



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:43 AM GMT

PDB ID : 3MUY
Title : E. coli (lacZ) beta-galactosidase (R599A)
Authors : Dugdale, M.L.; Vance, M.; Driedger, M.L.; Nibber, A.; Tran, A.; Huber, R.E.
Deposited on : 2010-05-03
Resolution : 2.50 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

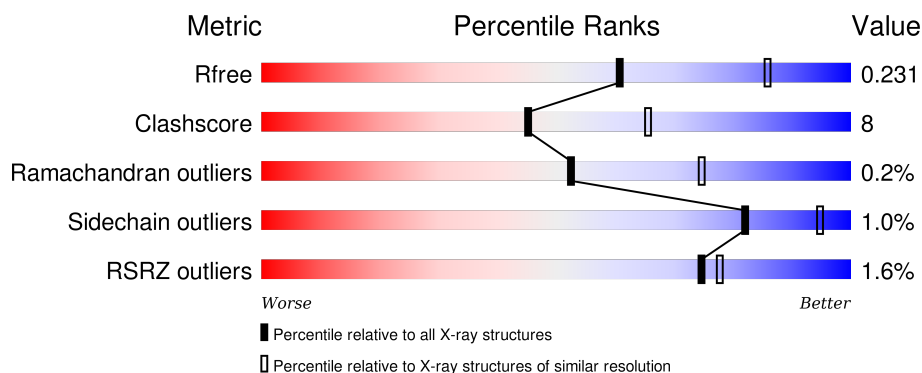
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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 ≥ 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	1	1023	<div> <div>2%</div> <div>80%</div> <div>18%</div> <div>.</div> </div>
1	2	1023	<div> <div>%</div> <div>78%</div> <div>20%</div> <div>.</div> </div>
1	3	1023	<div> <div>%</div> <div>78%</div> <div>20%</div> <div>.</div> </div>
1	4	1023	<div> <div>2%</div> <div>80%</div> <div>18%</div> <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
2	DMS	1	8402	-	-	-	X
2	DMS	1	8404	-	-	-	X
2	DMS	1	8405	-	-	-	X
2	DMS	1	8407	-	-	-	X
2	DMS	1	8412	-	-	-	X
2	DMS	1	8416	-	-	-	X
2	DMS	1	8419	-	-	-	X
2	DMS	1	8504	-	-	-	X
2	DMS	1	8607	-	-	-	X
2	DMS	2	8401	-	-	-	X
2	DMS	2	8402	-	-	-	X
2	DMS	2	8403	-	-	-	X
2	DMS	2	8404	-	-	-	X
2	DMS	2	8406	-	-	-	X
2	DMS	2	8410	-	-	-	X
2	DMS	2	8411	-	-	-	X
2	DMS	2	8412	-	-	-	X
2	DMS	2	8417	-	-	-	X
2	DMS	2	8420	-	-	-	X
2	DMS	2	8423	-	-	-	X
2	DMS	2	8425	-	-	-	X
2	DMS	2	8603	-	-	-	X
2	DMS	2	8609	-	-	-	X
2	DMS	2	8610	-	-	-	X
2	DMS	2	8613	-	-	-	X
2	DMS	3	8402	-	-	-	X
2	DMS	3	8403	-	-	-	X
2	DMS	3	8407	-	-	-	X
2	DMS	3	8408	-	-	-	X
2	DMS	3	8410	-	-	-	X
2	DMS	3	8411	-	-	-	X
2	DMS	3	8417	-	-	-	X
2	DMS	3	8420	-	-	-	X
2	DMS	3	8423	-	-	-	X
2	DMS	3	8425	-	-	-	X
2	DMS	3	8603	-	-	-	X
2	DMS	3	8606	-	-	-	X
2	DMS	3	8611	-	-	-	X
2	DMS	4	8402	-	-	-	X
2	DMS	4	8404	-	-	-	X
2	DMS	4	8405	-	-	-	X

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	DMS	4	8406	-	-	-	X
2	DMS	4	8410	-	-	-	X
2	DMS	4	8411	-	-	-	X
2	DMS	4	8417	-	-	-	X
2	DMS	4	8508	-	-	-	X
2	DMS	4	8613	-	-	-	X
2	DMS	4	8615	-	-	-	X
2	DMS	4	8617	-	-	-	X
2	DMS	4	8618	-	-	-	X
2	DMS	4	8701	-	-	-	X
3	MG	1	3002	-	-	-	X
4	NA	4	3104	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 36360 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 Beta-D-galactosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1	1011	Total	C	N	O	S	0	0	0
			8119	5135	1437	1509	38			
1	2	1011	Total	C	N	O	S	0	0	0
			8119	5135	1437	1509	38			
1	3	1011	Total	C	N	O	S	0	0	0
			8119	5135	1437	1509	38			
1	4	1011	Total	C	N	O	S	0	0	0
			8119	5135	1437	1509	38			

There are 36 discrepancies between the modelled and reference sequences:

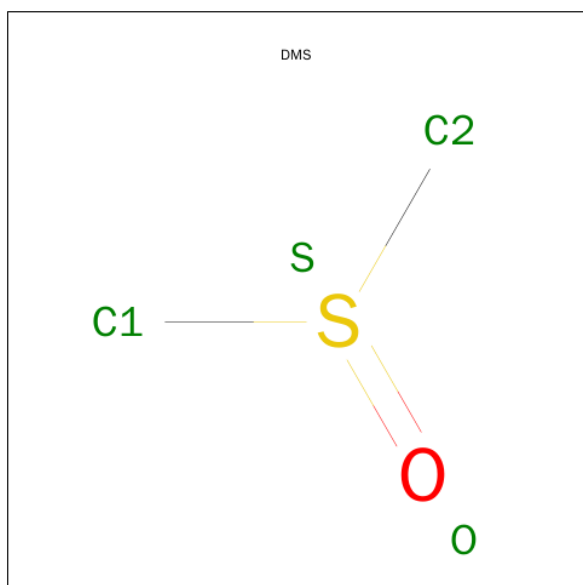
Chain	Residue	Modelled	Actual	Comment	Reference
1	1	GLY	-	EXPRESSION TAG	UNP C6UB28
1	2	SER	-	EXPRESSION TAG	UNP C6UB28
1	3	HIS	-	EXPRESSION TAG	UNP C6UB28
1	4	MET	-	EXPRESSION TAG	UNP C6UB28
1	5	LEU	-	EXPRESSION TAG	UNP C6UB28
1	6	GLU	-	EXPRESSION TAG	UNP C6UB28
1	7	ASP	-	EXPRESSION TAG	UNP C6UB28
1	8	PRO	-	EXPRESSION TAG	UNP C6UB28
1	599	ALA	ARG	ENGINEERED	UNP C6UB28
2	1	GLY	-	EXPRESSION TAG	UNP C6UB28
2	2	SER	-	EXPRESSION TAG	UNP C6UB28
2	3	HIS	-	EXPRESSION TAG	UNP C6UB28
2	4	MET	-	EXPRESSION TAG	UNP C6UB28
2	5	LEU	-	EXPRESSION TAG	UNP C6UB28
2	6	GLU	-	EXPRESSION TAG	UNP C6UB28
2	7	ASP	-	EXPRESSION TAG	UNP C6UB28
2	8	PRO	-	EXPRESSION TAG	UNP C6UB28
2	599	ALA	ARG	ENGINEERED	UNP C6UB28
3	1	GLY	-	EXPRESSION TAG	UNP C6UB28
3	2	SER	-	EXPRESSION TAG	UNP C6UB28
3	3	HIS	-	EXPRESSION TAG	UNP C6UB28

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
3	4	MET	-	EXPRESSION TAG	UNP C6UB28
3	5	LEU	-	EXPRESSION TAG	UNP C6UB28
3	6	GLU	-	EXPRESSION TAG	UNP C6UB28
3	7	ASP	-	EXPRESSION TAG	UNP C6UB28
3	8	PRO	-	EXPRESSION TAG	UNP C6UB28
3	599	ALA	ARG	ENGINEERED	UNP C6UB28
4	1	GLY	-	EXPRESSION TAG	UNP C6UB28
4	2	SER	-	EXPRESSION TAG	UNP C6UB28
4	3	HIS	-	EXPRESSION TAG	UNP C6UB28
4	4	MET	-	EXPRESSION TAG	UNP C6UB28
4	5	LEU	-	EXPRESSION TAG	UNP C6UB28
4	6	GLU	-	EXPRESSION TAG	UNP C6UB28
4	7	ASP	-	EXPRESSION TAG	UNP C6UB28
4	8	PRO	-	EXPRESSION TAG	UNP C6UB28
4	599	ALA	ARG	ENGINEERED	UNP C6UB28

- Molecule 2 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C₂H₆OS).



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

Continued on next page...

Continued from previous page...

[illegible]

Continued on next page...

Continued from previous page...

[illegible]

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

[illegible]

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

[illegible]

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	2	2	Total 2	Mg 2	0	0
3	1	3	Total 3	Mg 3	0	0
3	4	3	Total 3	Mg 3	0	0
3	3	2	Total 2	Mg 2	0	0

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	2	4	Total 4	Na 4	0	0
4	1	3	Total 3	Na 3	0	0
4	4	4	Total 4	Na 4	0	0
4	3	5	Total 5	Na 5	0	0

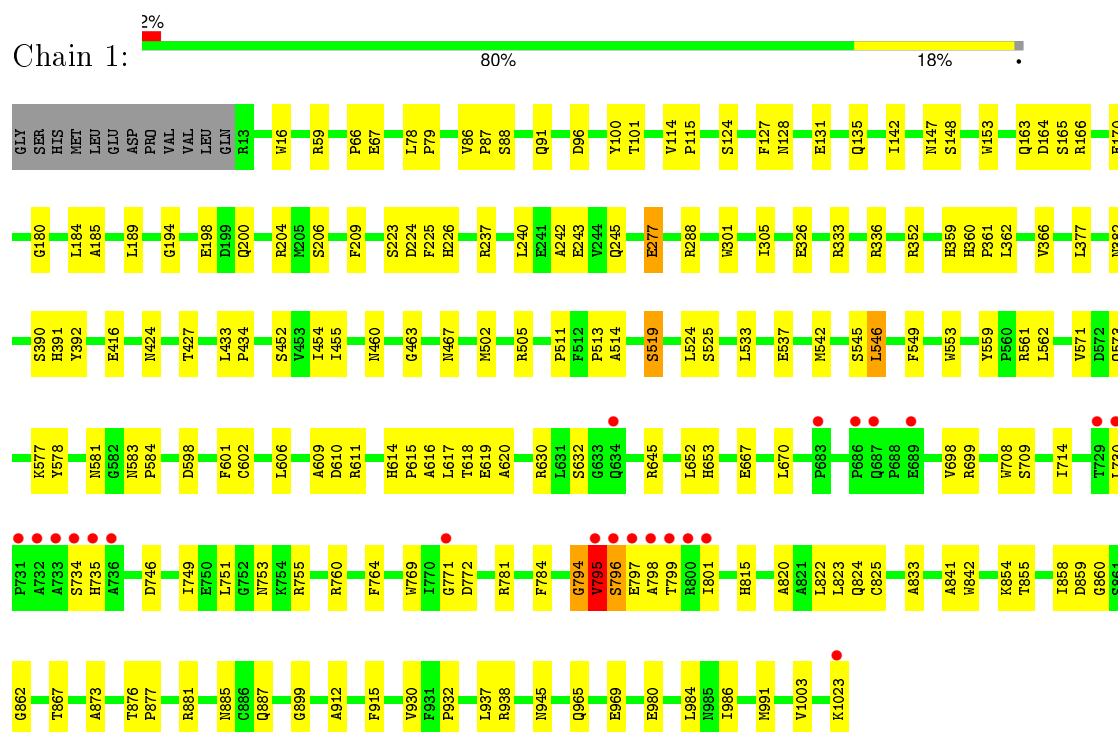
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	1	846	Total 846	O 846	0	0
5	2	821	Total 821	O 821	0	0
5	3	838	Total 838	O 838	0	0
5	4	833	Total 833	O 833	0	0

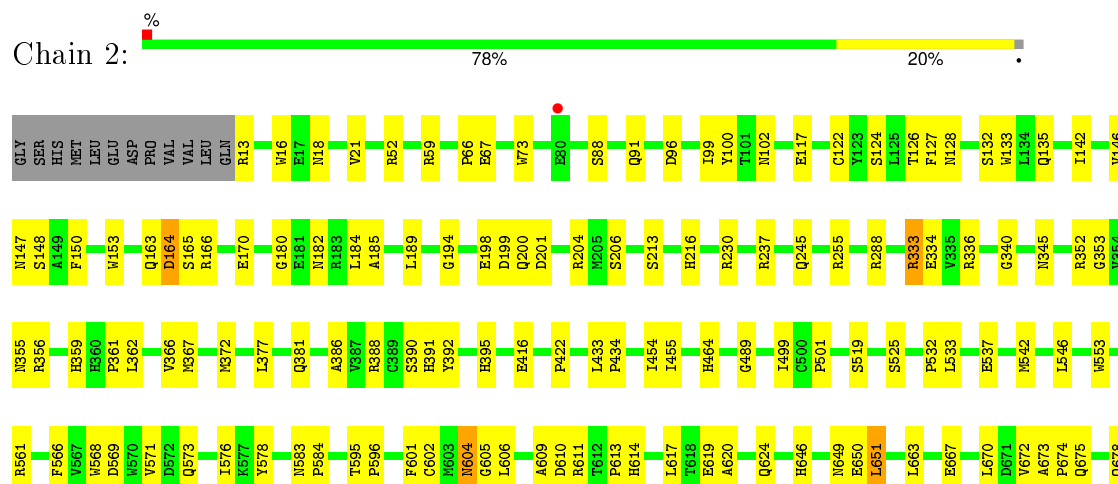
3 Residue-property plots

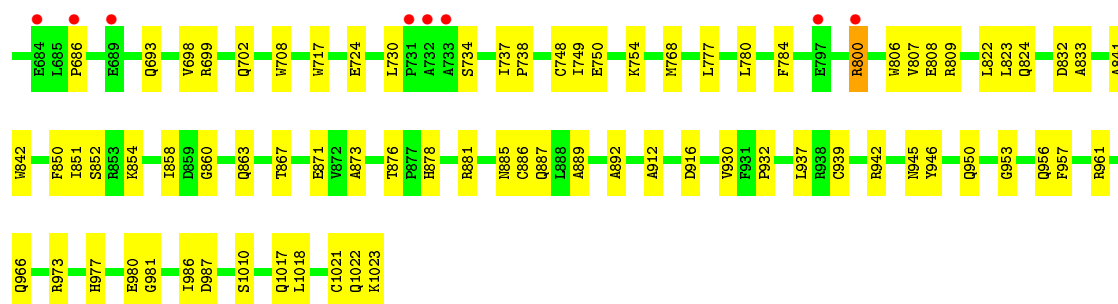
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: Beta-D-galactosidase



• Molecule 1: Beta-D-galactosidase

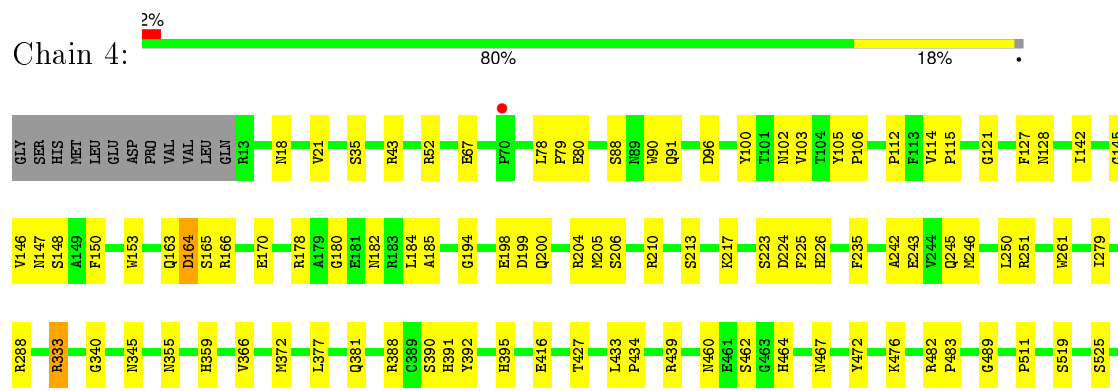


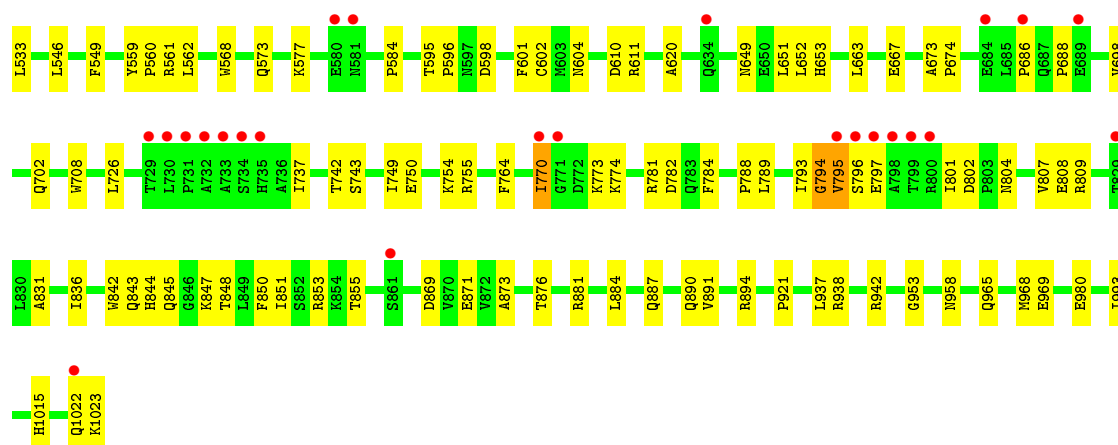


• Molecule 1: Beta-D-galactosidase



• Molecule 1: Beta-D-galactosidase





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	149.27Å 167.24Å 200.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	86.02 – 2.50 86.02 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.7 (86.02-2.50) 99.8 (86.02-2.50)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.82 (at 2.51Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.179 , 0.235 0.175 , 0.231	Depositor DCC
R_{free} test set	2456 reflections (1.42%)	DCC
Wilson B-factor (Å ²)	20.7	Xtriage
Anisotropy	0.718	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 58.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	1 of 172872 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	36360	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 37.76 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 4.0857e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NA, MG, DMS

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	1	0.33	0/8361	0.61	0/11408
1	2	0.33	0/8361	0.61	0/11408
1	3	0.33	0/8361	0.61	0/11408
1	4	0.33	0/8361	0.61	1/11408 (0.0%)
All	All	0.33	0/33444	0.61	1/45632 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	4	770	ILE	N-CA-C	-5.47	96.23	111.00

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	1	8119	0	7708	126	0
1	2	8119	0	7707	134	0
1	3	8119	0	7707	132	0
1	4	8119	0	7707	123	0
2	1	108	0	162	1	0
2	2	136	0	204	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	3	140	0	210	1	0
2	4	136	0	204	1	0
3	1	3	0	0	0	0
3	2	2	0	0	0	0
3	3	2	0	0	0	0
3	4	3	0	0	0	0
4	1	3	0	0	0	0
4	2	4	0	0	0	0
4	3	5	0	0	0	0
4	4	4	0	0	0	0
5	1	846	0	0	2	0
5	2	821	0	0	4	0
5	3	838	0	0	8	0
5	4	833	0	0	3	0
All	All	36360	0	31609	506	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 8.

All (506) 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)
1:4:142:ILE:HG12	1:4:170:GLU:HG2	1.37	1.05
1:2:966:GLN:HE22	1:2:977:HIS:H	1.04	0.93
1:1:142:ILE:HG12	1:1:170:GLU:HG2	1.52	0.92
1:2:142:ILE:HG12	1:2:170:GLU:HG2	1.54	0.87
1:4:804:ASN:ND2	1:4:809:ARG:HH21	1.73	0.86
1:4:804:ASN:HD22	1:4:809:ARG:HH21	1.24	0.83
1:1:794:GLY:O	1:1:795:VAL:HG13	1.77	0.83
1:3:44:THR:OG1	1:3:46:ARG:HD3	1.79	0.83
1:1:630:ARG:HH12	1:1:632:SER:HB2	1.43	0.81
1:1:245:GLN:HG2	1:1:288:ARG:HG2	1.63	0.80
1:3:142:ILE:HG12	1:3:170:GLU:HG2	1.64	0.79
1:1:147:ASN:HB3	1:1:206:SER:HA	1.66	0.77
1:2:966:GLN:NE2	1:2:977:HIS:H	1.83	0.75
1:1:88:SER:HA	1:1:366:VAL:HG21	1.68	0.75
1:2:873:ALA:O	1:2:876:THR:HG22	1.85	0.74
1:2:147:ASN:HB3	1:2:206:SER:HA	1.70	0.73
1:3:579:ASP:OD2	1:3:583:ASN:HB2	1.88	0.73
1:2:737:ILE:HD12	1:2:738:PRO:HD2	1.68	0.73
1:1:615:PRO:O	1:1:618:THR:HG22	1.89	0.73

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4:568:TRP:HE1	1:4:604:ASN:HD22	1.38	0.72
1:2:245:GLN:HG2	1:2:288:ARG:HG2	1.72	0.71
1:4:245:GLN:HG2	1:4:288:ARG:HG2	1.72	0.71
1:1:546:LEU:HG	1:1:616:ALA:HB1	1.73	0.71
1:4:147:ASN:HB3	1:4:206:SER:HA	1.73	0.71
1:1:730:LEU:HD21	1:2:823:LEU:O	1.91	0.69
1:1:542:MET:HE3	1:1:601:PHE:HA	1.74	0.69
1:1:965:GLN:O	1:1:969:GLU:HG3	1.93	0.69
1:3:755:ARG:HB3	1:3:769:TRP:HB2	1.75	0.69
1:3:416:GLU:HG3	1:3:460:ASN:O	1.93	0.69
1:4:250:LEU:O	1:4:251:ARG:HG2	1.93	0.69
1:2:966:GLN:HE22	1:2:977:HIS:N	1.87	0.68
1:4:377:LEU:HD22	1:4:708:TRP:HA	1.76	0.67
1:3:652:LEU:HD11	1:3:698:VAL:HB	1.76	0.67
1:3:147:ASN:HB3	1:3:206:SER:HA	1.75	0.67
1:3:88:SER:HA	1:3:366:VAL:HG21	1.75	0.67
1:3:615:PRO:O	1:3:618:THR:HG22	1.94	0.67
1:3:245:GLN:HG2	1:3:288:ARG:HG2	1.74	0.67
1:4:355:ASN:OD1	1:4:388:ARG:HD3	1.94	0.66
1:1:630:ARG:NH1	1:1:632:SER:HB2	2.10	0.66
1:2:737:ILE:HD13	1:2:832:ASP:HA	1.77	0.66
1:4:598:ASP:OD1	1:4:797:GLU:HA	1.96	0.65
1:3:651:LEU:HD12	1:3:651:LEU:O	1.96	0.65
1:4:804:ASN:HD22	1:4:809:ARG:NH2	1.94	0.65
1:4:651:LEU:HD12	1:4:651:LEU:O	1.97	0.65
1:3:454:ILE:HG13	1:3:455:ILE:HG13	1.79	0.64
1:2:127:PHE:HE2	1:2:184:LEU:HG	1.61	0.64
1:1:653:HIS:CD2	1:1:667:GLU:HG2	2.32	0.64
1:1:598:ASP:OD1	1:1:797:GLU:HA	1.96	0.64
1:2:748:CYS:C	1:2:749:ILE:HD12	2.18	0.64
1:3:623:GLN:HA	2:3:8402:DMS:H11	1.80	0.63
1:3:843:GLN:HG2	1:3:848:THR:HA	1.81	0.63
1:4:88:SER:HA	1:4:366:VAL:HG21	1.81	0.62
1:3:890:GLN:HG2	1:3:891:VAL:N	2.14	0.62
1:3:356:ARG:HD2	1:3:379:MET:CE	2.30	0.62
1:2:620:ALA:O	1:2:624:GLN:HG3	2.00	0.62
1:2:91:GLN:HG3	1:2:96:ASP:OD1	1.99	0.62
1:2:699:ARG:HG2	1:2:717:TRP:HB3	1.82	0.61
1:4:801:ILE:HD12	1:4:801:ILE:N	2.13	0.61
1:3:568:TRP:HE1	1:3:604:ASN:HD22	1.48	0.61
1:4:427:THR:HG21	1:4:462:SER:HB3	1.82	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4:793:ILE:HG22	1:4:795:VAL:HG22	1.83	0.61
1:3:251:ARG:HG3	1:3:251:ARG:HH11	1.66	0.61
1:2:124:SER:HA	1:2:184:LEU:O	2.01	0.61
1:4:794:GLY:O	1:4:795:VAL:HG13	2.01	0.60
1:1:945:ASN:HB3	1:1:1023:LYS:HE3	1.82	0.60
1:1:382:ASN:ND2	1:1:617:LEU:HD21	2.17	0.60
1:1:873:ALA:O	1:1:876:THR:HG22	2.01	0.60
1:2:18:ASN:ND2	1:2:21:VAL:HG23	2.17	0.60
1:2:377:LEU:HD22	1:2:708:TRP:HA	1.84	0.60
1:2:663:LEU:HD21	1:2:686:PRO:HG2	1.83	0.59
1:2:754:LYS:HE2	1:2:1022:GLN:NE2	2.18	0.59
1:2:942:ARG:HA	1:2:953:GLY:O	2.03	0.59
1:2:777:LEU:HG	1:2:889:ALA:HA	1.84	0.59
1:1:937:LEU:O	1:1:938:ARG:HD2	2.02	0.59
1:4:595:THR:HA	1:4:596:PRO:C	2.23	0.59
1:1:801:ILE:HD12	1:1:801:ILE:N	2.17	0.59
1:2:986:ILE:HD13	1:2:1018:LEU:HD13	1.85	0.59
1:3:749:ILE:N	1:3:749:ILE:HD12	2.17	0.59
1:4:142:ILE:HG12	1:4:170:GLU:CG	2.25	0.59
1:3:767:GLN:NE2	1:3:774:LYS:HD3	2.17	0.59
1:1:801:ILE:H	1:1:801:ILE:HD12	1.66	0.59
1:2:672:VAL:HG22	1:2:678:GLN:HB2	1.83	0.59
1:1:746:ASP:HA	1:1:760:ARG:HG3	1.83	0.58
1:1:377:LEU:HD22	1:1:708:TRP:HA	1.85	0.58
1:3:672:VAL:HG22	1:3:678:GLN:HB2	1.85	0.58
1:1:277:GLU:CD	1:1:277:GLU:H	2.06	0.58
1:2:88:SER:HA	1:2:366:VAL:HG21	1.86	0.58
1:3:240:LEU:HD23	1:3:240:LEU:C	2.24	0.58
1:1:545:SER:O	1:1:546:LEU:HB2	2.02	0.58
1:3:377:LEU:O	1:3:381:GLN:HG3	2.02	0.57
1:2:610:ASP:O	1:2:611:ARG:HB2	2.04	0.57
1:1:887:GLN:NE2	1:1:980:GLU:O	2.38	0.57
1:3:41:GLU:HG2	1:3:46:ARG:NH2	2.19	0.57
1:2:194:GLY:O	1:2:198:GLU:HG3	2.05	0.57
1:2:127:PHE:CE2	1:2:184:LEU:HG	2.40	0.57
1:1:764:PHE:CE1	1:1:781:ARG:NH1	2.72	0.57
1:1:749:ILE:HD12	1:1:749:ILE:N	2.19	0.57
1:3:890:GLN:OE1	1:3:947:GLY:HA3	2.05	0.56
1:4:965:GLN:O	1:4:969:GLU:HG3	2.06	0.56
1:4:416:GLU:HG3	1:4:460:ASN:O	2.05	0.56
1:4:788:PRO:HD2	1:4:968:MET:HG3	1.87	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4:153:TRP:HB2	1:4:185:ALA:HB3	1.88	0.56
1:3:356:ARG:HD2	1:3:379:MET:HE1	1.88	0.56
1:4:433:LEU:HB3	1:4:434:PRO:HD3	1.87	0.56
1:3:965:GLN:O	1:3:969:GLU:HG3	2.06	0.56
1:2:13:ARG:HG3	1:3:13:ARG:NH1	2.21	0.55
1:2:619:GLU:HA	1:2:912:ALA:HB2	1.88	0.55
1:3:823:LEU:HD11	1:3:841:ALA:HB2	1.89	0.55
1:2:153:TRP:HB2	1:2:185:ALA:HB3	1.87	0.55
1:4:546:LEU:HA	5:4:4130:HOH:O	2.07	0.55
1:2:573:GLN:HB2	1:2:602:CYS:O	2.06	0.55
1:4:942:ARG:HA	1:4:953:GLY:O	2.07	0.54
1:4:651:LEU:C	1:4:651:LEU:HD12	2.28	0.54
1:2:651:LEU:HD11	1:2:667:GLU:OE1	2.06	0.54
1:4:91:GLN:HG3	1:4:96:ASP:OD1	2.07	0.54
1:3:728:VAL:HG12	1:4:851:ILE:HD11	1.89	0.54
1:3:573:GLN:HB2	1:3:602:CYS:O	2.07	0.54
1:4:894:ARG:NH1	1:4:921:PRO:HG3	2.23	0.54
1:2:930:VAL:O	1:2:932:PRO:HD3	2.08	0.54
1:3:59:ARG:HB2	1:3:124:SER:OG	2.07	0.54
1:4:340:GLY:O	1:4:561:ARG:HG2	2.08	0.54
1:2:166:ARG:HG3	1:2:392:TYR:HB2	1.89	0.53
1:1:652:LEU:HD11	1:1:698:VAL:HB	1.90	0.53
1:4:784:PHE:HA	1:4:881:ARG:O	2.08	0.53
1:1:237:ARG:NH1	1:1:237:ARG:HB3	2.24	0.53
1:2:823:LEU:HD11	1:2:841:ALA:HB2	1.91	0.53
1:1:433:LEU:HB3	1:1:434:PRO:HD3	1.90	0.53
1:3:334:GLU:OE1	1:3:336:ARG:NH1	2.41	0.53
1:2:595:THR:HA	1:2:596:PRO:C	2.28	0.53
1:3:533:LEU:HD23	1:3:533:LEU:C	2.29	0.53
1:2:945:ASN:OD1	1:2:950:GLN:HG3	2.08	0.52
1:3:579:ASP:CG	1:3:583:ASN:HB2	2.29	0.52
1:4:802:ASP:O	1:4:808:GLU:HG3	2.09	0.52
1:4:549:PHE:CE2	1:4:620:ALA:HA	2.44	0.52
1:1:100:TYR:CE1	1:1:602:CYS:HB3	2.45	0.52
1:2:863:GLN:HG2	1:2:1021:CYS:CB	2.39	0.52
1:2:100:TYR:CE1	1:2:602:CYS:HB3	2.44	0.52
1:4:770:ILE:HG21	1:4:1022:GLN:HE22	1.75	0.52
1:3:230:ARG:HD3	5:3:7199:HOH:O	2.10	0.52
1:4:749:ILE:N	1:4:749:ILE:HD12	2.25	0.52
1:4:148:SER:HA	1:4:165:SER:OG	2.10	0.52
1:2:454:ILE:HG13	1:2:455:ILE:HG13	1.91	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:748:CYS:C	1:3:749:ILE:HD12	2.31	0.52
1:2:734:SER:HB3	1:2:860:GLY:HA3	1.92	0.52
1:2:646:HIS:HB3	5:2:6063:HOH:O	2.09	0.51
1:1:784:PHE:HA	1:1:881:ARG:O	2.09	0.51
1:4:686:PRO:O	1:4:688:PRO:HD3	2.11	0.51
1:3:251:ARG:HG3	1:3:251:ARG:NH1	2.24	0.51
1:3:839:ALA:HA	1:3:852:SER:O	2.10	0.51
1:4:937:LEU:O	1:4:938:ARG:HD2	2.10	0.51
1:1:301:TRP:CH2	1:1:452:SER:HA	2.45	0.51
1:4:873:ALA:O	1:4:876:THR:HG22	2.10	0.51
1:3:362:LEU:HD23	1:3:576:ILE:HB	1.92	0.51
1:1:336:ARG:HB3	2:1:8409:DMS:O	2.11	0.51
1:1:153:TRP:HB2	1:1:185:ALA:HB3	1.93	0.51
1:1:833:ALA:HB1	1:1:858:ILE:O	2.11	0.51
1:3:499:ILE:HG22	1:3:501:PRO:HD3	1.93	0.51
1:1:424:ASN:OD1	1:4:279:ILE:HD11	2.11	0.51
1:2:542:MET:HA	1:2:604:ASN:HA	1.92	0.51
1:2:433:LEU:HB3	1:2:434:PRO:HD3	1.94	0.50
1:1:755:ARG:HB2	1:1:769:TRP:HB2	1.94	0.50
1:2:499:ILE:HG22	1:2:501:PRO:HD3	1.94	0.50
1:3:458:LEU:HD11	1:3:472:TYR:HB2	1.93	0.50
1:2:362:LEU:HD23	1:2:576:ILE:HB	1.93	0.50
1:2:377:LEU:O	1:2:381:GLN:HG3	2.11	0.50
1:2:863:GLN:HG2	1:2:1021:CYS:HB3	1.92	0.50
1:3:738:PRO:HB2	1:3:834:VAL:HG23	1.94	0.50
1:1:542:MET:CE	1:1:601:PHE:HA	2.40	0.50
1:1:559:TYR:HB2	1:1:562:LEU:HD12	1.93	0.50
1:2:146:VAL:HG11	1:2:150:PHE:CD2	2.46	0.50
1:3:610:ASP:O	1:3:611:ARG:HB2	2.12	0.50
1:3:649:ASN:O	1:3:650:GLU:HG3	2.12	0.49
1:1:127:PHE:CE2	1:1:184:LEU:HG	2.47	0.49
1:4:673:ALA:HB1	1:4:674:PRO:HD2	1.93	0.49
1:3:646:HIS:HB3	5:3:6063:HOH:O	2.13	0.49
1:4:225:PHE:HA	1:4:243:GLU:O	2.12	0.49
1:1:734:SER:HB2	1:1:860:GLY:HA3	1.95	0.49
1:4:533:LEU:HD23	1:4:533:LEU:C	2.32	0.49
1:4:568:TRP:HE1	1:4:604:ASN:ND2	2.08	0.49
1:2:353:GLY:HA2	1:2:386:ALA:O	2.13	0.49
1:2:464:HIS:HB2	1:2:489:GLY:HA3	1.93	0.49
1:2:100:TYR:CZ	1:2:602:CYS:HB3	2.48	0.49
1:2:237:ARG:HG3	1:2:237:ARG:HH11	1.77	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:578:TYR:CE2	1:1:584:PRO:HB3	2.47	0.49
1:2:542:MET:CE	1:2:601:PHE:HA	2.43	0.49
1:3:126:THR:HA	1:3:182:ASN:O	2.12	0.49
1:3:1011:ALA:HB3	1:3:1014:TYR:CZ	2.48	0.49
1:4:651:LEU:HD11	1:4:653:HIS:CE1	2.48	0.49
1:4:573:GLN:HB2	1:4:602:CYS:O	2.11	0.49
1:4:843:GLN:HA	1:4:847:LYS:O	2.13	0.48
1:4:200:GLN:HG2	1:4:391:HIS:HB2	1.94	0.48
1:1:581:ASN:HB2	1:1:583:ASN:OD1	2.12	0.48
1:4:887:GLN:NE2	1:4:980:GLU:O	2.42	0.48
1:2:822:LEU:HD11	1:2:824:GLN:O	2.13	0.48
1:1:699:ARG:HD3	1:1:714:ILE:HD13	1.96	0.48
1:2:133:TRP:CE3	1:2:216:HIS:HB2	2.48	0.48
1:4:764:PHE:CD1	1:4:781:ARG:HG2	2.48	0.48
1:2:961:ARG:NE	1:2:981:GLY:O	2.43	0.48
1:4:742:THR:HG22	1:4:743:SER:N	2.27	0.48
1:2:352:ARG:HG2	1:2:553:TRP:CH2	2.48	0.48
1:1:245:GLN:HG2	1:1:288:ARG:CG	2.38	0.48
1:4:18:ASN:ND2	1:4:21:VAL:HG23	2.29	0.48
1:4:737:ILE:HD12	1:4:831:ALA:O	2.14	0.48
1:1:708:TRP:CE3	1:1:709:SER:HB3	2.47	0.48
1:4:128:ASN:HB3	1:4:180:GLY:O	2.13	0.48
1:2:881:ARG:HE	1:2:987:ASP:CG	2.17	0.48
1:4:114:VAL:HB	1:4:115:PRO:HD2	1.94	0.48
1:4:782:ASP:HA	1:4:884:LEU:HD23	1.95	0.48
1:1:533:LEU:HD23	1:1:533:LEU:C	2.34	0.48
1:2:255:ARG:HH11	1:2:255:ARG:HG2	1.79	0.48
1:3:749:ILE:HB	1:3:756:TRP:HB2	1.95	0.48
1:1:87:PRO:HB2	1:1:209:PHE:C	2.35	0.47
1:3:674:PRO:O	1:3:675:GLN:HB2	2.13	0.47
1:3:608:PHE:CE1	1:3:614:HIS:HD2	2.32	0.47
1:4:145:GLY:N	1:4:210:ARG:HB2	2.29	0.47
1:4:1022:GLN:O	1:4:1023:LYS:HB2	2.14	0.47
1:1:755:ARG:HD2	5:1:6193:HOH:O	2.13	0.47
1:1:854:LYS:HA	1:1:867:THR:O	2.14	0.47
1:3:833:ALA:HB1	1:3:858:ILE:O	2.14	0.47
1:2:613:PRO:HB3	1:2:617:LEU:HD23	1.94	0.47
1:4:91:GLN:OE1	1:4:205:MET:HB3	2.13	0.47
1:3:746:ASP:HA	1:3:760:ARG:HG3	1.95	0.47
1:2:355:ASN:OD1	1:2:388:ARG:HD3	2.14	0.47
1:3:356:ARG:HD2	1:3:379:MET:HE2	1.95	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:549:PHE:CE2	1:1:620:ALA:HA	2.49	0.47
1:4:843:GLN:HG2	1:4:848:THR:HA	1.96	0.47
1:4:194:GLY:O	1:4:198:GLU:HG3	2.14	0.47
1:4:146:VAL:HG11	1:4:150:PHE:CD2	2.49	0.47
1:1:454:ILE:HG13	1:1:455:ILE:HG13	1.97	0.47
1:2:698:VAL:O	1:2:717:TRP:HA	2.14	0.47
1:3:559:TYR:HB2	1:3:562:LEU:HD12	1.97	0.47
1:3:794:GLY:HA2	1:3:998:SER:O	2.15	0.47
1:2:750:GLU:HB3	5:2:5177:HOH:O	2.13	0.47
1:1:502:MET:HB2	1:1:537:GLU:HB2	1.95	0.47
1:3:166:ARG:HG3	1:3:392:TYR:HB2	1.97	0.47
1:1:795:VAL:C	1:1:797:GLU:H	2.17	0.47
1:4:750:GLU:OE2	1:4:755:ARG:HD3	2.15	0.47
1:3:809:ARG:HD2	5:3:4651:HOH:O	2.14	0.47
1:2:334:GLU:OE1	1:2:336:ARG:NH1	2.46	0.46
1:3:549:PHE:CE2	1:3:620:ALA:HA	2.49	0.46
1:4:164:ASP:OD2	1:4:439:ARG:HG2	2.15	0.46
1:4:890:GLN:HG3	1:4:891:VAL:N	2.30	0.46
1:3:377:LEU:HD22	1:3:708:TRP:HA	1.97	0.46
1:2:986:ILE:HG23	1:2:986:ILE:O	2.15	0.46
1:1:573:GLN:HB2	1:1:602:CYS:O	2.16	0.46
1:3:73:TRP:CE2	1:3:122:CYS:HB3	2.51	0.46
1:1:200:GLN:HG2	1:1:391:HIS:HB2	1.97	0.46
1:2:390:SER:HA	1:2:391:HIS:HA	1.74	0.46
1:2:833:ALA:HB1	1:2:858:ILE:O	2.15	0.46
1:4:250:LEU:C	1:4:251:ARG:HG2	2.36	0.46
1:4:390:SER:HA	1:4:391:HIS:HA	1.76	0.46
1:4:79:PRO:HG2	1:4:80:GLU:OE2	2.16	0.46
1:2:148:SER:HA	1:2:165:SER:OG	2.16	0.46
1:2:754:LYS:HE2	1:2:1022:GLN:HE21	1.80	0.46
1:3:100:TYR:CZ	1:3:602:CYS:HB3	2.51	0.46
1:1:114:VAL:HB	1:1:115:PRO:HD2	1.97	0.46
1:2:533:LEU:C	1:2:533:LEU:HD23	2.36	0.46
1:1:361:PRO:HB3	1:1:609:ALA:HB1	1.97	0.46
1:3:35:SER:HB2	1:3:217:LYS:HD2	1.97	0.46
1:4:601:PHE:CD1	1:4:796:SER:HA	2.51	0.46
1:4:333:ARG:HA	1:4:345:ASN:OD1	2.15	0.46
1:1:930:VAL:O	1:1:932:PRO:HD3	2.15	0.46
1:1:166:ARG:HG3	1:1:392:TYR:HB2	1.97	0.46
1:3:372:MET:HE3	1:3:397:LEU:HD23	1.97	0.46
1:1:359:HIS:CD2	1:1:573:GLN:HA	2.51	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:99:ILE:O	1:2:204:ARG:HG2	2.16	0.46
1:2:230:ARG:HD3	5:2:7562:HOH:O	2.14	0.46
1:1:546:LEU:HA	1:1:546:LEU:HD22	1.80	0.45
1:1:237:ARG:HH11	1:1:237:ARG:HB3	1.80	0.45
1:3:554:GLN:HG3	5:3:7553:HOH:O	2.15	0.45
1:3:433:LEU:N	1:3:434:PRO:CD	2.78	0.45
1:2:166:ARG:HG3	1:2:392:TYR:CB	2.46	0.45
1:3:595:THR:HA	1:3:596:PRO:C	2.37	0.45
1:1:799:THR:HG22	1:1:799:THR:O	2.16	0.45
1:1:147:ASN:HA	1:1:148:SER:HA	1.63	0.45
1:3:245:GLN:HG2	1:3:288:ARG:CG	2.46	0.45
1:1:194:GLY:O	1:1:198:GLU:HG3	2.16	0.45
1:1:101:THR:HG23	1:1:204:ARG:NH2	2.31	0.45
1:2:245:GLN:HG2	1:2:288:ARG:CG	2.43	0.45
1:4:163:GLN:O	1:4:164:ASP:HB3	2.17	0.45
1:4:235:PHE:CE2	1:4:345:ASN:HA	2.52	0.45
1:2:887:GLN:NE2	1:2:980:GLU:O	2.49	0.45
1:2:892:ALA:HB3	1:2:946:TYR:CE1	2.51	0.45
1:4:90:TRP:CZ3	1:4:121:GLY:HA3	2.52	0.45
1:2:66:PRO:HG2	1:2:67:GLU:OE1	2.17	0.45
1:2:132:SER:HA	1:2:135:GLN:CD	2.37	0.45
1:2:16:TRP:CG	1:2:189:LEU:HD13	2.52	0.45
1:1:66:PRO:HG2	1:1:67:GLU:OE1	2.15	0.45
1:2:163:GLN:O	1:2:164:ASP:HB3	2.17	0.45
1:3:233:ASP:OD1	1:3:234:ASP:N	2.49	0.45
1:2:537:GLU:HA	1:2:566:PHE:O	2.17	0.45
1:1:305:ILE:HD11	1:1:645:ARG:HB3	1.98	0.45
1:2:52:ARG:O	1:2:213:SER:HB2	2.16	0.45
1:2:780:LEU:HA	1:2:886:CYS:HB3	1.99	0.45
1:1:822:LEU:HD11	1:1:824:GLN:O	2.17	0.45
1:3:789:LEU:HD11	1:3:993:ILE:HG22	1.97	0.45
1:3:356:ARG:HH22	1:3:367:MET:CE	2.30	0.44
1:3:153:TRP:HB2	1:3:185:ALA:HB3	1.99	0.44
1:3:505:ARG:O	1:3:519:SER:HA	2.16	0.44
1:1:619:GLU:HA	1:1:912:ALA:HB2	1.99	0.44
1:1:390:SER:HA	1:1:391:HIS:HA	1.72	0.44
1:1:505:ARG:O	1:1:519:SER:HA	2.17	0.44
1:4:958:ASN:C	1:4:958:ASN:OD1	2.55	0.44
1:4:100:TYR:CE1	1:4:602:CYS:HB3	2.51	0.44
1:3:433:LEU:HB3	1:3:434:PRO:HD3	1.99	0.44
1:3:194:GLY:O	1:3:198:GLU:HG3	2.18	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:1006:GLU:HG2	1:3:1007:PHE:CD1	2.53	0.44
1:2:59:ARG:HB2	1:2:124:SER:OG	2.18	0.44
1:1:223:SER:O	1:1:224:ASP:HB2	2.17	0.44
1:2:674:PRO:O	1:2:675:GLN:HB2	2.18	0.44
1:1:91:GLN:HG3	1:1:96:ASP:OD1	2.17	0.44
1:4:472:TYR:O	1:4:476:LYS:HG2	2.17	0.44
1:1:795:VAL:O	1:1:797:GLU:N	2.50	0.44
1:2:117:GLU:OE1	1:2:117:GLU:HA	2.18	0.44
1:3:147:ASN:HA	1:3:148:SER:HA	1.70	0.44
1:1:571:VAL:CG2	1:1:609:ALA:HA	2.48	0.44
1:3:353:GLY:HA2	1:3:386:ALA:O	2.18	0.44
1:3:390:SER:HA	1:3:391:HIS:HA	1.78	0.44
1:1:525:SER:O	1:2:561:ARG:HD3	2.17	0.44
1:3:225:PHE:HA	1:3:243:GLU:O	2.18	0.44
1:4:245:GLN:HG2	1:4:288:ARG:CG	2.46	0.44
1:4:223:SER:O	1:4:224:ASP:HB2	2.17	0.44
1:2:102:ASN:OD1	1:2:201:ASP:HB2	2.18	0.44
1:3:690:SER:HB2	5:3:5032:HOH:O	2.18	0.44
1:2:606:LEU:O	1:2:614:HIS:HB2	2.17	0.44
1:3:606:LEU:O	1:3:614:HIS:HB2	2.18	0.43
1:1:128:ASN:HA	1:1:180:GLY:O	2.18	0.43
1:1:163:GLN:O	1:1:164:ASP:HB3	2.18	0.43
1:2:945:ASN:HB3	1:2:1023:LYS:HE2	1.99	0.43
1:4:773:LYS:HE3	1:4:774:LYS:O	2.19	0.43
1:2:372:MET:CE	1:2:395:HIS:HB3	2.48	0.43
1:2:245:GLN:CG	1:2:288:ARG:HG2	2.45	0.43
1:1:801:ILE:CD1	1:1:801:ILE:H	2.29	0.43
1:3:359:HIS:CD2	1:3:573:GLN:HA	2.53	0.43
1:1:855:THR:OG1	1:1:867:THR:HB	2.19	0.43
1:3:546:LEU:HA	5:3:4130:HOH:O	2.17	0.43
1:1:226:HIS:O	1:1:242:ALA:HA	2.19	0.43
1:2:73:TRP:CE2	1:2:122:CYS:HB3	2.52	0.43
1:2:939:CYS:SG	1:2:956:GLN:HG3	2.58	0.43
1:3:764:PHE:CE1	1:3:781:ARG:NH1	2.86	0.43
1:4:127:PHE:CE2	1:4:184:LEU:HG	2.53	0.43
1:4:359:HIS:CD2	1:4:573:GLN:HA	2.53	0.43
1:4:67:GLU:N	1:4:67:GLU:OE1	2.45	0.43
1:4:427:THR:O	1:4:467:ASN:HB2	2.17	0.43
1:4:807:VAL:HG13	1:4:808:GLU:N	2.33	0.43
1:1:815:HIS:HE1	1:1:877:PRO:O	2.00	0.43
1:4:651:LEU:HD22	1:4:667:GLU:OE1	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4:750:GLU:HG3	1:4:755:ARG:HG2	1.99	0.43
1:2:422:PRO:HG3	1:3:285:TYR:CE1	2.52	0.43
1:2:800:ARG:HH11	1:2:800:ARG:HB3	1.83	0.43
1:2:663:LEU:HD23	1:2:663:LEU:C	2.39	0.43
1:3:301:TRP:CH2	1:3:452:SER:HA	2.53	0.43
1:3:663:LEU:HD21	1:3:686:PRO:HG2	2.01	0.43
1:3:963:SER:HB3	1:3:983:TRP:NE1	2.33	0.43
1:1:610:ASP:O	1:1:611:ARG:HB2	2.18	0.43
1:1:240:LEU:HD23	1:1:240:LEU:C	2.38	0.43
1:2:569:ASP:O	1:2:605:GLY:HA2	2.19	0.43
1:3:577:LYS:O	1:3:584:PRO:HA	2.19	0.43
1:4:102:ASN:ND2	1:4:103:VAL:HG23	2.34	0.43
1:2:356:ARG:HH22	1:2:367:MET:HE2	1.83	0.43
1:3:843:GLN:HA	1:3:847:LYS:O	2.19	0.43
1:1:708:TRP:CZ3	1:1:709:SER:HB3	2.54	0.43
1:1:59:ARG:HB2	1:1:124:SER:OG	2.18	0.43
1:4:166:ARG:HG3	1:4:392:TYR:HB2	2.01	0.43
1:1:352:ARG:HG2	1:1:553:TRP:CH2	2.54	0.43
1:4:869:ASP:OD1	1:4:1015:HIS:ND1	2.42	0.43
1:3:807:VAL:HG13	1:3:808:GLU:N	2.32	0.43
1:3:367:MET:HE2	1:3:372:MET:HG2	2.01	0.43
1:2:237:ARG:NH1	1:2:237:ARG:HG3	2.34	0.43
1:4:737:ILE:HG23	1:4:737:ILE:O	2.18	0.43
1:3:619:GLU:HA	1:3:912:ALA:HB2	2.01	0.43
1:2:878:HIS:NE2	1:2:1010:SER:HB3	2.34	0.43
1:4:464:HIS:HB2	1:4:489:GLY:HA3	2.01	0.43
1:1:984:LEU:HD21	1:1:986:ILE:HD11	2.00	0.43
1:3:305:ILE:HD11	1:3:645:ARG:HB3	2.01	0.43
1:1:606:LEU:O	1:1:614:HIS:HB2	2.19	0.43
1:2:128:ASN:HA	1:2:180:GLY:O	2.19	0.43
1:2:126:THR:HA	1:2:182:ASN:O	2.19	0.43
1:3:930:VAL:O	1:3:932:PRO:HD3	2.19	0.42
1:1:823:LEU:HD11	1:1:841:ALA:HB2	2.01	0.42
1:1:795:VAL:C	1:1:797:GLU:N	2.72	0.42
1:3:651:LEU:HD12	1:3:651:LEU:C	2.40	0.42
1:3:608:PHE:CE1	1:3:614:HIS:CD2	3.07	0.42
1:3:887:GLN:NE2	1:3:980:GLU:O	2.52	0.42
1:4:652:LEU:HD11	1:4:698:VAL:HB	2.00	0.42
1:1:427:THR:O	1:1:467:ASN:HB2	2.19	0.42
1:3:163:GLN:O	1:3:164:ASP:HB3	2.19	0.42
1:2:147:ASN:HA	1:2:148:SER:HA	1.67	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:433:LEU:N	1:1:434:PRO:CD	2.82	0.42
1:3:127:PHE:CE2	1:3:184:LEU:HG	2.55	0.42
1:4:853:ARG:NH1	1:4:871:GLU:OE2	2.42	0.42
1:1:751:LEU:HD23	1:1:862:GLY:HA2	2.01	0.42
1:3:111:PRO:HA	1:3:112:PRO:HA	1.85	0.42
1:3:442:ARG:HD3	5:3:4049:HOH:O	2.19	0.42
1:2:651:LEU:HD23	1:2:651:LEU:C	2.40	0.42
1:3:754:LYS:HE3	1:3:1022:GLN:OE1	2.20	0.42
1:4:52:ARG:O	1:4:213:SER:HB2	2.20	0.42
1:1:326:GLU:OE1	1:1:326:GLU:HA	2.20	0.42
1:1:463:GLY:HA2	5:1:4629:HOH:O	2.19	0.42
1:3:261:TRP:CZ3	1:3:266:GLN:HB2	2.55	0.42
1:4:377:LEU:O	1:4:381:GLN:HB2	2.20	0.42
1:3:751:LEU:HD23	1:3:862:GLY:HA2	2.01	0.42
1:1:899:GLY:HA2	1:1:915:PHE:CE1	2.55	0.42
1:3:375:ASP:O	1:3:379:MET:HG3	2.20	0.42
1:4:742:THR:CG2	1:4:743:SER:N	2.82	0.42
1:2:1017:GLN:HB2	5:2:7130:HOH:O	2.19	0.42
1:4:43:ARG:HD2	1:4:261:TRP:CD2	2.55	0.42
1:4:782:ASP:OD1	1:4:842:TRP:HH2	2.03	0.42
1:1:502:MET:CB	1:1:537:GLU:HB2	2.50	0.42
1:2:340:GLY:O	1:2:532:PRO:HB3	2.19	0.42
1:1:524:LEU:HD11	1:1:562:LEU:HG	2.02	0.42
1:2:784:PHE:HA	1:2:881:ARG:O	2.19	0.42
1:1:824:GLN:HG2	1:1:825:CYS:N	2.35	0.42
1:3:730:LEU:HA	1:3:731:PRO:HD3	1.92	0.42
1:3:361:PRO:HB3	1:3:609:ALA:HB1	2.01	0.42
1:1:225:PHE:HA	1:1:243:GLU:O	2.20	0.42
1:1:561:ARG:HD3	1:2:525:SER:O	2.19	0.42
1:3:355:ASN:OD1	1:3:388:ARG:HD3	2.20	0.42
1:1:86:VAL:HG13	1:1:87:PRO:HA	2.01	0.42
1:3:133:TRP:CE3	1:3:216:HIS:HB2	2.54	0.42
1:4:35:SER:HB2	1:4:217:LYS:HD2	2.02	0.42
1:4:246:MET:SD	1:4:246:MET:C	2.99	0.42
1:2:930:VAL:HA	1:2:973:ARG:HD3	2.01	0.41
1:1:127:PHE:CD2	1:1:127:PHE:N	2.88	0.41
1:2:583:ASN:HA	1:2:584:PRO:HD3	1.81	0.41
1:4:844:HIS:ND1	1:4:845:GLN:HG2	2.34	0.41
1:1:991:MET:CE	1:1:1003:VAL:HG21	2.50	0.41
1:2:571:VAL:CG2	1:2:609:ALA:HA	2.49	0.41
1:3:907:PRO:HG2	1:3:990:HIS:O	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:78:LEU:HA	1:1:79:PRO:HD3	1.92	0.41
1:2:842:TRP:HZ3	1:2:852:SER:HB3	1.85	0.41
1:4:178:ARG:HG2	1:4:182:ASN:OD1	2.20	0.41
1:1:16:TRP:CG	1:1:189:LEU:HD13	2.55	0.41
1:1:416:GLU:HG3	1:1:460:ASN:O	2.19	0.41
1:3:963:SER:HB3	1:3:983:TRP:CE2	2.56	0.41
1:3:127:PHE:CD2	1:3:127:PHE:N	2.88	0.41
1:1:753:ASN:HB2	1:1:771:GLY:HA2	2.00	0.41
1:4:726:LEU:HA	5:4:7519:HOH:O	2.20	0.41
1:3:482:ARG:HA	1:3:483:PRO:HD3	1.94	0.41
1:4:663:LEU:O	1:4:663:LEU:HD23	2.21	0.41
1:4:702:GLN:HE22	1:4:708:TRP:HH2	1.67	0.41
1:4:894:ARG:HH12	1:4:921:PRO:HG3	1.85	0.41
1:3:105:TYR:CE2	1:3:199:ASP:HB2	2.54	0.41
1:4:559:TYR:HB2	1:4:562:LEU:HD12	2.02	0.41
1:1:237:ARG:HH11	1:1:237:ARG:CB	2.34	0.41
1:2:646:HIS:CD2	1:2:673:ALA:HA	2.54	0.41
1:2:578:TYR:CE2	1:2:584:PRO:HG3	2.55	0.41
1:4:78:LEU:HD23	5:4:4504:HOH:O	2.20	0.41
1:2:649:ASN:O	1:2:702:GLN:HA	2.21	0.41
1:2:372:MET:HE1	1:2:395:HIS:HB3	2.03	0.41
1:2:806:TRP:CE2	1:2:809:ARG:NH2	2.89	0.41
1:4:105:TYR:CE2	1:4:199:ASP:HB2	2.55	0.41
1:2:851:ILE:HB	1:2:871:GLU:HB2	2.01	0.41
1:2:199:ASP:C	1:2:416:GLU:HG2	2.41	0.41
1:2:693:GLN:OE1	1:2:724:GLU:HB2	2.21	0.41
1:1:755:ARG:HH21	1:1:772:ASP:HA	1.86	0.41
1:4:482:ARG:HA	1:4:483:PRO:HD3	1.96	0.41
1:4:610:ASP:O	1:4:611:ARG:HB2	2.20	0.41
1:3:372:MET:HE1	1:3:397:LEU:HB3	2.03	0.41
1:2:542:MET:HE3	1:2:601:PHE:HA	2.02	0.41
1:2:361:PRO:HB3	1:2:609:ALA:HB1	2.03	0.41
1:3:542:MET:CE	1:3:600:GLN:HG2	2.51	0.41
1:1:797:GLU:C	1:1:799:THR:H	2.24	0.41
1:1:601:PHE:CE2	1:1:796:SER:HA	2.56	0.41
1:3:651:LEU:HD11	1:3:701:VAL:HB	2.03	0.41
1:1:801:ILE:CD1	1:1:801:ILE:N	2.84	0.41
1:3:767:GLN:HE21	1:3:774:LYS:HD3	1.86	0.41
1:1:833:ALA:HB2	1:1:859:ASP:HA	2.02	0.41
1:3:578:TYR:CE2	1:3:584:PRO:HB3	2.56	0.41
1:4:789:LEU:HD11	1:4:993:ILE:HG22	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:650:GLU:HB3	1:2:670:LEU:HD12	2.02	0.41
1:2:937:LEU:HA	1:2:957:PHE:O	2.21	0.41
1:2:807:VAL:HG13	1:2:808:GLU:N	2.35	0.41
1:1:513:PRO:O	1:1:514:ALA:HB3	2.21	0.41
1:3:883:GLY:HA3	1:3:987:ASP:HA	2.02	0.41
1:4:836:ILE:O	1:4:855:THR:HA	2.21	0.41
1:1:131:GLU:O	1:1:135:GLN:HG2	2.21	0.41
1:4:372:MET:CE	1:4:395:HIS:HB3	2.50	0.41
1:1:630:ARG:HG2	1:1:630:ARG:HH11	1.86	0.40
1:4:147:ASN:HA	1:4:148:SER:HA	1.64	0.40
1:2:749:ILE:N	1:2:749:ILE:HD12	2.36	0.40
1:3:522:LYS:HE3	1:4:560:PRO:HD3	2.03	0.40
1:3:873:ALA:O	1:3:876:THR:HG22	2.20	0.40
1:1:820:ALA:HB2	1:1:842:TRP:CE2	2.56	0.40
1:1:148:SER:HA	1:1:165:SER:OG	2.20	0.40
1:1:577:LYS:O	1:1:584:PRO:HA	2.21	0.40
1:2:200:GLN:HG2	1:2:391:HIS:HB2	2.04	0.40
1:3:146:VAL:HG11	1:3:150:PHE:CD2	2.56	0.40
1:4:106:PRO:HD3	1:4:204:ARG:NH1	2.36	0.40
1:4:754:LYS:HE2	1:4:1022:GLN:OE1	2.21	0.40
1:2:568:TRP:CD2	1:2:569:ASP:HB3	2.55	0.40
1:3:561:ARG:HD3	1:4:525:SER:O	2.22	0.40
1:4:577:LYS:O	1:4:584:PRO:HA	2.21	0.40
1:1:360:HIS:CE1	1:1:362:LEU:HB2	2.56	0.40
1:3:749:ILE:N	1:3:749:ILE:CD1	2.83	0.40
1:2:359:HIS:CD2	1:2:573:GLN:HA	2.56	0.40
1:3:725:ASN:HB2	5:3:6007:HOH:O	2.21	0.40
1:2:854:LYS:HA	1:2:867:THR:O	2.21	0.40
1:4:649:ASN:HA	2:4:1024:DMS:H21	2.04	0.40
1:4:226:HIS:O	1:4:242:ALA:HA	2.21	0.40
1:3:778:THR:HG23	1:3:887:GLN:OE1	2.22	0.40
1:3:630:ARG:HB2	1:3:637:GLU:HB3	2.04	0.40
1:3:825:CYS:HA	1:3:837:THR:O	2.22	0.40
1:3:782:ASP:HB2	1:3:842:TRP:CH2	2.56	0.40
1:2:333:ARG:HA	1:2:345:ASN:OD1	2.21	0.40
1:1:670:LEU:HD23	1:1:670:LEU:HA	1.90	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	1	1009/1023 (99%)	948 (94%)	56 (6%)	5 (0%)	34	55
1	2	1009/1023 (99%)	959 (95%)	49 (5%)	1 (0%)	56	78
1	3	1009/1023 (99%)	953 (94%)	55 (6%)	1 (0%)	56	78
1	4	1009/1023 (99%)	946 (94%)	60 (6%)	3 (0%)	46	68
All	All	4036/4092 (99%)	3806 (94%)	220 (6%)	10 (0%)	52	75

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1	795	VAL
1	1	794	GLY
1	4	794	GLY
1	1	796	SER
1	1	798	ALA
1	3	164	ASP
1	4	164	ASP
1	2	164	ASP
1	1	511	PRO
1	4	511	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	1	863/874 (99%)	856 (99%)	7 (1%)	86	96

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	2	863/874 (99%)	852 (99%)	11 (1%)	76	92
1	3	863/874 (99%)	853 (99%)	10 (1%)	78	93
1	4	863/874 (99%)	858 (99%)	5 (1%)	90	97
All	All	3452/3496 (99%)	3419 (99%)	33 (1%)	82	95

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1	277	GLU
1	1	333	ARG
1	1	519	SER
1	1	546	LEU
1	1	735	HIS
1	1	795	VAL
1	1	885	ASN
1	2	333	ARG
1	2	519	SER
1	2	546	LEU
1	2	604	ASN
1	2	651	LEU
1	2	730	LEU
1	2	768	MET
1	2	800	ARG
1	2	850	PHE
1	2	885	ASN
1	2	916	ASP
1	3	135	GLN
1	3	178	ARG
1	3	262	GLN
1	3	333	ARG
1	3	519	SER
1	3	604	ASN
1	3	687	GLN
1	3	772	ASP
1	3	956	GLN
1	3	1017	GLN
1	4	112	PRO
1	4	333	ARG
1	4	519	SER
1	4	795	VAL
1	4	850	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	1	510	GLN
1	1	817	GLN
1	1	863	GLN
1	2	266	GLN
1	2	381	GLN
1	2	624	GLN
1	2	804	ASN
1	2	966	GLN
1	2	1022	GLN
1	3	266	GLN
1	3	634	GLN
1	3	824	GLN
1	4	804	ASN
1	4	863	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](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 156 ligands modelled in this entry, 26 are monoatomic - leaving 130 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
2	DMS	1	8401	-	3,3,3	0.21	0	3,3,3	0.57	0
2	DMS	1	8402	-	3,3,3	0.19	0	3,3,3	0.58	0
2	DMS	1	8403	-	3,3,3	0.22	0	3,3,3	0.59	0
2	DMS	1	8404	-	3,3,3	0.28	0	3,3,3	0.60	0
2	DMS	1	8405	-	3,3,3	0.26	0	3,3,3	0.60	0
2	DMS	1	8406	-	3,3,3	0.24	0	3,3,3	0.60	0
2	DMS	1	8407	-	3,3,3	0.21	0	3,3,3	0.59	0
2	DMS	1	8408	-	3,3,3	0.23	0	3,3,3	0.62	0
2	DMS	1	8409	-	3,3,3	0.25	0	3,3,3	0.58	0
2	DMS	1	8411	-	3,3,3	0.28	0	3,3,3	0.60	0
2	DMS	1	8412	-	3,3,3	0.24	0	3,3,3	0.54	0
2	DMS	1	8414	-	3,3,3	0.25	0	3,3,3	0.58	0
2	DMS	1	8416	-	3,3,3	0.25	0	3,3,3	0.59	0
2	DMS	1	8419	-	3,3,3	0.23	0	3,3,3	0.60	0
2	DMS	1	8421	-	3,3,3	0.25	0	3,3,3	0.59	0
2	DMS	1	8425	4	3,3,3	0.20	0	3,3,3	0.57	0
2	DMS	1	8501	-	3,3,3	0.21	0	3,3,3	0.62	0
2	DMS	1	8503	-	3,3,3	0.24	0	3,3,3	0.58	0
2	DMS	1	8504	-	3,3,3	0.27	0	3,3,3	0.60	0
2	DMS	1	8602	-	3,3,3	0.24	0	3,3,3	0.59	0
2	DMS	1	8603	-	3,3,3	0.18	0	3,3,3	0.58	0
2	DMS	1	8604	-	3,3,3	0.25	0	3,3,3	0.60	0
2	DMS	1	8605	-	3,3,3	0.23	0	3,3,3	0.60	0
2	DMS	1	8606	-	3,3,3	0.24	0	3,3,3	0.57	0
2	DMS	1	8607	-	3,3,3	0.22	0	3,3,3	0.59	0
2	DMS	1	8609	-	3,3,3	0.23	0	3,3,3	0.62	0
2	DMS	1	8610	-	3,3,3	0.32	0	3,3,3	0.65	0
2	DMS	2	8401	-	3,3,3	0.27	0	3,3,3	0.62	0
2	DMS	2	8402	-	3,3,3	0.28	0	3,3,3	0.56	0
2	DMS	2	8403	-	3,3,3	0.29	0	3,3,3	0.59	0
2	DMS	2	8404	-	3,3,3	0.24	0	3,3,3	0.59	0
2	DMS	2	8405	-	3,3,3	0.16	0	3,3,3	0.55	0
2	DMS	2	8406	-	3,3,3	0.19	0	3,3,3	0.57	0
2	DMS	2	8408	-	3,3,3	0.23	0	3,3,3	0.61	0
2	DMS	2	8409	-	3,3,3	0.25	0	3,3,3	0.63	0
2	DMS	2	8410	-	3,3,3	0.23	0	3,3,3	0.61	0
2	DMS	2	8411	-	3,3,3	0.26	0	3,3,3	0.58	0
2	DMS	2	8412	-	3,3,3	0.29	0	3,3,3	0.60	0
2	DMS	2	8414	-	3,3,3	0.23	0	3,3,3	0.59	0
2	DMS	2	8416	-	3,3,3	0.21	0	3,3,3	0.59	0
2	DMS	2	8417	-	3,3,3	0.25	0	3,3,3	0.59	0
2	DMS	2	8420	-	3,3,3	0.25	0	3,3,3	0.57	0
2	DMS	2	8421	-	3,3,3	0.24	0	3,3,3	0.61	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	DMS	2	8423	-	3,3,3	0.23	0	3,3,3	0.58	0
2	DMS	2	8425	4	3,3,3	0.24	0	3,3,3	0.58	0
2	DMS	2	8502	-	3,3,3	0.24	0	3,3,3	0.61	0
2	DMS	2	8504	-	3,3,3	0.23	0	3,3,3	0.59	0
2	DMS	2	8508	-	3,3,3	0.24	0	3,3,3	0.59	0
2	DMS	2	8601	-	3,3,3	0.26	0	3,3,3	0.59	0
2	DMS	2	8602	-	3,3,3	0.25	0	3,3,3	0.57	0
2	DMS	2	8603	-	3,3,3	0.26	0	3,3,3	0.60	0
2	DMS	2	8604	-	3,3,3	0.23	0	3,3,3	0.59	0
2	DMS	2	8605	-	3,3,3	0.22	0	3,3,3	0.59	0
2	DMS	2	8606	-	3,3,3	0.22	0	3,3,3	0.59	0
2	DMS	2	8607	-	3,3,3	0.20	0	3,3,3	0.58	0
2	DMS	2	8608	-	3,3,3	0.24	0	3,3,3	0.59	0
2	DMS	2	8609	-	3,3,3	0.22	0	3,3,3	0.57	0
2	DMS	2	8610	-	3,3,3	0.29	0	3,3,3	0.61	0
2	DMS	2	8611	-	3,3,3	0.26	0	3,3,3	0.61	0
2	DMS	2	8612	-	3,3,3	0.22	0	3,3,3	0.59	0
2	DMS	2	8613	-	3,3,3	0.24	0	3,3,3	0.60	0
2	DMS	3	1024	-	3,3,3	0.22	0	3,3,3	0.59	0
2	DMS	3	8401	-	3,3,3	0.22	0	3,3,3	0.58	0
2	DMS	3	8402	-	3,3,3	0.30	0	3,3,3	0.64	0
2	DMS	3	8403	-	3,3,3	0.29	0	3,3,3	0.62	0
2	DMS	3	8404	-	3,3,3	0.19	0	3,3,3	0.62	0
2	DMS	3	8405	-	3,3,3	0.20	0	3,3,3	0.59	0
2	DMS	3	8407	-	3,3,3	0.24	0	3,3,3	0.58	0
2	DMS	3	8408	-	3,3,3	0.22	0	3,3,3	0.61	0
2	DMS	3	8409	-	3,3,3	0.25	0	3,3,3	0.57	0
2	DMS	3	8410	-	3,3,3	0.24	0	3,3,3	0.59	0
2	DMS	3	8411	-	3,3,3	0.25	0	3,3,3	0.60	0
2	DMS	3	8412	-	3,3,3	0.24	0	3,3,3	0.58	0
2	DMS	3	8414	-	3,3,3	0.26	0	3,3,3	0.59	0
2	DMS	3	8415	-	3,3,3	0.25	0	3,3,3	0.59	0
2	DMS	3	8416	-	3,3,3	0.25	0	3,3,3	0.60	0
2	DMS	3	8417	-	3,3,3	0.24	0	3,3,3	0.61	0
2	DMS	3	8420	-	3,3,3	0.24	0	3,3,3	0.58	0
2	DMS	3	8421	-	3,3,3	0.25	0	3,3,3	0.57	0
2	DMS	3	8423	-	3,3,3	0.25	0	3,3,3	0.59	0
2	DMS	3	8425	4	3,3,3	0.24	0	3,3,3	0.58	0
2	DMS	3	8428	-	3,3,3	0.22	0	3,3,3	0.59	0
2	DMS	3	8501	-	3,3,3	0.23	0	3,3,3	0.61	0
2	DMS	3	8601	-	3,3,3	0.25	0	3,3,3	0.57	0
2	DMS	3	8602	-	3,3,3	0.21	0	3,3,3	0.57	0
2	DMS	3	8603	-	3,3,3	0.22	0	3,3,3	0.56	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	DMS	3	8604	-	3,3,3	0.20	0	3,3,3	0.56	0
2	DMS	3	8605	-	3,3,3	0.22	0	3,3,3	0.59	0
2	DMS	3	8606	-	3,3,3	0.18	0	3,3,3	0.60	0
2	DMS	3	8607	-	3,3,3	0.20	0	3,3,3	0.56	0
2	DMS	3	8608	-	3,3,3	0.21	0	3,3,3	0.60	0
2	DMS	3	8609	-	3,3,3	0.20	0	3,3,3	0.61	0
2	DMS	3	8610	-	3,3,3	0.28	0	3,3,3	0.62	0
2	DMS	3	8611	-	3,3,3	0.24	0	3,3,3	0.57	0
2	DMS	3	8612	-	3,3,3	0.26	0	3,3,3	0.63	0
2	DMS	3	8613	-	3,3,3	0.19	0	3,3,3	0.57	0
2	DMS	4	1024	4	3,3,3	0.21	0	3,3,3	0.58	0
2	DMS	4	8401	-	3,3,3	0.22	0	3,3,3	0.61	0
2	DMS	4	8402	-	3,3,3	0.17	0	3,3,3	0.58	0
2	DMS	4	8403	-	3,3,3	0.18	0	3,3,3	0.57	0
2	DMS	4	8404	-	3,3,3	0.24	0	3,3,3	0.63	0
2	DMS	4	8405	-	3,3,3	0.26	0	3,3,3	0.63	0
2	DMS	4	8406	-	3,3,3	0.30	0	3,3,3	0.55	0
2	DMS	4	8408	-	3,3,3	0.25	0	3,3,3	0.60	0
2	DMS	4	8409	-	3,3,3	0.24	0	3,3,3	0.61	0
2	DMS	4	8410	-	3,3,3	0.24	0	3,3,3	0.62	0
2	DMS	4	8411	-	3,3,3	0.29	0	3,3,3	0.59	0
2	DMS	4	8412	-	3,3,3	0.22	0	3,3,3	0.58	0
2	DMS	4	8414	-	3,3,3	0.26	0	3,3,3	0.59	0
2	DMS	4	8416	-	3,3,3	0.22	0	3,3,3	0.58	0
2	DMS	4	8417	-	3,3,3	0.23	0	3,3,3	0.59	0
2	DMS	4	8419	-	3,3,3	0.21	0	3,3,3	0.59	0
2	DMS	4	8421	-	3,3,3	0.23	0	3,3,3	0.61	0
2	DMS	4	8423	-	3,3,3	0.25	0	3,3,3	0.58	0
2	DMS	4	8501	-	3,3,3	0.23	0	3,3,3	0.59	0
2	DMS	4	8503	-	3,3,3	0.26	0	3,3,3	0.58	0
2	DMS	4	8508	-	3,3,3	0.20	0	3,3,3	0.57	0
2	DMS	4	8607	-	3,3,3	0.23	0	3,3,3	0.58	0
2	DMS	4	8608	-	3,3,3	0.25	0	3,3,3	0.60	0
2	DMS	4	8610	-	3,3,3	0.24	0	3,3,3	0.56	0
2	DMS	4	8611	-	3,3,3	0.19	0	3,3,3	0.56	0
2	DMS	4	8612	-	3,3,3	0.21	0	3,3,3	0.60	0
2	DMS	4	8613	-	3,3,3	0.24	0	3,3,3	0.60	0
2	DMS	4	8614	-	3,3,3	0.24	0	3,3,3	0.57	0
2	DMS	4	8615	-	3,3,3	0.24	0	3,3,3	0.61	0
2	DMS	4	8617	-	3,3,3	0.23	0	3,3,3	0.58	0
2	DMS	4	8618	-	3,3,3	0.20	0	3,3,3	0.57	0
2	DMS	4	8701	-	3,3,3	0.28	0	3,3,3	0.58	0
2	DMS	4	8703	-	3,3,3	0.19	0	3,3,3	0.54	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	DMS	4	8705	-	3,3,3	0.22	0	3,3,3	0.62	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	DMS	1	8401	-	-	0/0/0/0	0/0/0/0
2	DMS	1	8402	-	-	0/0/0/0	0/0/0/0
2	DMS	1	8403	-	-	0/0/0/0	0/0/0/0
2	DMS	1	8404	-	-	0/0/0/0	0/0/0/0
2	DMS	1	8405	-	-	0/0/0/0	0/0/0/0
2	DMS	1	8406	-	-	0/0/0/0	0/0/0/0
2	DMS	1	8407	-	-	0/0/0/0	0/0/0/0
2	DMS	1	8408	-	-	0/0/0/0	0/0/0/0
2	DMS	1	8409	-	-	0/0/0/0	0/0/0/0
2	DMS	1	8411	-	-	0/0/0/0	0/0/0/0
2	DMS	1	8412	-	-	0/0/0/0	0/0/0/0
2	DMS	1	8414	-	-	0/0/0/0	0/0/0/0
2	DMS	1	8416	-	-	0/0/0/0	0/0/0/0
2	DMS	1	8419	-	-	0/0/0/0	0/0/0/0
2	DMS	1	8421	-	-	0/0/0/0	0/0/0/0
2	DMS	1	8425	4	-	0/0/0/0	0/0/0/0
2	DMS	1	8501	-	-	0/0/0/0	0/0/0/0
2	DMS	1	8503	-	-	0/0/0/0	0/0/0/0
2	DMS	1	8504	-	-	0/0/0/0	0/0/0/0
2	DMS	1	8602	-	-	0/0/0/0	0/0/0/0
2	DMS	1	8603	-	-	0/0/0/0	0/0/0/0
2	DMS	1	8604	-	-	0/0/0/0	0/0/0/0
2	DMS	1	8605	-	-	0/0/0/0	0/0/0/0
2	DMS	1	8606	-	-	0/0/0/0	0/0/0/0
2	DMS	1	8607	-	-	0/0/0/0	0/0/0/0
2	DMS	1	8609	-	-	0/0/0/0	0/0/0/0
2	DMS	1	8610	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8401	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8402	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8403	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8404	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8405	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8406	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8408	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8409	-	-	0/0/0/0	0/0/0/0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	DMS	2	8410	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8411	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8412	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8414	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8416	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8417	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8420	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8421	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8423	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8425	4	-	0/0/0/0	0/0/0/0
2	DMS	2	8502	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8504	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8508	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8601	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8602	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8603	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8604	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8605	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8606	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8607	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8608	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8609	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8610	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8611	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8612	-	-	0/0/0/0	0/0/0/0
2	DMS	2	8613	-	-	0/0/0/0	0/0/0/0
2	DMS	3	1024	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8401	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8402	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8403	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8404	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8405	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8407	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8408	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8409	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8410	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8411	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8412	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8414	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8415	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8416	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8417	-	-	0/0/0/0	0/0/0/0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	DMS	3	8420	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8421	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8423	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8425	4	-	0/0/0/0	0/0/0/0
2	DMS	3	8428	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8501	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8601	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8602	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8603	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8604	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8605	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8606	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8607	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8608	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8609	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8610	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8611	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8612	-	-	0/0/0/0	0/0/0/0
2	DMS	3	8613	-	-	0/0/0/0	0/0/0/0
2	DMS	4	1024	4	-	0/0/0/0	0/0/0/0
2	DMS	4	8401	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8402	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8403	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8404	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8405	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8406	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8408	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8409	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8410	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8411	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8412	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8414	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8416	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8417	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8419	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8421	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8423	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8501	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8503	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8508	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8607	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8608	-	-	0/0/0/0	0/0/0/0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	DMS	4	8610	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8611	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8612	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8613	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8614	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8615	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8617	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8618	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8701	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8703	-	-	0/0/0/0	0/0/0/0
2	DMS	4	8705	-	-	0/0/0/0	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.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	1	8409	DMS	1	0
2	3	8402	DMS	1	0
2	4	1024	DMS	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, 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	1	1011/1023 (98%)	-0.35	22 (2%) 65 69	5, 17, 37, 78	0
1	2	1011/1023 (98%)	-0.40	9 (0%) 85 88	4, 17, 37, 68	0
1	3	1011/1023 (98%)	-0.43	8 (0%) 87 89	4, 17, 39, 70	0
1	4	1011/1023 (98%)	-0.29	25 (2%) 61 65	4, 17, 38, 81	0
All	All	4044/4092 (98%)	-0.37	64 (1%) 74 78	4, 17, 38, 81	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	1	799	THR	8.4
1	1	800	ARG	8.2
1	4	800	ARG	7.3
1	4	798	ALA	7.2
1	1	798	ALA	7.1
1	1	796	SER	6.9
1	1	795	VAL	6.8
1	4	799	THR	6.7
1	4	735	HIS	5.3
1	4	732	ALA	5.3
1	1	801	ILE	5.1
1	4	795	VAL	5.1
1	1	689	GLU	5.0
1	1	686	PRO	4.9
1	4	797	GLU	4.7
1	3	800	ARG	4.6
1	4	796	SER	4.6
1	1	797	GLU	4.3
1	3	731	PRO	4.2
1	1	732	ALA	4.2
1	4	686	PRO	4.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	1	735	HIS	4.1
1	4	734	SER	4.0
1	1	730	LEU	3.9
1	4	731	PRO	3.7
1	3	730	LEU	3.7
1	4	689	GLU	3.7
1	4	634	GLN	3.6
1	1	731	PRO	3.6
1	1	733	ALA	3.6
1	4	730	LEU	3.6
1	2	684	GLU	3.5
1	1	771	GLY	3.4
1	4	733	ALA	3.3
1	1	687	GLN	3.2
1	2	800	ARG	3.2
1	1	634	GLN	3.0
1	2	689	GLU	2.9
1	1	734	SER	2.8
1	3	732	ALA	2.8
1	4	684	GLU	2.7
1	4	729	THR	2.7
1	4	861	SER	2.6
1	1	1023	LYS	2.5
1	2	731	PRO	2.5
1	3	689	GLU	2.5
1	4	580	GLU	2.5
1	1	729	THR	2.4
1	4	1022	GLN	2.4
1	3	735	HIS	2.4
1	2	80	GLU	2.3
1	2	797	GLU	2.3
1	3	76	CYS	2.3
1	4	829	THR	2.3
1	2	686	PRO	2.2
1	2	732	ALA	2.2
1	2	733	ALA	2.1
1	4	770	ILE	2.1
1	4	771	GLY	2.1
1	1	683	PRO	2.1
1	1	736	ALA	2.0
1	4	70	PRO	2.0
1	3	762	SER	2.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	4	581	ASN	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, 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	LLDF	B-factors(Å ²)	Q<0.9
2	DMS	2	8603	4/4	0.91	0.26	21.01	71,72,72,73	0
2	DMS	4	8417	4/4	0.80	0.38	17.81	91,91,91,92	0
2	DMS	3	8606	4/4	0.93	0.26	16.91	54,54,54,55	0
2	DMS	2	8417	4/4	0.86	0.28	16.03	63,65,65,65	0
2	DMS	1	8407	4/4	0.89	0.22	14.37	72,72,73,73	0
2	DMS	3	8417	4/4	0.94	0.27	14.24	66,66,67,67	0
2	DMS	3	8407	4/4	0.92	0.23	10.16	69,70,70,71	0
2	DMS	1	8504	4/4	0.96	0.17	9.68	43,43,43,44	0
2	DMS	3	8420	4/4	0.86	0.26	9.01	73,74,74,75	0
2	DMS	4	8615	4/4	0.92	0.25	7.62	49,50,51,52	0
2	DMS	1	8416	4/4	0.92	0.27	7.49	57,57,57,58	0
2	DMS	3	8403	4/4	0.98	0.17	7.43	34,34,35,35	0
2	DMS	2	8610	4/4	0.94	0.24	7.13	51,51,52,52	0
2	DMS	3	8603	4/4	0.96	0.23	6.95	64,64,64,65	0
2	DMS	1	8607	4/4	0.97	0.18	6.92	53,53,53,54	0
2	DMS	4	8410	4/4	0.95	0.35	6.83	65,65,65,65	0
2	DMS	3	8425	4/4	0.94	0.27	6.77	58,58,59,59	0
2	DMS	3	8611	4/4	0.94	0.30	6.40	60,61,62,62	0
2	DMS	4	8613	4/4	0.88	0.17	5.67	56,57,58,58	0
2	DMS	3	8402	4/4	0.97	0.19	5.18	27,27,27,29	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	DMS	2	8406	4/4	0.96	0.20	5.12	58,58,59,59	0
2	DMS	3	8411	4/4	0.99	0.18	5.10	38,38,38,38	0
2	DMS	2	8411	4/4	0.96	0.16	4.95	38,40,40,40	0
2	DMS	4	8402	4/4	0.98	0.15	4.74	25,28,28,29	0
2	DMS	2	8423	4/4	0.92	0.18	4.73	76,76,76,76	0
2	DMS	2	8410	4/4	0.88	0.23	4.72	87,87,88,88	0
2	DMS	2	8420	4/4	0.93	0.18	4.55	57,57,58,58	0
2	DMS	1	8412	4/4	0.96	0.23	4.52	44,45,46,47	0
2	DMS	2	8402	4/4	0.96	0.17	4.05	28,28,29,32	0
2	DMS	4	8404	4/4	0.98	0.16	3.92	45,46,47,48	0
2	DMS	4	8406	4/4	0.96	0.15	3.88	34,34,34,35	0
2	DMS	2	8609	4/4	0.89	0.24	3.67	67,68,68,68	0
2	DMS	4	8618	4/4	0.89	0.18	3.61	59,59,60,61	0
2	DMS	1	8404	4/4	0.98	0.15	3.48	38,39,39,39	0
2	DMS	1	8419	4/4	0.92	0.21	3.25	68,68,68,68	0
2	DMS	2	8401	4/4	0.99	0.15	3.23	14,17,17,19	0
2	DMS	4	8508	4/4	0.95	0.19	3.22	58,58,58,58	0
2	DMS	2	8425	4/4	0.97	0.28	3.03	52,53,53,53	0
2	DMS	1	8405	4/4	0.98	0.16	3.01	32,32,33,33	0
2	DMS	2	8403	4/4	0.98	0.15	2.87	29,29,29,30	0
2	DMS	4	8411	4/4	0.95	0.24	2.79	38,40,41,42	0
2	DMS	4	8701	4/4	0.97	0.14	2.69	21,22,23,25	0
2	DMS	4	8617	4/4	0.96	0.16	2.55	70,71,71,71	0
4	NA	4	3104	1/1	0.79	0.19	2.50	54,54,54,54	0
2	DMS	2	8613	4/4	0.92	0.19	2.43	63,64,65,65	0
2	DMS	3	8408	4/4	0.97	0.18	2.43	38,39,40,41	0
2	DMS	4	8405	4/4	0.97	0.22	2.42	42,43,43,43	0
2	DMS	2	8404	4/4	0.97	0.14	2.39	38,39,40,41	0
2	DMS	3	8423	4/4	0.96	0.14	2.30	63,63,64,64	0
2	DMS	3	8410	4/4	0.91	0.25	2.29	77,78,78,78	0
2	DMS	2	8412	4/4	0.97	0.19	2.28	37,37,38,38	0
2	DMS	1	8402	4/4	0.97	0.15	2.26	28,29,31,31	0
3	MG	1	3002	1/1	0.99	0.17	2.15	23,23,23,23	0
2	DMS	4	8423	4/4	0.96	0.13	2.00	63,63,63,64	0
2	DMS	4	8611	4/4	0.94	0.16	1.87	67,67,67,68	0
2	DMS	4	8401	4/4	0.99	0.13	1.85	20,20,20,22	0
2	DMS	2	8502	4/4	0.96	0.16	1.74	48,48,48,49	0
2	DMS	4	8614	4/4	0.86	0.17	1.72	61,61,62,62	0
2	DMS	1	8501	4/4	0.95	0.18	1.69	47,47,48,48	0
4	NA	3	3104	1/1	0.91	0.18	1.64	39,39,39,39	0
2	DMS	1	8606	4/4	0.98	0.15	1.62	39,40,40,41	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	DMS	4	8419	4/4	0.96	0.15	1.60	52,52,52,53	0
2	DMS	4	8703	4/4	0.95	0.18	1.53	59,59,60,60	0
2	DMS	4	8408	4/4	0.97	0.18	1.53	34,36,37,37	0
2	DMS	3	8412	4/4	0.96	0.17	1.52	43,44,44,45	0
2	DMS	4	8705	4/4	0.96	0.20	1.50	57,57,58,58	0
2	DMS	2	8504	4/4	0.98	0.20	1.44	63,63,63,63	0
2	DMS	2	8611	4/4	0.96	0.20	1.40	60,60,61,62	0
2	DMS	4	8412	4/4	0.99	0.17	1.39	33,33,34,35	0
2	DMS	4	1024	4/4	0.87	0.22	1.30	70,70,70,70	0
2	DMS	1	8408	4/4	0.96	0.17	1.27	45,46,47,47	0
2	DMS	1	8406	4/4	0.96	0.14	1.16	58,59,60,60	0
2	DMS	3	8404	4/4	0.97	0.13	1.12	30,31,32,33	0
2	DMS	1	8610	4/4	0.82	0.19	1.11	66,66,67,68	0
2	DMS	2	8408	4/4	0.96	0.16	1.10	55,55,55,56	0
4	NA	3	3102	1/1	0.98	0.14	0.97	17,17,17,17	0
2	DMS	2	8602	4/4	0.93	0.19	0.96	63,64,64,65	0
2	DMS	3	8401	4/4	0.99	0.13	0.90	16,17,17,18	0
3	MG	3	3002	1/1	0.98	0.13	0.86	17,17,17,17	0
2	DMS	3	8501	4/4	0.97	0.13	0.86	34,36,36,36	0
2	DMS	1	8425	4/4	0.95	0.17	0.75	49,49,49,49	0
4	NA	4	3103	1/1	0.90	0.14	0.75	41,41,41,41	0
4	NA	3	3103	1/1	0.81	0.14	0.73	34,34,34,34	0
2	DMS	4	8610	4/4	0.94	0.14	0.62	55,55,55,56	0
4	NA	4	3102	1/1	0.97	0.12	0.61	18,18,18,18	0
2	DMS	1	8609	4/4	0.92	0.17	0.54	43,43,45,45	0
2	DMS	1	8403	4/4	0.99	0.11	0.52	29,29,30,31	0
2	DMS	3	8604	4/4	0.98	0.16	0.48	44,44,44,44	0
2	DMS	2	8405	4/4	0.98	0.12	0.33	40,40,40,40	0
2	DMS	2	8605	4/4	0.95	0.12	0.24	62,62,63,63	0
2	DMS	3	8613	4/4	0.94	0.17	0.22	61,61,61,63	0
2	DMS	4	8612	4/4	0.94	0.14	0.21	60,60,61,62	0
4	NA	2	3103	1/1	0.98	0.13	0.19	28,28,28,28	0
2	DMS	3	8405	4/4	0.98	0.12	0.06	32,32,33,34	0
2	DMS	4	8501	4/4	0.97	0.12	-0.17	43,43,44,45	0
2	DMS	3	8605	4/4	0.95	0.11	-0.40	63,64,64,65	0
2	DMS	2	8606	4/4	0.94	0.12	-0.44	46,47,47,48	0
2	DMS	3	1024	4/4	0.95	0.11	-0.59	77,77,77,77	0
4	NA	4	3101	1/1	0.93	0.10	-0.67	18,18,18,18	0
2	DMS	4	8403	4/4	0.98	0.10	-0.87	26,26,27,29	0
4	NA	1	3101	1/1	0.98	0.09	-0.88	17,17,17,17	0
2	DMS	1	8401	4/4	0.99	0.10	-0.95	12,12,13,15	0
3	MG	4	3003	1/1	0.98	0.11	-1.14	29,29,29,29	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	NA	2	3102	1/1	0.97	0.11	-1.23	29,29,29,29	0
4	NA	2	3104	1/1	0.94	0.10	-1.30	27,27,27,27	0
3	MG	4	3002	1/1	0.97	0.09	-1.49	11,11,11,11	0
4	NA	1	3103	1/1	0.94	0.09	-1.55	30,30,30,30	0
3	MG	2	3002	1/1	0.97	0.07	-2.06	12,12,12,12	0
4	NA	2	3101	1/1	0.99	0.09	-2.34	12,12,12,12	0
4	NA	1	3102	1/1	0.97	0.10	-2.39	16,16,16,16	0
4	NA	3	3101	1/1	0.98	0.06	-2.70	10,10,10,10	0
3	MG	4	3001	1/1	0.97	0.06	-3.69	7,7,7,7	0
3	MG	3	3001	1/1	0.98	0.06	-4.41	15,15,15,15	0
3	MG	1	3001	1/1	0.97	0.05	-4.59	14,14,14,14	0
3	MG	2	3001	1/1	0.97	0.06	-13.82	11,11,11,11	0
2	DMS	2	8601	4/4	0.89	0.24	-	69,69,70,70	0
2	DMS	2	8508	4/4	0.94	0.17	-	72,72,73,73	0
2	DMS	3	8601	4/4	0.94	0.25	-	59,59,59,60	0
2	DMS	3	8421	4/4	0.95	0.18	-	58,58,58,58	0
2	DMS	1	8603	4/4	0.98	0.18	-	57,57,58,58	0
3	MG	1	3003	1/1	0.92	0.09	-	41,41,41,41	0
2	DMS	4	8414	4/4	0.94	0.16	-	52,52,53,54	0
2	DMS	3	8610	4/4	0.93	0.20	-	49,49,49,50	0
2	DMS	3	8415	4/4	0.90	0.17	-	60,61,61,62	0
2	DMS	4	8608	4/4	0.96	0.12	-	52,52,52,53	0
2	DMS	2	8608	4/4	0.94	0.16	-	53,54,55,55	0
2	DMS	1	8421	4/4	0.94	0.24	-	69,69,69,69	0
2	DMS	2	8421	4/4	0.98	0.17	-	52,53,53,53	0
2	DMS	2	8607	4/4	0.98	0.14	-	44,45,46,46	0
2	DMS	3	8607	4/4	0.94	0.17	-	65,65,65,66	0
2	DMS	3	8602	4/4	0.97	0.11	-	55,55,56,56	0
2	DMS	4	8503	4/4	0.82	0.28	-	83,83,84,84	0
2	DMS	1	8414	4/4	0.93	0.14	-	50,50,50,52	0
2	DMS	2	8612	4/4	0.93	0.18	-	48,49,50,52	0
2	DMS	1	8503	4/4	0.96	0.15	-	63,63,64,64	0
2	DMS	3	8428	4/4	0.90	0.21	-	79,79,79,79	0
2	DMS	4	8607	4/4	0.96	0.12	-	53,54,54,55	0
4	NA	3	3105	1/1	0.93	0.37	-	54,54,54,54	0
2	DMS	2	8604	4/4	0.95	0.18	-	62,63,63,63	0
2	DMS	3	8416	4/4	0.93	0.18	-	70,70,70,71	0
2	DMS	3	8612	4/4	0.94	0.18	-	47,47,48,49	0
2	DMS	1	8602	4/4	0.93	0.16	-	80,80,80,80	0
2	DMS	2	8409	4/4	0.93	0.22	-	42,43,44,45	0
2	DMS	2	8416	4/4	0.98	0.09	-	52,52,53,54	0
2	DMS	3	8609	4/4	0.89	0.17	-	52,52,54,54	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	DMS	1	8604	4/4	0.91	0.18	-	66,67,67,68	0
2	DMS	4	8416	4/4	0.96	0.15	-	51,51,52,53	0
2	DMS	1	8605	4/4	0.94	0.11	-	71,71,71,72	0
2	DMS	4	8409	4/4	0.96	0.18	-	45,45,45,46	0
2	DMS	2	8414	4/4	0.98	0.22	-	50,51,52,52	0
2	DMS	1	8411	4/4	0.98	0.17	-	40,41,41,42	0
2	DMS	1	8409	4/4	0.96	0.16	-	51,52,52,52	0
2	DMS	3	8409	4/4	0.96	0.17	-	39,39,40,40	0
2	DMS	3	8608	4/4	0.91	0.17	-	58,59,59,60	0
2	DMS	3	8414	4/4	0.97	0.18	-	41,41,43,43	0
2	DMS	4	8421	4/4	0.94	0.15	-	60,61,61,62	0

6.5 Other polymers [i](#)

There are no such residues in this entry.