B	154	ASN
2	B	178	ASN

### 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 ⓘ

2 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	$\# Z  > 2$
3	EDO	B	301	-	3,3,3	0.46	0	2,2,2	0.44	0
3	EDO	B	302	-	3,3,3	1.02	0	2,2,2	0.27	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
3	EDO	B	301	-	-	0/1/1/1	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	B	302	-	-	0/1/1/1	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	301	EDO	8	0
3	B	302	EDO	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	215/245 (87%)	1.15	50 (23%)	1 1	20, 44, 85, 105	0
2	B	191/213 (89%)	0.43	20 (10%)	7 9	21, 38, 69, 91	0
All	All	406/458 (88%)	0.81	70 (17%)	2 3	20, 41, 81, 105	0

All (70) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	151	VAL	8.0
2	B	107	THR	7.5
1	A	207	TYR	6.8
1	A	214	SER	6.6
1	A	154	LEU	6.0
1	A	152	ILE	5.6
1	A	124	ASP	5.6
1	A	206	LEU	5.1
1	A	239	ALA	5.0
2	B	128	PHE	4.8
1	A	231	ARG	4.8
1	A	217	LYS	4.5
1	A	65	THR	4.5
1	A	228	VAL	4.3
1	A	150	ASP	4.2
1	A	229	ASP	3.9
1	A	127	ASN	3.9
1	A	238	ALA	3.9
1	A	6	ASN	3.9
1	A	10	TYR	3.7
1	A	87	HIS	3.6
2	B	177	LYS	3.5
2	B	32	HIS	3.5
1	A	31	ASN	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	33	ILE	3.3
2	B	176	LYS	3.3
2	B	144	LEU	3.3
2	B	75	LEU	3.1
1	A	106	PHE	3.1
1	A	75	ILE	3.1
1	A	98	ILE	3.1
1	A	39	SER	3.1
1	A	105	VAL	3.0
2	B	143	LEU	3.0
1	A	34	SER	3.0
1	A	95	LEU	3.0
1	A	97	CYS	3.0
1	A	227	VAL	2.9
1	A	8	ARG	2.9
1	A	19	THR	2.9
2	B	155	GLU	2.8
1	A	37	GLN	2.8
1	A	51[A]	PHE	2.8
2	B	99	GLN	2.8
2	B	193	ILE	2.7
2	B	97	ASN	2.6
1	A	36	GLU	2.6
2	B	146	LEU	2.6
1	A	29	LEU	2.6
1	A	73	ILE	2.5
1	A	120[A]	ARG	2.5
1	A	213	ASP	2.4
1	A	94	SER	2.4
1	A	233	GLN	2.4
1	A	35	GLU	2.3
1	A	102	GLY	2.3
2	B	206	TYR	2.3
1	A	96	SER	2.3
2	B	132	PRO	2.3
1	A	67	ASP	2.3
1	A	103	LEU	2.3
1	A	109	LEU	2.3
1	A	41	LEU	2.2
2	B	130	SER	2.2
2	B	148	VAL	2.2
1	A	40	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
2	B	207	TYR	2.1
1	A	76	VAL	2.1
2	B	159	ILE	2.1
2	B	139	LEU	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
3	EDO	B	302	4/4	0.86	0.10	-0.20	48,49,53,57	0
3	EDO	B	301	4/4	0.85	0.18	-	39,49,52,58	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.