



Full wwPDB X-ray Structure Validation Report

Sep 3, 2023 – 08:45 PM EDT

PDB ID : 3SBP
Title : Pseudomonas stutzeri nitrous oxide reductase, P1 crystal form
Authors : Pomowski, A.; Zumft, W.G.; Kroneck, P.M.H.; Einsle, O.
Deposited on : 2011-06-06
Resolution : 2.10 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  symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : 2.35
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) : 2.35

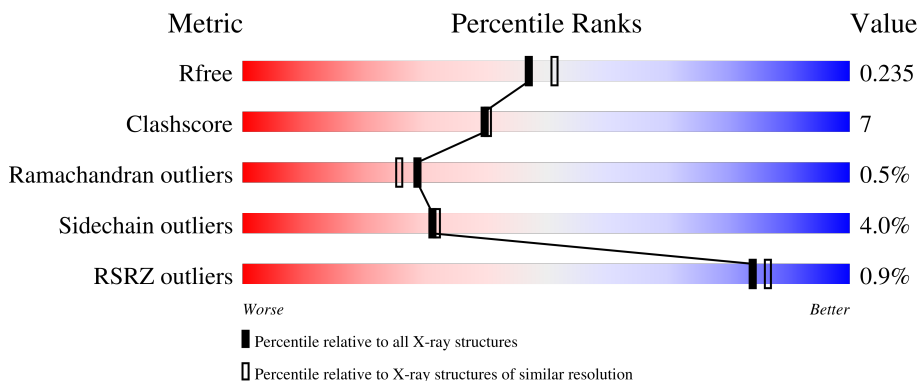
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 $\leq 5\%$. 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	638	 3% 74% 15% • 9%
1	B	638	 2% 76% 13% • 9%
1	C	638	 77% 12% • 9%
1	D	638	 78% 12% • 8%
1	E	638	 79% 11% • 9%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	638	 79% 10% • 9%
1	G	638	 79% 12% • 8%
1	H	638	 77% 13% • 9%

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
7	IMD	H	639	-	-	X	-

2 Entry composition

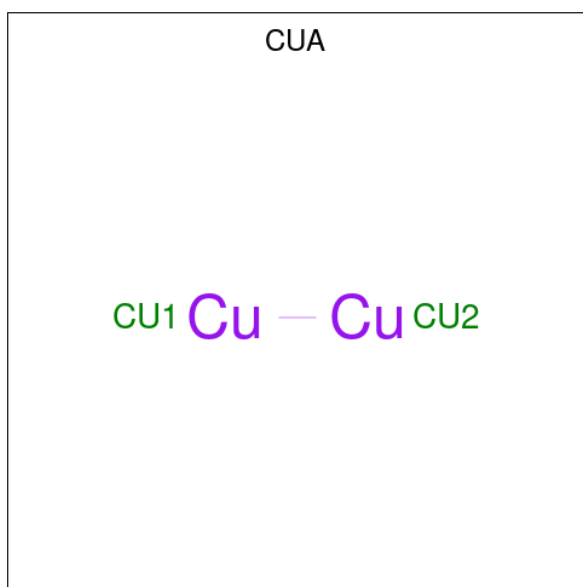
There are 8 unique types of molecules in this entry. The entry contains 39843 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Nitrous-oxide reductase.

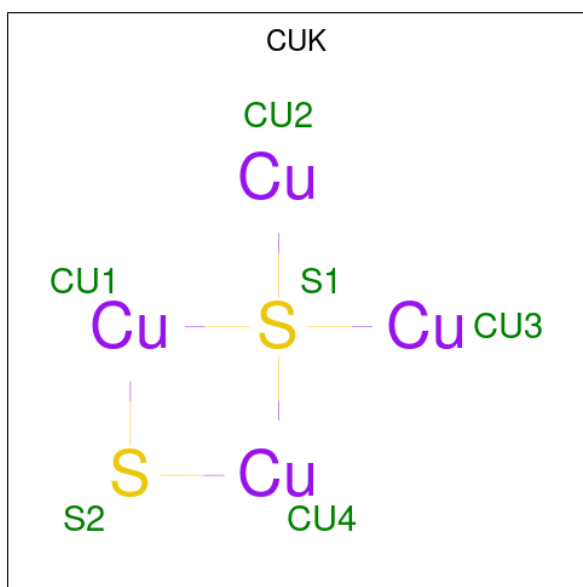
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	581	4573	2891	788	862	32	0	1	0
1	B	581	4592	2902	792	866	32	0	3	0
1	C	581	4590	2900	790	868	32	0	3	0
1	D	588	4636	2929	799	876	32	0	2	0
1	E	581	4575	2892	788	863	32	0	1	0
1	F	581	4593	2902	790	869	32	0	3	0
1	G	585	4606	2911	794	869	32	0	1	0
1	H	581	4590	2900	790	868	32	0	3	0

- Molecule 2 is DINUCLEAR COPPER ION (three-letter code: CUA) (formula: Cu₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Cu 2 2	0	0
2	B	1	Total Cu 2 2	0	0
2	C	1	Total Cu 2 2	0	0
2	D	1	Total Cu 2 2	0	0
2	E	1	Total Cu 2 2	0	0
2	F	1	Total Cu 2 2	0	0
2	G	1	Total Cu 2 2	0	0
2	H	1	Total Cu 2 2	0	0

- Molecule 3 is [4Cu:2S] cluster (three-letter code: CUK) (formula: Cu₄S₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	Cu	S	0	0
			6	4	2		
3	B	1	Total	Cu	S	0	0
			6	4	2		
3	C	1	Total	Cu	S	0	0
			6	4	2		
3	D	1	Total	Cu	S	0	0
			6	4	2		
3	E	1	Total	Cu	S	0	0
			6	4	2		
3	F	1	Total	Cu	S	0	0
			6	4	2		
3	G	1	Total	Cu	S	0	0
			6	4	2		
3	H	1	Total	Cu	S	0	0
			6	4	2		

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Ca	0	0
			1	1		
4	B	1	Total	Ca	0	0
			1	1		
4	C	1	Total	Ca	0	0
			1	1		
4	D	1	Total	Ca	0	0
			1	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	E	1	Total Ca 1 1	0	0
4	F	1	Total Ca 1 1	0	0
4	G	1	Total Ca 1 1	0	0
4	H	1	Total Ca 1 1	0	0

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Cl 1 1	0	0
5	B	1	Total Cl 1 1	0	0
5	C	1	Total Cl 1 1	0	0
5	D	1	Total Cl 1 1	0	0
5	E	1	Total Cl 1 1	0	0
5	F	1	Total Cl 1 1	0	0
5	G	1	Total Cl 1 1	0	0
5	H	1	Total Cl 1 1	0	0

- Molecule 6 is POTASSIUM ION (three-letter code: K) (formula: K).

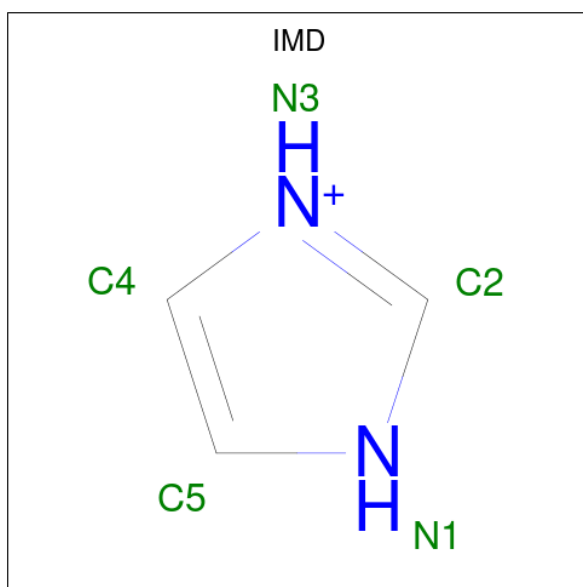
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total K 1 1	0	0
6	B	1	Total K 1 1	0	0
6	C	1	Total K 1 1	0	0
6	D	1	Total K 1 1	0	0
6	E	1	Total K 1 1	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	F	1	Total K 1 1	0	0
6	G	1	Total K 1 1	0	0
6	H	1	Total K 1 1	0	0

- Molecule 7 is IMIDAZOLE (three-letter code: IMD) (formula: C₃H₅N₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	D	1	Total C N 5 3 2	0	0
7	E	1	Total C N 5 3 2	0	0
7	E	1	Total C N 5 3 2	0	0
7	F	1	Total C N 5 3 2	0	0
7	G	1	Total C N 5 3 2	0	0
7	H	1	Total C N 5 3 2	0	0

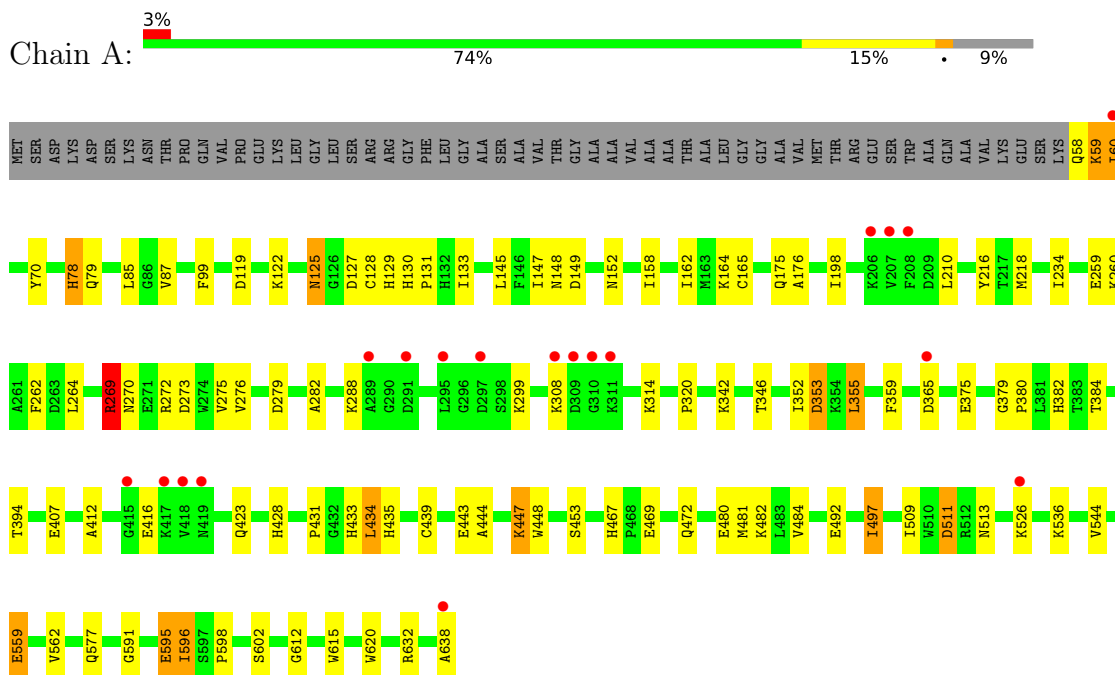
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	232	Total 232	O 232	0	0
8	B	218	Total 218	O 218	0	0
8	C	409	Total 409	O 409	0	0
8	D	419	Total 419	O 419	0	0
8	E	439	Total 439	O 439	0	0
8	F	446	Total 446	O 446	0	0
8	G	406	Total 406	O 406	0	0
8	H	401	Total 401	O 401	0	0

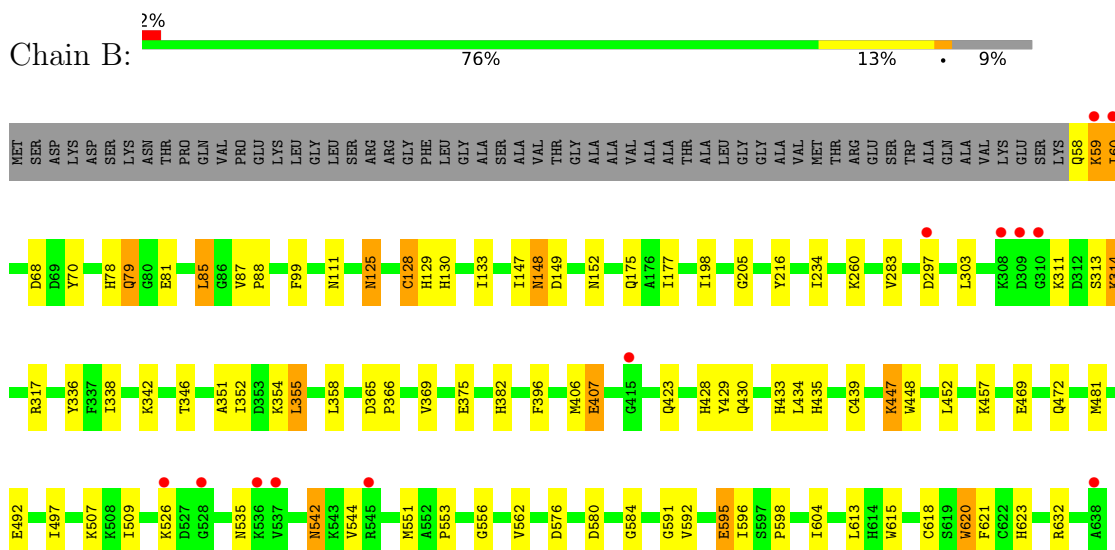
3 Residue-property plots [i](#)

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: Nitrous-oxide reductase

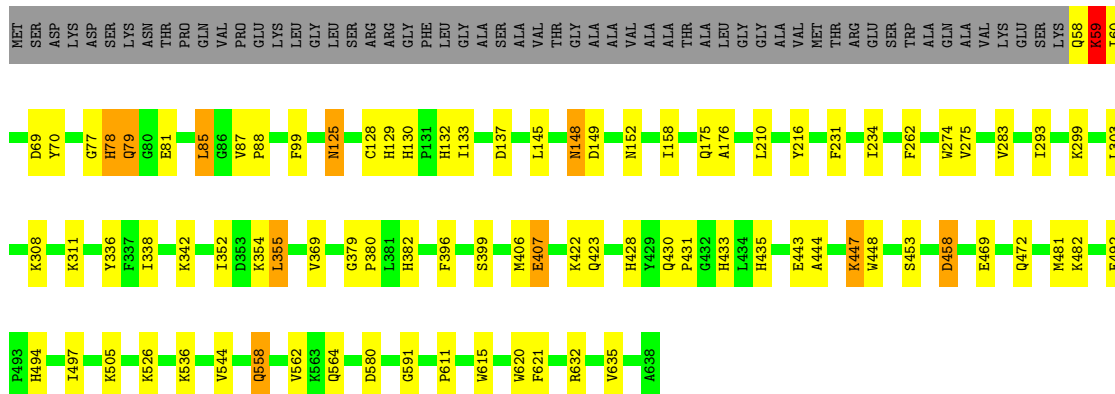


- Molecule 1: Nitrous-oxide reductase




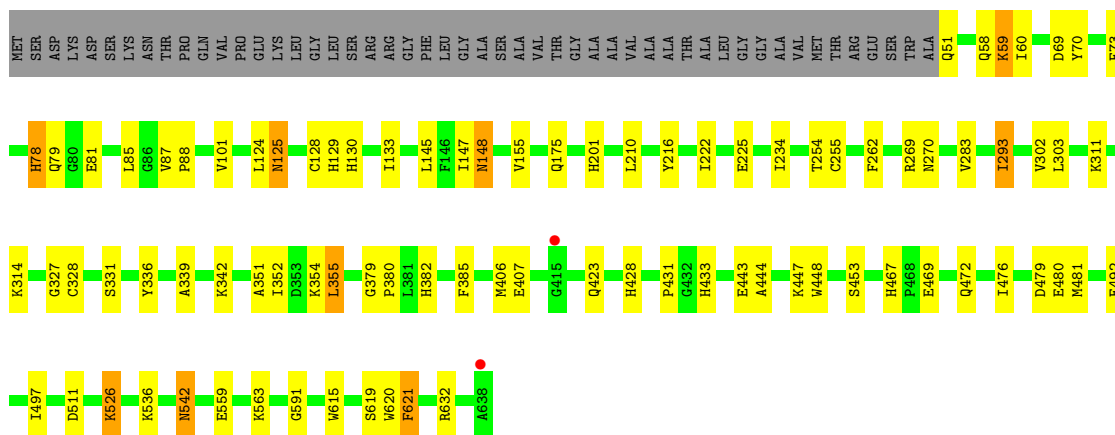
- Molecule 1: Nitrous-oxide reductase

Chain C:  77% 12% 9%




- Molecule 1: Nitrous-oxide reductase

Chain D:  78% 12% 8%




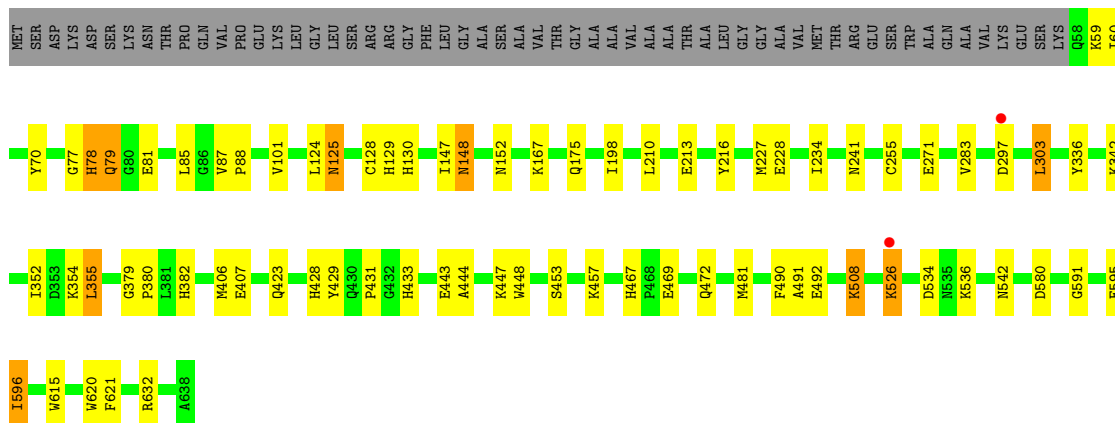
- Molecule 1: Nitrous-oxide reductase

Chain E:  79% 11% 9%




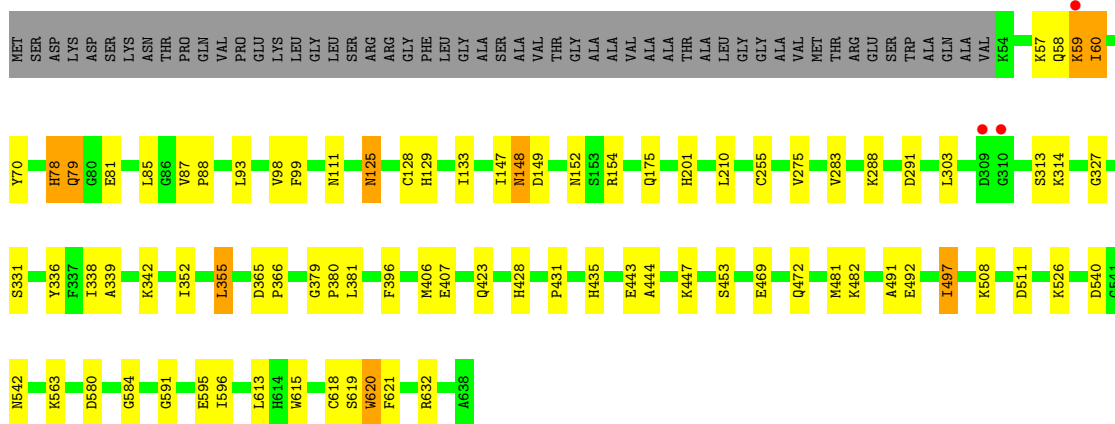
- Molecule 1: Nitrous-oxide reductase

Chain F:  79% 10% 9%




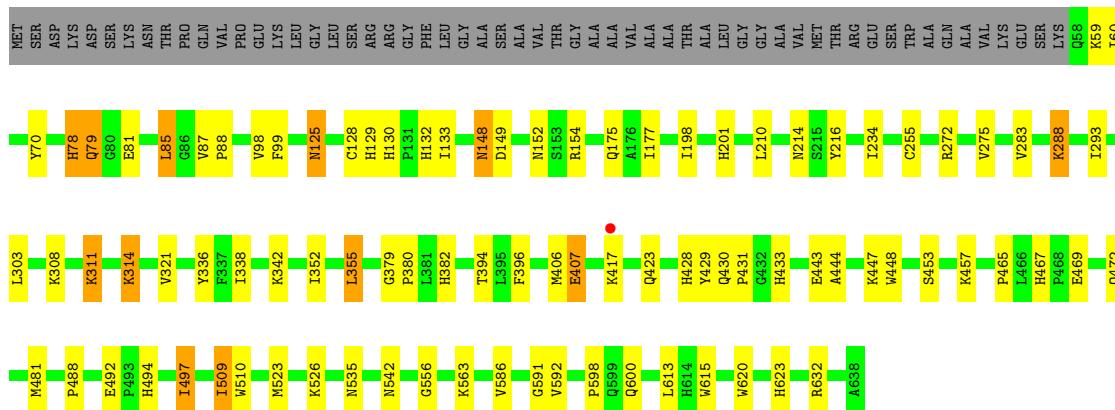
• Molecule 1: Nitrous-oxide reductase

Chain G:  79% 12% 8%



• Molecule 1: Nitrous-oxide reductase

Chain H:  77% 13% 9%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	96.89Å 106.70Å 131.14Å 111.34° 107.33° 90.74°	Depositor
Resolution (Å)	46.02 – 2.10 45.81 – 2.10	Depositor EDS
% Data completeness (in resolution range)	94.7 (46.02-2.10) 94.7 (45.81-2.10)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.75 (at 2.10Å)	Xtrriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.177 , 0.236 0.178 , 0.235	Depositor DCC
R_{free} test set	12842 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	22.9	Xtrriage
Anisotropy	0.021	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 38.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.013 for -h,k,-k-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	39843	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.89% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: CUA, IMD, CUK, CL, K, CA

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.44	0/4685	0.61	1/6345 (0.0%)
1	B	0.45	0/4705	0.61	1/6372 (0.0%)
1	C	0.53	0/4702	0.66	1/6368 (0.0%)
1	D	0.52	0/4748	0.66	1/6428 (0.0%)
1	E	0.53	0/4687	0.68	2/6348 (0.0%)
1	F	0.54	0/4705	0.66	1/6372 (0.0%)
1	G	0.52	0/4718	0.66	0/6387
1	H	0.53	0/4702	0.65	1/6368 (0.0%)
All	All	0.51	0/37652	0.65	8/50988 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1
1	D	0	1
1	G	0	1
All	All	0	3

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	85	LEU	CA-CB-CG	7.97	133.64	115.30
1	H	85	LEU	CA-CB-CG	5.97	129.03	115.30
1	B	85	LEU	CA-CB-CG	5.71	128.43	115.30
1	D	85	LEU	CA-CB-CG	5.66	128.32	115.30
1	F	85	LEU	CA-CB-CG	5.49	127.92	115.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	85	LEU	CA-CB-CG	5.26	127.41	115.30
1	E	269	ARG	NE-CZ-NH2	-5.14	117.73	120.30
1	E	85	LEU	CA-CB-CG	5.04	126.88	115.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	274	TRP	Peptide
1	D	58	GLN	Peptide
1	G	58	GLN	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	4573	0	4441	71	0
1	B	4592	0	4452	80	0
1	C	4590	0	4449	74	0
1	D	4636	0	4505	74	0
1	E	4575	0	4440	70	0
1	F	4593	0	4450	61	0
1	G	4606	0	4478	65	0
1	H	4590	0	4449	77	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	F	2	0	0	0	0
2	G	2	0	0	0	0
2	H	2	0	0	0	0
3	A	6	0	0	0	0
3	B	6	0	0	0	0
3	C	6	0	0	0	0
3	D	6	0	0	0	0
3	E	6	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	F	6	0	0	0	0
3	G	6	0	0	0	0
3	H	6	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
4	G	1	0	0	0	0
4	H	1	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
5	E	1	0	0	0	0
5	F	1	0	0	1	0
5	G	1	0	0	0	0
5	H	1	0	0	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
6	E	1	0	0	0	0
6	F	1	0	0	0	0
6	G	1	0	0	0	0
6	H	1	0	0	0	0
7	D	5	0	5	2	0
7	E	10	0	10	4	0
7	F	5	0	5	3	0
7	G	5	0	5	0	0
7	H	5	0	5	4	0
8	A	232	0	0	5	0
8	B	218	0	0	4	0
8	C	409	0	0	6	0
8	D	419	0	0	13	0
8	E	439	0	0	10	0
8	F	446	0	0	10	0
8	G	406	0	0	10	0
8	H	401	0	0	12	0
All	All	39843	0	35694	532	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 7.

All (532) 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:H:338:ILE:HD11	1:H:406:MET:CE	1.89	1.03
8:D:2328:HOH:O	1:E:542:ASN:HB3	1.60	1.02
1:H:423:GLN:HE22	1:H:481:MET:H	1.08	1.01
1:E:423:GLN:HE22	1:E:481:MET:H	1.09	0.97
1:C:338:ILE:HD11	1:C:406:MET:HE3	1.45	0.96
1:H:469:GLU:HG3	1:H:492:GLU:HA	1.48	0.96
1:C:458:ASP:HB3	8:C:743:HOH:O	1.66	0.94
1:F:423:GLN:HE22	1:F:481:MET:H	1.12	0.94
1:E:336:TYR:HD2	1:E:406:MET:HE1	1.32	0.94
1:B:469:GLU:HG3	1:B:492:GLU:HA	1.51	0.93
1:G:283:VAL:HG13	1:G:303:LEU:HD13	1.49	0.93
1:A:125:ASN:HD21	1:B:591:GLY:HA2	1.34	0.92
1:C:336:TYR:HD2	1:C:406:MET:HE1	1.36	0.91
1:H:283:VAL:HG13	1:H:303:LEU:HD12	1.51	0.90
1:G:288:LYS:HG2	8:G:1278:HOH:O	1.69	0.90
1:A:264:LEU:HD21	1:B:553:PRO:HG2	1.54	0.90
1:E:125:ASN:HD21	1:F:591:GLY:HA2	1.38	0.89
1:A:269:ARG:HE	1:A:269:ARG:HA	1.39	0.88
1:D:352:ILE:HA	1:D:355:LEU:HD22	1.55	0.88
1:H:338:ILE:HD11	1:H:406:MET:HE2	1.55	0.87
1:F:336:TYR:HD2	1:F:406:MET:CE	1.86	0.87
1:G:423:GLN:HE22	1:G:481:MET:H	1.23	0.86
1:C:423:GLN:HE22	1:C:481:MET:H	1.19	0.86
1:E:336:TYR:CD2	1:E:406:MET:HE1	2.11	0.86
1:E:428:HIS:H	1:E:472:GLN:HE22	1.20	0.85
1:G:125:ASN:HD21	1:H:591:GLY:HA2	1.42	0.85
1:H:283:VAL:HG13	1:H:303:LEU:CD1	2.07	0.85
1:D:423:GLN:HE22	1:D:481:MET:H	1.22	0.84
1:C:469:GLU:HG3	1:C:492:GLU:HA	1.60	0.83
1:A:269:ARG:HA	1:A:269:ARG:NE	1.94	0.83
1:C:129:HIS:H	1:C:148:ASN:HD21	1.27	0.82
1:H:129:HIS:H	1:H:148:ASN:HD21	1.28	0.82
1:H:338:ILE:HD11	1:H:406:MET:HE3	1.61	0.82
1:F:283:VAL:HG13	1:F:303:LEU:HD13	1.60	0.82
1:A:423:GLN:HE22	1:A:481:MET:H	1.27	0.81
1:F:129:HIS:H	1:F:148:ASN:HD21	1.29	0.81
1:G:331:SER:HB3	1:G:406:MET:HE3	1.60	0.81
1:F:78:HIS:ND1	8:F:2846:HOH:O	2.02	0.80

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:133:ILE:HG13	1:D:497:ILE:HD12	1.64	0.79
1:A:259:GLU:HG2	1:A:269:ARG:HB3	1.64	0.79
1:B:423:GLN:HE22	1:B:481:MET:H	1.27	0.79
1:E:125:ASN:ND2	1:F:591:GLY:HA2	1.98	0.79
1:G:563:LYS:HD3	8:G:714:HOH:O	1.81	0.79
1:F:336:TYR:CD2	1:F:406:MET:CE	2.65	0.78
1:C:125:ASN:HD21	1:D:591:GLY:HA2	1.46	0.78
1:G:428:HIS:H	1:G:472:GLN:HE22	1.29	0.78
1:D:428:HIS:H	1:D:472:GLN:HE22	1.30	0.78
1:E:382:HIS:HB3	8:E:1097:HOH:O	1.84	0.77
1:E:336:TYR:HD2	1:E:406:MET:CE	1.98	0.77
1:F:469:GLU:HG3	1:F:492:GLU:HA	1.67	0.76
1:G:469:GLU:HG3	1:G:492:GLU:HA	1.68	0.75
1:F:198:ILE:H	7:F:639:IMD:H2	1.49	0.75
1:C:338:ILE:HD11	1:C:406:MET:CE	2.14	0.75
1:H:338:ILE:CD1	1:H:406:MET:HE3	2.16	0.75
1:E:129:HIS:H	1:E:148:ASN:HD21	1.34	0.75
1:E:269:ARG:HD2	8:E:820:HOH:O	1.86	0.75
1:D:283:VAL:HG13	1:D:303:LEU:HD13	1.68	0.75
1:C:283:VAL:HG13	1:C:303:LEU:CD1	2.17	0.74
1:D:469:GLU:HG3	1:D:492:GLU:HA	1.68	0.74
1:C:428:HIS:H	1:C:472:GLN:HE22	1.36	0.74
1:E:469:GLU:HG3	1:E:492:GLU:HA	1.69	0.74
1:B:129:HIS:H	1:B:148:ASN:HD21	1.36	0.73
1:A:577:GLN:CD	8:A:654:HOH:O	2.27	0.73
1:E:283:VAL:HG13	1:E:303:LEU:CD1	2.19	0.73
1:E:338:ILE:HD11	1:E:406:MET:HE3	1.71	0.73
1:E:632:ARG:HD3	8:E:2177:HOH:O	1.87	0.72
1:G:129:HIS:H	1:G:148:ASN:HD21	1.35	0.72
1:D:129:HIS:H	1:D:148:ASN:HD21	1.36	0.72
1:D:336:TYR:HD2	1:D:406:MET:CE	2.02	0.72
1:E:428:HIS:H	1:E:472:GLN:NE2	1.88	0.71
1:D:632:ARG:HD3	8:D:2130:HOH:O	1.90	0.71
1:D:542:ASN:HB3	8:D:654:HOH:O	1.90	0.71
1:C:382:HIS:CE1	1:C:433:HIS:CE1	2.78	0.71
1:A:469:GLU:HG3	1:A:492:GLU:HA	1.71	0.70
1:E:59:LYS:NZ	1:E:448:TRP:HE1	1.87	0.70
1:E:59:LYS:HE3	1:E:69:ASP:OD2	1.90	0.70
1:A:352:ILE:HA	1:A:355:LEU:HD22	1.73	0.70
1:B:59:LYS:O	1:B:60:ILE:HG22	1.91	0.70
1:H:382:HIS:CE1	1:H:433:HIS:CE1	2.79	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:336:TYR:HD2	1:F:406:MET:HE1	1.57	0.69
1:H:133:ILE:HG13	1:H:497:ILE:HD12	1.73	0.69
1:F:352:ILE:HA	1:F:355:LEU:HD22	1.73	0.69
1:C:336:TYR:CD2	1:C:406:MET:HE1	2.24	0.69
1:D:59:LYS:HZ1	1:D:448:TRP:HE1	1.41	0.69
1:H:509:ILE:HG22	1:H:598:PRO:HB2	1.75	0.68
1:C:336:TYR:HD2	1:C:406:MET:CE	2.07	0.68
1:E:336:TYR:CD2	1:E:406:MET:CE	2.74	0.68
1:E:433:HIS:HB2	1:E:494:HIS:O	1.94	0.68
1:B:428:HIS:H	1:B:472:GLN:HE22	1.40	0.68
1:H:314:LYS:CE	8:H:762:HOH:O	2.42	0.68
1:A:125:ASN:ND2	1:B:591:GLY:HA2	2.07	0.68
1:H:314:LYS:HE3	8:H:762:HOH:O	1.94	0.67
1:E:613:LEU:HD11	1:E:632:ARG:HG2	1.75	0.67
1:G:615:TRP:CH2	7:H:639:IMD:H4	2.29	0.67
1:B:70:TYR:HB2	1:B:87:VAL:HB	1.77	0.66
1:E:428:HIS:N	1:E:472:GLN:HE22	1.94	0.66
1:C:133:ILE:HG13	1:C:497:ILE:HD12	1.77	0.66
1:B:283:VAL:HG13	1:B:303:LEU:HD13	1.77	0.65
1:H:275:VAL:HG13	1:H:321:VAL:HG21	1.78	0.65
1:C:128:CYS:HB3	1:C:148:ASN:O	1.97	0.65
1:H:613:LEU:HD11	1:H:632:ARG:HB3	1.77	0.65
1:B:542:ASN:C	1:B:542:ASN:HD22	1.99	0.65
1:C:262:PHE:HB2	1:D:632:ARG:HD2	1.79	0.65
1:E:59:LYS:HE2	1:E:88:PRO:HG3	1.79	0.65
1:G:591:GLY:HA2	1:H:125:ASN:HD21	1.61	0.64
1:C:352:ILE:HA	1:C:355:LEU:HD22	1.79	0.64
1:D:336:TYR:CD2	1:D:406:MET:CE	2.80	0.64
1:F:382:HIS:CE1	1:F:433:HIS:CE1	2.86	0.64
1:H:59:LYS:HE2	1:H:88:PRO:HG3	1.80	0.64
1:F:428:HIS:H	1:F:472:GLN:HE22	1.46	0.64
1:F:129:HIS:H	1:F:148:ASN:ND2	1.97	0.63
1:A:544:VAL:HG21	1:A:562:VAL:HG12	1.79	0.63
1:B:338:ILE:HD11	1:B:406:MET:HE3	1.80	0.63
1:D:51:GLN:HA	8:D:1483:HOH:O	1.98	0.62
1:D:133:ILE:HG13	1:D:497:ILE:CD1	2.28	0.62
1:E:615:TRP:H	1:F:175:GLN:HE22	1.47	0.62
1:E:70:TYR:HB2	1:E:87:VAL:HB	1.81	0.62
1:B:429:TYR:CD1	1:B:457:LYS:HD2	2.34	0.62
1:C:133:ILE:HG13	1:C:497:ILE:CD1	2.30	0.62
1:C:336:TYR:CD2	1:C:406:MET:CE	2.81	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:331:SER:HB3	1:G:406:MET:CE	2.27	0.62
1:D:431:PRO:HA	1:D:453:SER:HA	1.81	0.62
1:B:469:GLU:CG	1:B:492:GLU:HA	2.28	0.62
1:D:480:GLU:HG3	8:D:1442:HOH:O	2.00	0.62
1:B:79:GLN:HE22	1:B:81:GLU:CG	2.13	0.61
1:B:79:GLN:HE22	1:B:81:GLU:HG2	1.64	0.61
1:H:59:LYS:NZ	1:H:448:TRP:HE1	1.98	0.61
1:H:338:ILE:CD1	1:H:406:MET:CE	2.70	0.61
1:H:128:CYS:HB3	1:H:148:ASN:O	2.00	0.61
1:E:129:HIS:H	1:E:148:ASN:ND2	1.98	0.61
1:A:394:THR:HG23	1:A:434:LEU:HD13	1.83	0.61
1:C:591:GLY:HA2	1:D:125:ASN:HD21	1.66	0.61
1:C:615:TRP:H	1:D:175:GLN:HE22	1.47	0.61
1:H:308:LYS:O	1:H:311:LYS:HD2	2.00	0.60
1:D:293:ILE:HG22	1:D:302:VAL:HB	1.82	0.60
7:H:639:IMD:H5	8:H:688:HOH:O	2.02	0.60
1:E:591:GLY:HA2	1:F:125:ASN:HD21	1.67	0.60
1:F:271[B]:GLU:OE1	8:F:2876:HOH:O	2.17	0.60
1:G:595:GLU:HG2	1:G:596:ILE:N	2.17	0.60
1:A:129:HIS:H	1:A:148:ASN:HD21	1.47	0.59
1:A:198:ILE:HD13	1:A:260:LYS:HE3	1.83	0.59
1:G:508:LYS:HE3	8:H:1007:HOH:O	2.02	0.59
1:C:125:ASN:ND2	1:D:591:GLY:HA2	2.16	0.59
1:F:336:TYR:CD2	1:F:406:MET:HE1	2.36	0.59
1:F:198:ILE:H	7:F:639:IMD:C2	2.15	0.59
1:B:317:ARG:HG3	1:B:358:LEU:HG	1.84	0.59
1:A:577:GLN:HE21	1:A:577:GLN:HA	1.67	0.59
1:C:338:ILE:CD1	1:C:406:MET:HE3	2.26	0.59
1:C:407:GLU:HG2	1:H:563:LYS:HD2	1.83	0.59
1:G:336:TYR:HD2	1:G:406:MET:CE	2.16	0.59
1:G:59:LYS:HE3	1:G:88:PRO:HG3	1.85	0.58
1:B:407:GLU:HG3	8:B:2163:HOH:O	2.01	0.58
1:A:428:HIS:H	1:A:472:GLN:HE22	1.52	0.58
1:E:198:ILE:H	7:E:640:IMD:HN1	1.50	0.58
1:D:79:GLN:HE22	1:D:81:GLU:CG	2.17	0.58
1:G:435:HIS:CE1	1:G:497:ILE:HG22	2.39	0.58
1:F:77:GLY:HA2	1:F:128:CYS:O	2.04	0.58
1:H:129:HIS:N	1:H:148:ASN:HD21	2.01	0.58
1:C:129:HIS:H	1:C:148:ASN:ND2	1.98	0.58
1:D:129:HIS:H	1:D:148:ASN:ND2	2.02	0.57
1:G:59:LYS:O	1:G:60:ILE:HG23	2.05	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:382:HIS:CE1	1:E:433:HIS:CE1	2.93	0.57
1:B:133:ILE:HG13	1:B:497:ILE:HD12	1.85	0.57
1:E:338:ILE:HD11	1:E:406:MET:CE	2.34	0.57
1:H:535:ASN:OD1	1:H:556:GLY:HA3	2.04	0.57
1:C:428:HIS:H	1:C:472:GLN:NE2	2.02	0.57
1:C:137:ASP:HB3	8:C:1790:HOH:O	2.03	0.57
1:C:632:ARG:HD3	8:C:2156:HOH:O	2.05	0.57
1:H:308:LYS:O	1:H:311:LYS:CD	2.53	0.57
1:H:129:HIS:H	1:H:148:ASN:ND2	1.99	0.56
1:B:336:TYR:CD2	1:B:406:MET:HE2	2.40	0.56
1:F:78:HIS:CE1	8:F:2846:HOH:O	2.50	0.56
1:H:79:GLN:HE22	1:H:81:GLU:CG	2.18	0.56
1:F:336:TYR:CD2	1:F:406:MET:HE2	2.40	0.56
1:D:59:LYS:CE	1:D:88:PRO:HG3	2.35	0.56
1:D:70:TYR:HB2	1:D:87:VAL:HB	1.88	0.56
1:E:447:LYS:HD3	8:E:2352:HOH:O	2.04	0.56
1:E:447:LYS:HE2	8:E:1948:HOH:O	2.05	0.56
1:C:615:TRP:CH2	7:D:639:IMD:H2	2.40	0.55
1:G:615:TRP:CZ2	7:H:639:IMD:H4	2.41	0.55
1:B:352:ILE:HA	1:B:355:LEU:HD22	1.87	0.55
1:D:336:TYR:CD2	1:D:406:MET:HE2	2.42	0.55
1:F:70:TYR:HB2	1:F:87:VAL:HB	1.87	0.55
1:A:60:ILE:HD13	1:A:484:VAL:HB	1.88	0.55
1:A:70:TYR:HB2	1:A:87:VAL:HB	1.88	0.55
1:F:632:ARG:HD3	8:F:1451:HOH:O	2.07	0.55
1:A:509:ILE:HG22	1:A:598:PRO:HB2	1.89	0.55
1:B:125:ASN:ND2	1:B:152:ASN:HD21	2.03	0.55
1:E:283:VAL:HG13	1:E:303:LEU:HD13	1.88	0.55
1:A:615:TRP:H	1:B:175:GLN:HE22	1.55	0.55
1:G:632:ARG:HD3	8:G:2045:HOH:O	2.07	0.55
1:C:632:ARG:HD2	1:D:262:PHE:HB2	1.89	0.54
1:C:129:HIS:N	1:C:148:ASN:HD21	2.01	0.54
1:C:431:PRO:HA	1:C:453:SER:HA	1.88	0.54
1:G:619:SER:O	1:H:78:HIS:CE1	2.61	0.54
1:B:338:ILE:HD11	1:B:406:MET:CE	2.37	0.54
1:D:73:PHE:HB2	1:D:497:ILE:HG13	1.90	0.54
1:H:431:PRO:HA	1:H:453:SER:HA	1.90	0.54
1:E:59:LYS:HZ3	1:E:448:TRP:HE1	1.55	0.54
1:H:396:PHE:CE1	1:H:430:GLN:HB3	2.43	0.54
1:A:272:ARG:HD2	8:A:968:HOH:O	2.07	0.54
1:F:59:LYS:HE2	1:F:448:TRP:HZ2	1.73	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:125:ASN:ND2	1:F:152:ASN:HD21	2.06	0.54
1:G:70:TYR:HB2	1:G:87:VAL:HB	1.90	0.54
1:G:431:PRO:HA	1:G:453:SER:HA	1.90	0.54
1:H:132:HIS:HA	1:H:497:ILE:HD13	1.90	0.54
1:H:314:LYS:HD3	8:H:2281:HOH:O	2.07	0.54
1:H:428:HIS:H	1:H:472:GLN:HE22	1.56	0.54
1:A:262:PHE:HB2	1:B:632:ARG:HD2	1.90	0.54
1:A:591:GLY:HA2	1:B:125:ASN:HD21	1.72	0.54
1:C:70:TYR:HB2	1:C:87:VAL:HB	1.88	0.54
1:F:128:CYS:HB2	1:F:147:ILE:HG12	1.90	0.54
1:E:396:PHE:CE1	1:E:430:GLN:HB3	2.43	0.53
1:F:428:HIS:H	1:F:472:GLN:NE2	2.06	0.53
1:A:382:HIS:CE1	1:A:433:HIS:CE1	2.97	0.53
1:C:526:LYS:HB2	1:C:526:LYS:NZ	2.24	0.53
1:E:101:VAL:HG21	1:E:124:LEU:HD22	1.90	0.53
1:G:79:GLN:HE22	1:G:81:GLU:CG	2.20	0.53
1:G:469:GLU:CG	1:G:492:GLU:HA	2.39	0.53
1:G:125:ASN:ND2	1:H:591:GLY:HA2	2.18	0.53
1:H:429:TYR:CD2	1:H:457:LYS:HD2	2.43	0.53
1:B:497:ILE:HG21	8:B:2451:HOH:O	2.09	0.53
1:D:133:ILE:CG1	1:D:497:ILE:HD12	2.36	0.52
1:E:125:ASN:ND2	1:E:152:ASN:HD21	2.07	0.52
1:D:526:LYS:HD3	8:D:1185:HOH:O	2.10	0.52
1:E:129:HIS:N	1:E:148:ASN:HD21	2.03	0.52
1:A:269:ARG:NE	1:A:269:ARG:CA	2.66	0.52
1:D:51:GLN:HG3	1:E:605:THR:CG2	2.40	0.52
1:F:354:LYS:NZ	8:F:777:HOH:O	2.42	0.52
1:G:128:CYS:HB2	1:G:147:ILE:HG12	1.90	0.52
1:D:78:HIS:ND1	8:D:2779:HOH:O	2.11	0.52
1:A:480:GLU:OE1	1:F:526:LYS:HE2	2.10	0.52
1:D:130:HIS:H	1:D:148:ASN:ND2	2.08	0.52
1:H:586:VAL:HA	1:H:592:VAL:O	2.09	0.52
1:C:125:ASN:ND2	1:C:152:ASN:HD21	2.08	0.51
1:D:269:ARG:NH1	1:D:270:ASN:OD1	2.43	0.51
1:E:591:GLY:HA2	1:F:125:ASN:ND2	2.25	0.51
1:G:615:TRP:H	1:H:175:GLN:HE22	1.58	0.51
1:B:595:GLU:HB2	1:B:620:TRP:CZ3	2.46	0.51
1:B:125:ASN:HD21	1:B:152:ASN:HD21	1.57	0.51
1:F:125:ASN:HD21	1:F:152:ASN:HD21	1.58	0.51
1:A:210:LEU:O	1:A:260:LYS:HE2	2.10	0.51
1:B:428:HIS:HB3	1:B:429:TYR:CE1	2.45	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:175:GLN:HE22	1:B:615:TRP:H	1.57	0.51
1:D:51:GLN:HG3	1:E:605:THR:HG21	1.93	0.51
1:B:382[A]:HIS:CE1	1:B:433:HIS:CE1	2.99	0.51
1:E:59:LYS:O	1:E:60:ILE:HG23	2.11	0.51
1:A:282:ALA:HB1	1:A:314:LYS:HD2	1.92	0.51
1:C:59:LYS:HE3	1:C:69:ASP:OD2	2.10	0.51
8:D:715:HOH:O	7:E:639:IMD:H5	2.10	0.51
1:A:133:ILE:HG13	1:A:497:ILE:HD13	1.93	0.51
1:A:99:PHE:CE2	1:A:149:ASP:HB2	2.46	0.50
1:A:130:HIS:H	1:A:148:ASN:ND2	2.09	0.50
1:G:148:ASN:HD22	1:G:148:ASN:H	1.58	0.50
1:H:198:ILE:H	7:H:639:IMD:HN3	1.59	0.50
1:H:214:ASN:ND2	8:H:751:HOH:O	2.45	0.50
1:A:577:GLN:HA	1:A:577:GLN:NE2	2.27	0.50
1:D:476:ILE:HG22	1:D:481:MET:HG2	1.94	0.50
1:A:467:HIS:HB2	1:B:580:ASP:OD1	2.12	0.50
1:B:428:HIS:H	1:B:472:GLN:NE2	2.07	0.50
1:B:452:LEU:N	1:B:452:LEU:HD12	2.27	0.50
1:G:125:ASN:ND2	1:G:152:ASN:HD21	2.09	0.50
1:C:536:LYS:HE2	8:C:1127:HOH:O	2.10	0.50
1:C:175:GLN:HE22	1:D:615:TRP:H	1.59	0.50
1:E:175:GLN:HE22	1:F:615:TRP:H	1.60	0.50
1:G:352:ILE:HA	1:G:355:LEU:HD22	1.93	0.50
1:B:125:ASN:HD22	1:B:125:ASN:H	1.59	0.50
1:C:379:GLY:N	1:C:380:PRO:HD3	2.26	0.50
1:C:433:HIS:HB2	1:C:494:HIS:O	2.12	0.50
1:H:125:ASN:ND2	1:H:152:ASN:HD21	2.10	0.50
1:A:412:ALA:HA	1:A:416:GLU:O	2.12	0.49
1:B:351:ALA:HB3	1:B:354:LYS:HG3	1.93	0.49
1:D:559:GLU:HA	1:D:632:ARG:O	2.12	0.49
1:G:540:ASP:HB3	8:G:699:HOH:O	2.12	0.49
1:G:591:GLY:HA2	1:H:125:ASN:ND2	2.27	0.49
1:C:216:TYR:CD1	1:C:234:ILE:HG23	2.47	0.49
8:G:1326:HOH:O	1:H:465:PRO:HD2	2.13	0.49
1:G:365:ASP:OD1	1:G:366:PRO:HD2	2.12	0.49
1:A:58:GLN:HE22	1:A:447:LYS:HG2	1.78	0.49
1:A:125:ASN:ND2	1:A:152:ASN:HD21	2.11	0.49
7:E:640:IMD:H2	1:F:615:TRP:CZ2	2.47	0.49
1:H:379:GLY:N	1:H:380:PRO:HD3	2.27	0.49
1:C:435:HIS:CE1	1:C:497:ILE:HG22	2.48	0.49
1:D:59:LYS:HE2	1:D:88:PRO:HG3	1.94	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:201:HIS:HE1	1:D:216:TYR:O	1.95	0.49
1:F:534:ASP:HB3	1:F:536:LYS:HD2	1.94	0.49
1:G:129:HIS:H	1:G:148:ASN:ND2	2.07	0.49
1:E:58:GLN:N	8:E:1461:HOH:O	2.46	0.49
1:H:336:TYR:HD2	1:H:406:MET:HE1	1.77	0.49
1:D:379:GLY:N	1:D:380:PRO:HD3	2.27	0.48
1:C:79:GLN:HE22	1:C:81:GLU:CG	2.25	0.48
1:F:443:GLU:O	1:F:444:ALA:C	2.51	0.48
1:B:79:GLN:NE2	1:B:81:GLU:HG2	2.29	0.48
1:E:580:ASP:OD1	1:F:467:HIS:HB2	2.14	0.48
1:G:175:GLN:HE22	1:H:615:TRP:H	1.59	0.48
1:D:428:HIS:H	1:D:472:GLN:NE2	2.04	0.48
1:G:580:ASP:OD1	1:H:467:HIS:HB2	2.13	0.48
1:E:99:PHE:CE2	1:E:149:ASP:HB2	2.49	0.48
1:H:125:ASN:HD21	1:H:152:ASN:HD21	1.62	0.48
1:H:216:TYR:CD1	1:H:234:ILE:HG23	2.49	0.48
1:A:129:HIS:H	1:A:148:ASN:ND2	2.10	0.47
1:F:429:TYR:CD1	1:F:457:LYS:HD2	2.49	0.47
1:A:125:ASN:HD21	1:A:152:ASN:HD21	1.61	0.47
1:F:447:LYS:HE2	8:F:2850:HOH:O	2.14	0.47
1:F:379:GLY:N	1:F:380:PRO:HD3	2.29	0.47
1:H:382:HIS:CD2	1:H:433:HIS:HA	2.50	0.47
1:B:148:ASN:H	1:B:148:ASN:HD22	1.63	0.47
1:D:336:TYR:HD2	1:D:406:MET:HE1	1.77	0.47
1:G:78:HIS:ND1	8:G:2902:HOH:O	2.08	0.47
1:G:336:TYR:HD2	1:G:406:MET:HE2	1.79	0.47
1:B:336:TYR:CD2	1:B:406:MET:CE	2.98	0.47
1:C:492:GLU:OE2	1:D:621:PHE:HB2	2.15	0.47
1:D:314:LYS:HB3	1:D:314:LYS:HE3	1.48	0.47
1:E:467:HIS:HB2	1:F:580:ASP:OD1	2.14	0.47
1:H:59:LYS:HZ3	1:H:448:TRP:HE1	1.60	0.47
1:A:131:PRO:O	1:A:497:ILE:HG12	2.15	0.47
1:B:59:LYS:NZ	1:B:448:TRP:HE1	2.12	0.47
1:G:336:TYR:CD2	1:G:406:MET:HE2	2.50	0.47
1:C:399[B]:SER:O	1:C:399[B]:SER:OG	2.31	0.47
1:E:327:GLY:O	1:E:339:ALA:HA	2.15	0.47
1:A:119:ASP:O	1:A:122:LYS:HG2	2.16	0.46
1:H:428:HIS:H	1:H:472:GLN:NE2	2.13	0.46
1:D:148:ASN:H	1:D:148:ASN:HD22	1.64	0.46
1:G:99:PHE:CE2	1:G:149:ASP:HB2	2.50	0.46
1:A:59:LYS:NZ	1:A:448:TRP:HE1	2.12	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:111:ASN:ND2	8:B:2638:HOH:O	2.48	0.46
1:C:99:PHE:CE2	1:C:149:ASP:HB2	2.50	0.46
1:G:125:ASN:HD22	1:G:125:ASN:H	1.63	0.46
1:G:428:HIS:H	1:G:472:GLN:NE2	2.05	0.46
1:G:613:LEU:HD11	1:G:632:ARG:HG2	1.97	0.46
1:D:59:LYS:O	8:D:2707:HOH:O	2.21	0.46
1:D:479:ASP:CB	8:D:1442:HOH:O	2.63	0.46
1:B:128:CYS:HB3	1:B:148:ASN:O	2.14	0.46
1:D:145:LEU:CD1	1:D:497:ILE:HD11	2.45	0.46
1:E:216:TYR:CD1	1:E:234:ILE:HG23	2.51	0.46
1:A:162:ILE:HD12	1:A:164:LYS:HB2	1.97	0.46
1:A:379:GLY:N	1:A:380:PRO:HD3	2.30	0.46
1:C:615:TRP:CZ3	7:D:639:IMD:H2	2.51	0.46
1:C:77:GLY:HA2	1:C:128:CYS:O	2.15	0.46
1:D:59:LYS:HE3	1:D:88:PRO:HG3	1.97	0.46
1:B:382[B]:HIS:HD2	1:B:434:LEU:HD23	1.80	0.45
1:G:59:LYS:HB3	1:G:60:ILE:H	1.32	0.45
1:B:336:TYR:HD2	1:B:406:MET:CE	2.29	0.45
1:C:137:ASP:CB	8:C:1790:HOH:O	2.63	0.45
1:C:423:GLN:HE22	1:C:481:MET:N	2.00	0.45
1:E:59:LYS:HZ1	1:E:448:TRP:HE1	1.60	0.45
1:G:595:GLU:HB2	1:G:620:TRP:CZ3	2.51	0.45
1:C:580:ASP:OD1	1:D:467:HIS:HB2	2.15	0.45
1:F:490:PHE:CE2	1:F:491:ALA:HB2	2.51	0.45
1:B:346:THR:HG22	1:B:375:GLU:HA	1.99	0.45
1:D:128:CYS:HB2	1:D:147:ILE:HG12	1.99	0.45
1:A:492:GLU:OE2	1:B:621:PHE:HB2	2.17	0.45
1:A:591:GLY:HA2	1:B:125:ASN:ND2	2.31	0.45
1:B:314:LYS:O	1:B:314:LYS:HG2	2.17	0.45
1:E:431:PRO:HA	1:E:453:SER:HA	1.97	0.45
1:F:59:LYS:HE2	1:F:448:TRP:CZ2	2.51	0.45
1:F:79:GLN:HE22	1:F:81:GLU:CG	2.30	0.45
1:H:338:ILE:HD12	1:H:406:MET:HE3	1.97	0.45
1:C:148:ASN:HD22	1:C:148:ASN:H	1.65	0.45
1:D:101:VAL:HG21	1:D:124:LEU:HD22	1.99	0.45
1:H:407:GLU:OE1	8:H:2968:HOH:O	2.21	0.45
1:E:79:GLN:NE2	1:E:83:ARG:HH21	2.14	0.45
1:E:90:MET:HE2	8:E:1945:HOH:O	2.15	0.45
1:H:149:ASP:HB3	1:H:154:ARG:HB2	1.99	0.45
1:A:78:HIS:HA	1:A:127:ASP:HA	1.99	0.44
1:A:273:ASP:O	1:A:320:PRO:HA	2.17	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:435:HIS:CE1	1:A:439:CYS:SG	3.10	0.44
1:D:59:LYS:HE3	1:D:69:ASP:OD2	2.17	0.44
1:D:128:CYS:HB3	1:D:148:ASN:O	2.17	0.44
1:D:382:HIS:CE1	1:D:433:HIS:NE2	2.85	0.44
1:F:129:HIS:N	1:F:148:ASN:HD21	2.07	0.44
1:A:443:GLU:O	1:A:444:ALA:C	2.55	0.44
1:B:535:ASN:OD1	1:B:556:GLY:HA3	2.17	0.44
1:C:494:HIS:HE1	8:D:1439:HOH:O	1.99	0.44
1:C:611:PRO:HA	1:C:635:VAL:HB	1.99	0.44
1:D:563:LYS:HE3	1:D:563:LYS:HB2	1.84	0.44
1:G:201:HIS:HD2	8:G:984:HOH:O	2.00	0.44
1:A:269:ARG:NH2	8:A:1918:HOH:O	2.47	0.44
1:E:99:PHE:CZ	1:E:149:ASP:HB2	2.52	0.44
1:E:128:CYS:HB3	1:E:148:ASN:O	2.18	0.44
1:H:70:TYR:HB2	1:H:87:VAL:HB	1.99	0.44
1:B:58:GLN:HE22	1:B:447:LYS:CG	2.30	0.44
1:B:435:HIS:CE1	1:B:439:CYS:SG	3.11	0.44
1:E:125:ASN:HD21	1:E:152:ASN:HD21	1.66	0.44
1:A:128:CYS:HB2	1:A:147:ILE:HG12	2.00	0.44
1:C:125:ASN:HD21	1:C:152:ASN:HD21	1.64	0.44
1:G:584:GLY:O	1:G:618:CYS:HA	2.18	0.44
1:H:563:LYS:HE2	8:H:755:HOH:O	2.18	0.44
1:E:563:LYS:HB2	1:E:563:LYS:HE3	1.67	0.44
1:B:365:ASP:OD1	1:B:366:PRO:HD2	2.18	0.43
1:C:396:PHE:CE1	1:C:430:GLN:HB3	2.53	0.43
1:F:241:ASN:ND2	5:F:704:CL:CL	2.88	0.43
1:H:99:PHE:CE2	1:H:149:ASP:HB2	2.53	0.43
1:C:231:PHE:CE1	1:C:283:VAL:HG11	2.53	0.43
1:E:577:GLN:HE21	1:E:577:GLN:HB3	1.65	0.43
1:F:101:VAL:HG21	1:F:124:LEU:HD22	1.99	0.43
1:F:148:ASN:H	1:F:148:ASN:HD22	1.65	0.43
1:F:431:PRO:HA	1:F:453:SER:HA	1.98	0.43
1:H:352:ILE:HA	1:H:355:LEU:HD22	1.99	0.43
1:H:542:ASN:HB3	8:H:1267:HOH:O	2.19	0.43
1:D:536:LYS:HG2	8:D:2767:HOH:O	2.17	0.43
1:E:469:GLU:CG	1:E:492:GLU:HA	2.44	0.43
1:F:130:HIS:H	1:F:148:ASN:ND2	2.17	0.43
1:G:149:ASP:HB3	1:G:154:ARG:HB2	2.00	0.43
1:A:638:ALA:HA	8:A:1042:HOH:O	2.17	0.43
1:B:59:LYS:HA	8:B:2512:HOH:O	2.18	0.43
1:C:130:HIS:H	1:C:148:ASN:ND2	2.16	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:595:GLU:HG2	1:F:596:ILE:N	2.33	0.43
1:B:366:PRO:O	1:B:369:VAL:HG22	2.18	0.43
1:F:59:LYS:HE3	1:F:88:PRO:HG3	2.01	0.43
1:G:125:ASN:HD21	1:G:152:ASN:HD21	1.65	0.43
1:B:542:ASN:C	1:B:542:ASN:ND2	2.71	0.43
1:C:59:LYS:NZ	1:C:448:TRP:HE1	2.17	0.43
1:D:254:THR:HG23	1:D:328:CYS:HB2	2.01	0.43
1:G:79:GLN:HE22	1:G:81:GLU:HG2	1.83	0.43
1:A:158:ILE:HA	1:A:165:CYS:HA	2.00	0.43
1:A:379:GLY:H	1:A:380:PRO:HD3	1.83	0.43
1:B:613:LEU:HD11	1:B:632:ARG:HB3	2.00	0.43
1:C:443:GLU:O	1:C:444:ALA:C	2.57	0.43
1:G:111:ASN:ND2	8:G:691:HOH:O	2.52	0.43
1:C:78:HIS:CE1	1:D:619:SER:O	2.72	0.43
1:E:494:HIS:HE1	8:F:1431:HOH:O	2.01	0.43
1:F:382:HIS:CD2	1:F:433:HIS:HA	2.54	0.43
1:G:291:ASP:HB3	8:G:2572:HOH:O	2.17	0.43
1:B:58:GLN:HE22	1:B:447:LYS:HG3	1.83	0.43
1:C:145:LEU:HD22	1:C:158:ILE:HD12	2.01	0.43
1:B:130:HIS:H	1:B:148:ASN:ND2	2.16	0.42
1:B:509:ILE:HG22	1:B:598:PRO:HB2	2.01	0.42
1:F:167:LYS:HB2	1:F:227:MET:HG3	2.01	0.42
1:B:435:HIS:CE1	1:B:497:ILE:HG22	2.53	0.42
1:C:125:ASN:HD22	1:C:125:ASN:H	1.66	0.42
1:E:380:PRO:HA	1:E:394:THR:O	2.19	0.42
1:F:198:ILE:N	7:F:639:IMD:H2	2.26	0.42
1:F:407:GLU:OE1	8:F:2856:HOH:O	2.21	0.42
1:G:327:GLY:O	1:G:339:ALA:HA	2.19	0.42
1:H:148:ASN:HB2	1:H:177:ILE:HG22	2.01	0.42
1:A:612:GLY:HA2	1:B:205:GLY:HA2	2.02	0.42
1:G:99:PHE:CZ	1:G:149:ASP:HB2	2.53	0.42
1:H:433:HIS:HB2	1:H:494:HIS:O	2.19	0.42
1:B:128:CYS:HB2	1:B:147:ILE:HD11	2.02	0.42
1:B:129:HIS:H	1:B:148:ASN:ND2	2.10	0.42
1:C:564:GLN:NE2	8:C:680:HOH:O	2.42	0.42
1:E:79:GLN:HE21	1:E:83:ARG:HH21	1.67	0.42
1:E:552:ALA:HA	1:E:553:PRO:HA	1.83	0.42
1:F:216:TYR:CD1	1:F:234:ILE:HG23	2.54	0.42
1:G:79:GLN:HB2	1:G:491:ALA:CB	2.50	0.42
1:A:380:PRO:HA	1:A:394:THR:O	2.19	0.42
1:G:133:ILE:HG13	1:G:497:ILE:CD1	2.49	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:198:ILE:HD13	1:B:260:LYS:HG2	2.01	0.42
1:D:331:SER:HA	1:D:385:PHE:CE2	2.53	0.42
1:F:508:LYS:HE2	8:F:2836:HOH:O	2.20	0.42
1:G:93:LEU:HD23	1:H:488:PRO:HG3	2.02	0.42
1:G:379:GLY:N	1:G:380:PRO:HD3	2.34	0.42
1:G:381:LEU:CD1	1:G:396:PHE:HB2	2.50	0.42
1:G:381:LEU:HD11	1:G:396:PHE:HB2	2.00	0.42
1:C:354:LYS:HD3	1:C:369:VAL:HA	2.00	0.42
1:F:128:CYS:HB3	1:F:148:ASN:O	2.20	0.42
1:A:431:PRO:HA	1:A:453:SER:HA	2.00	0.42
1:H:130:HIS:H	1:H:148:ASN:ND2	2.18	0.42
1:A:577:GLN:HE21	1:A:577:GLN:CA	2.29	0.42
1:C:469:GLU:CG	1:C:492:GLU:HA	2.40	0.42
1:B:314:LYS:HE2	1:B:314:LYS:HB3	1.69	0.42
1:B:595:GLU:HB2	1:B:620:TRP:CH2	2.55	0.42
1:C:58:GLN:HE22	1:C:447:LYS:HG3	1.85	0.42
1:D:155:VAL:HG21	1:D:222:ILE:CD1	2.50	0.41
1:E:79:GLN:HE22	1:E:81:GLU:CG	2.32	0.41
1:E:148:ASN:HB2	1:E:177:ILE:HG22	2.01	0.41
1:E:476:ILE:HG22	1:E:481:MET:HG2	2.02	0.41
1:F:59:LYS:HG2	8:F:1420:HOH:O	2.19	0.41
1:D:216:TYR:CD1	1:D:234:ILE:HG23	2.56	0.41
1:E:391:ALA:HB3	1:E:404:TRP:CE2	2.54	0.41
8:E:1197:HOH:O	1:H:288:LYS:HE3	2.18	0.41
1:A:511:ASP:HB3	1:A:513:ASN:OD1	2.20	0.41
1:B:99:PHE:CE2	1:B:149:ASP:HB2	2.55	0.41
1:B:59:LYS:HE2	1:B:88:PRO:HG3	2.02	0.41
1:B:68:ASP:HB3	1:B:87:VAL:O	2.21	0.41
1:B:148:ASN:HB2	1:B:177:ILE:HG22	2.02	0.41
1:B:544:VAL:HG21	1:B:562:VAL:HG12	2.02	0.41
1:B:592:VAL:HG13	1:B:604:ILE:HD13	2.01	0.41
1:D:79:GLN:HE22	1:D:81:GLU:HG2	1.83	0.41
1:G:338:ILE:HD11	1:G:406:MET:CE	2.51	0.41
1:H:469:GLU:HG3	1:H:492:GLU:CA	2.36	0.41
1:C:132:HIS:HA	1:C:497:ILE:HD13	2.03	0.41
1:C:422:LYS:HA	1:C:422:LYS:HD3	1.94	0.41
1:H:125:ASN:HD22	1:H:125:ASN:H	1.68	0.41
1:H:510:TRP:CD1	1:H:600:GLN:HB2	2.56	0.41
1:A:78:HIS:CE1	1:A:492:GLU:HB3	2.55	0.41
1:B:59:LYS:HB3	1:B:60:ILE:H	1.57	0.41
1:B:396:PHE:CE1	1:B:430:GLN:HB3	2.55	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:D:2328:HOH:O	7:E:639:IMD:H4	2.20	0.41
1:E:260:LYS:HD2	8:E:642:HOH:O	2.20	0.41
1:A:218:MET:HG2	1:A:234:ILE:HA	2.01	0.41
1:A:279:ASP:HB2	1:A:359:PHE:CE2	2.56	0.41
1:A:595:GLU:HG2	1:A:596:ILE:N	2.35	0.41
1:B:553:PRO:HG3	1:B:623:HIS:CE1	2.56	0.41
1:D:133:ILE:CD1	1:D:497:ILE:HD12	2.51	0.41
1:D:145:LEU:HD11	1:D:497:ILE:HD11	2.01	0.41
1:H:148:ASN:H	1:H:148:ASN:HD22	1.69	0.41
1:C:591:GLY:HA2	1:D:125:ASN:ND2	2.34	0.41
1:D:351:ALA:HB3	1:D:354:LYS:HG3	2.02	0.41
1:D:382:HIS:NE2	1:D:433:HIS:CD2	2.89	0.41
1:A:423:GLN:HE22	1:A:481:MET:N	2.07	0.41
1:A:536:LYS:CD	8:A:650:HOH:O	2.68	0.41
1:A:559:GLU:OE1	1:A:632:ARG:NH1	2.53	0.41
1:C:544:VAL:HG21	1:C:562:VAL:HG12	2.03	0.41
1:D:331:SER:HB3	1:D:406:MET:HE3	2.03	0.41
1:D:443:GLU:O	1:D:444:ALA:C	2.58	0.41
1:E:435:HIS:CE1	1:E:497:ILE:HA	2.56	0.41
1:G:125:ASN:HD22	1:G:125:ASN:N	2.19	0.41
1:H:509:ILE:HD12	8:H:943:HOH:O	2.19	0.41
1:B:59:LYS:O	1:B:60:ILE:CG2	2.65	0.41
1:C:59:LYS:HE2	1:C:88:PRO:HG3	2.03	0.41
1:C:505:LYS:HE3	1:C:505:LYS:HB3	1.85	0.41
1:C:558:GLN:HE21	1:C:558:GLN:HB3	1.68	0.41
1:G:497:ILE:HB	8:G:675:HOH:O	2.20	0.41
1:A:145:LEU:C	1:A:145:LEU:HD23	2.42	0.40
1:B:133:ILE:HG13	1:B:497:ILE:CD1	2.48	0.40
1:B:216:TYR:CD1	1:B:234:ILE:HG23	2.57	0.40
1:E:201:HIS:HD2	8:E:2808:HOH:O	2.04	0.40
1:G:443:GLU:O	1:G:444:ALA:C	2.59	0.40
1:A:216:TYR:CD1	1:A:234:ILE:HG23	2.56	0.40
1:A:346:THR:HG22	1:A:375:GLU:HA	2.03	0.40
1:A:384:THR:HG22	1:A:434:LEU:HG	2.03	0.40
1:B:584:GLY:O	1:B:618:CYS:HA	2.22	0.40
1:D:327:GLY:O	1:D:339:ALA:HA	2.22	0.40
1:D:469:GLU:CG	1:D:492:GLU:HA	2.46	0.40
1:H:447:LYS:HD3	8:H:1866:HOH:O	2.22	0.40
1:H:129:HIS:CE1	1:H:494:HIS:CE1	3.10	0.40
1:H:201:HIS:HE1	1:H:216:TYR:O	2.04	0.40
1:H:272:ARG:NH2	8:H:682:HOH:O	2.42	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:443:GLU:O	1:H:444:ALA:C	2.58	0.40
1:H:380:PRO:HA	1:H:394:THR:O	2.22	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	580/638 (91%)	544 (94%)	30 (5%)	6 (1%)	15 11
1	B	582/638 (91%)	547 (94%)	32 (6%)	3 (0%)	29 26
1	C	582/638 (91%)	557 (96%)	22 (4%)	3 (0%)	29 26
1	D	588/638 (92%)	557 (95%)	29 (5%)	2 (0%)	41 41
1	E	580/638 (91%)	555 (96%)	24 (4%)	1 (0%)	47 49
1	F	582/638 (91%)	556 (96%)	25 (4%)	1 (0%)	47 49
1	G	584/638 (92%)	551 (94%)	30 (5%)	3 (0%)	29 26
1	H	582/638 (91%)	554 (95%)	25 (4%)	3 (0%)	29 26
All	All	4660/5104 (91%)	4421 (95%)	217 (5%)	22 (0%)	29 26

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	59	LYS
1	B	60	ILE
1	C	59	LYS
1	A	269	ARG
1	A	308	LYS
1	A	342	LYS
1	B	342	LYS
1	C	342	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	E	342	LYS
1	F	342	LYS
1	G	342	LYS
1	A	59	LYS
1	D	59	LYS
1	D	342	LYS
1	H	342	LYS
1	H	623	HIS
1	A	353	ASP
1	G	59	LYS
1	A	176	ALA
1	C	176	ALA
1	H	98	VAL
1	G	98	VAL

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	497/537 (93%)	472 (95%)	25 (5%)	24	23
1	B	499/537 (93%)	478 (96%)	21 (4%)	30	30
1	C	499/537 (93%)	478 (96%)	21 (4%)	30	30
1	D	504/537 (94%)	487 (97%)	17 (3%)	37	39
1	E	497/537 (93%)	482 (97%)	15 (3%)	41	44
1	F	499/537 (93%)	480 (96%)	19 (4%)	33	34
1	G	501/537 (93%)	479 (96%)	22 (4%)	28	28
1	H	499/537 (93%)	479 (96%)	20 (4%)	31	32
All	All	3995/4296 (93%)	3835 (96%)	160 (4%)	31	32

All (160) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	60	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	78	HIS
1	A	79	GLN
1	A	125	ASN
1	A	269	ARG
1	A	270	ASN
1	A	275	VAL
1	A	276	VAL
1	A	288	LYS
1	A	299	LYS
1	A	353	ASP
1	A	355	LEU
1	A	365	ASP
1	A	407	GLU
1	A	434	LEU
1	A	447	LYS
1	A	482	LYS
1	A	497	ILE
1	A	511	ASP
1	A	526	LYS
1	A	559	GLU
1	A	595	GLU
1	A	596	ILE
1	A	602	SER
1	A	620	TRP
1	B	78	HIS
1	B	79	GLN
1	B	85	LEU
1	B	125	ASN
1	B	128	CYS
1	B	148	ASN
1	B	297	ASP
1	B	311	LYS
1	B	313	SER
1	B	314	LYS
1	B	355	LEU
1	B	407	GLU
1	B	447	LYS
1	B	507	LYS
1	B	526	LYS
1	B	542	ASN
1	B	551	MET
1	B	576	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	595	GLU
1	B	596	ILE
1	B	620	TRP
1	C	59	LYS
1	C	60	ILE
1	C	78	HIS
1	C	79	GLN
1	C	85	LEU
1	C	125	ASN
1	C	148	ASN
1	C	210	LEU
1	C	275	VAL
1	C	293	ILE
1	C	299	LYS
1	C	308	LYS
1	C	311	LYS
1	C	355	LEU
1	C	407	GLU
1	C	447	LYS
1	C	458	ASP
1	C	482	LYS
1	C	558	GLN
1	C	620	TRP
1	C	621	PHE
1	D	60	ILE
1	D	78	HIS
1	D	125	ASN
1	D	148	ASN
1	D	210	LEU
1	D	225	GLU
1	D	255	CYS
1	D	293	ILE
1	D	311	LYS
1	D	355	LEU
1	D	407	GLU
1	D	447	LYS
1	D	511	ASP
1	D	526	LYS
1	D	542	ASN
1	D	620	TRP
1	D	621	PHE
1	E	60	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	E	78	HIS
1	E	79	GLN
1	E	85	LEU
1	E	125	ASN
1	E	213	GLU
1	E	275	VAL
1	E	297	ASP
1	E	311	LYS
1	E	355	LEU
1	E	407	GLU
1	E	497	ILE
1	E	542	ASN
1	E	620	TRP
1	E	621	PHE
1	F	60	ILE
1	F	78	HIS
1	F	79	GLN
1	F	125	ASN
1	F	148	ASN
1	F	210	LEU
1	F	213[A]	GLU
1	F	213[B]	GLU
1	F	228	GLU
1	F	255	CYS
1	F	297	ASP
1	F	303	LEU
1	F	355	LEU
1	F	508	LYS
1	F	526	LYS
1	F	542	ASN
1	F	596	ILE
1	F	620	TRP
1	F	621	PHE
1	G	57	LYS
1	G	60	ILE
1	G	78	HIS
1	G	79	GLN
1	G	85	LEU
1	G	125	ASN
1	G	148	ASN
1	G	210	LEU
1	G	255	CYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	G	275	VAL
1	G	313	SER
1	G	314	LYS
1	G	355	LEU
1	G	407	GLU
1	G	447	LYS
1	G	482	LYS
1	G	497	ILE
1	G	511	ASP
1	G	526	LYS
1	G	542	ASN
1	G	620	TRP
1	G	621	PHE
1	H	60	ILE
1	H	78	HIS
1	H	79	GLN
1	H	85	LEU
1	H	125	ASN
1	H	148	ASN
1	H	210	LEU
1	H	255	CYS
1	H	288	LYS
1	H	293	ILE
1	H	311	LYS
1	H	314	LYS
1	H	355	LEU
1	H	407	GLU
1	H	417	LYS
1	H	497	ILE
1	H	509	ILE
1	H	523	MET
1	H	526	LYS
1	H	620	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (104) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	58	GLN
1	A	79	GLN
1	A	111	ASN
1	A	125	ASN
1	A	129	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	148	ASN
1	A	175	GLN
1	A	241	ASN
1	A	390	ASN
1	A	423	GLN
1	A	472	GLN
1	A	577	GLN
1	B	58	GLN
1	B	79	GLN
1	B	111	ASN
1	B	125	ASN
1	B	129	HIS
1	B	148	ASN
1	B	175	GLN
1	B	201	HIS
1	B	423	GLN
1	B	472	GLN
1	B	542	ASN
1	B	577	GLN
1	C	58	GLN
1	C	78	HIS
1	C	79	GLN
1	C	111	ASN
1	C	125	ASN
1	C	129	HIS
1	C	148	ASN
1	C	175	GLN
1	C	201	HIS
1	C	214	ASN
1	C	423	GLN
1	C	467	HIS
1	C	472	GLN
1	C	494	HIS
1	C	558	GLN
1	C	577	GLN
1	D	58	GLN
1	D	79	GLN
1	D	111	ASN
1	D	125	ASN
1	D	129	HIS
1	D	148	ASN
1	D	175	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	201	HIS
1	D	214	ASN
1	D	241	ASN
1	D	423	GLN
1	D	472	GLN
1	D	542	ASN
1	E	79	GLN
1	E	111	ASN
1	E	125	ASN
1	E	129	HIS
1	E	148	ASN
1	E	175	GLN
1	E	201	HIS
1	E	214	ASN
1	E	423	GLN
1	E	472	GLN
1	E	542	ASN
1	E	558	GLN
1	E	577	GLN
1	F	79	GLN
1	F	111	ASN
1	F	125	ASN
1	F	129	HIS
1	F	148	ASN
1	F	175	GLN
1	F	201	HIS
1	F	241	ASN
1	F	423	GLN
1	F	472	GLN
1	F	542	ASN
1	F	558	GLN
1	F	577	GLN
1	G	58	GLN
1	G	79	GLN
1	G	111	ASN
1	G	125	ASN
1	G	129	HIS
1	G	148	ASN
1	G	175	GLN
1	G	423	GLN
1	G	472	GLN
1	G	542	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	G	558	GLN
1	G	599	GLN
1	H	58	GLN
1	H	79	GLN
1	H	111	ASN
1	H	125	ASN
1	H	129	HIS
1	H	148	ASN
1	H	175	GLN
1	H	201	HIS
1	H	423	GLN
1	H	472	GLN
1	H	494	HIS
1	H	577	GLN
1	H	599	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 46 ligands modelled in this entry, 24 are monoatomic - leaving 22 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
7	IMD	G	639	-	3,5,5	0.47	0	4,5,5	0.54	0
2	CUA	E	701	1	0,1,1	-	-	-	-	-
2	CUA	C	701	1	0,1,1	-	-	-	-	-
2	CUA	G	701	1	0,1,1	-	-	-	-	-
3	CUK	F	702	1	0,6,6	-	-	-	-	-
3	CUK	E	702	1	0,6,6	-	-	-	-	-
2	CUA	A	701	1	0,1,1	-	-	-	-	-
7	IMD	H	639	-	3,5,5	0.32	0	4,5,5	0.50	0
3	CUK	D	702	1	0,6,6	-	-	-	-	-
3	CUK	B	702	1	0,6,6	-	-	-	-	-
2	CUA	H	701	1	0,1,1	-	-	-	-	-
2	CUA	D	701	1	0,1,1	-	-	-	-	-
3	CUK	A	702	1	0,6,6	-	-	-	-	-
2	CUA	B	701	1	0,1,1	-	-	-	-	-
7	IMD	E	640	-	3,5,5	0.37	0	4,5,5	0.41	0
7	IMD	F	639	-	3,5,5	0.37	0	4,5,5	0.72	0
3	CUK	H	702	1	0,6,6	-	-	-	-	-
2	CUA	F	701	1	0,1,1	-	-	-	-	-
3	CUK	G	702	1	0,6,6	-	-	-	-	-
7	IMD	D	639	-	3,5,5	0.41	0	4,5,5	0.54	0
7	IMD	E	639	-	3,5,5	0.44	0	4,5,5	0.47	0
3	CUK	C	702	1	0,6,6	-	-	-	-	-

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
7	IMD	G	639	-	-	-	0/1/1/1
3	CUK	G	702	1	-	-	0/1/1/1
7	IMD	E	640	-	-	-	0/1/1/1
3	CUK	D	702	1	-	-	0/1/1/1
3	CUK	B	702	1	-	-	0/1/1/1
7	IMD	F	639	-	-	-	0/1/1/1
7	IMD	D	639	-	-	-	0/1/1/1
3	CUK	H	702	1	-	-	0/1/1/1
3	CUK	F	702	1	-	-	0/1/1/1
7	IMD	E	639	-	-	-	0/1/1/1
3	CUK	A	702	1	-	-	0/1/1/1
7	IMD	H	639	-	-	-	0/1/1/1
3	CUK	E	702	1	-	-	0/1/1/1
3	CUK	C	702	1	-	-	0/1/1/1

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.

5 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	H	639	IMD	4	0
7	E	640	IMD	2	0
7	F	639	IMD	3	0
7	D	639	IMD	2	0
7	E	639	IMD	2	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	A	581/638 (91%)	-0.02	19 (3%) 46 53	20, 33, 56, 70	0
1	B	581/638 (91%)	-0.01	13 (2%) 62 66	20, 33, 51, 62	0
1	C	581/638 (91%)	-0.49	0 100 100	10, 18, 31, 40	0
1	D	588/638 (92%)	-0.38	2 (0%) 94 94	9, 22, 36, 44	0
1	E	581/638 (91%)	-0.48	1 (0%) 95 95	8, 17, 29, 37	0
1	F	581/638 (91%)	-0.45	2 (0%) 94 94	10, 17, 31, 40	0
1	G	585/638 (91%)	-0.37	3 (0%) 91 92	10, 22, 39, 50	0
1	H	581/638 (91%)	-0.42	1 (0%) 95 95	11, 20, 35, 45	0
All	All	4659/5104 (91%)	-0.33	41 (0%) 84 86	8, 22, 43, 70	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	638	ALA	4.1
1	A	310	GLY	4.0
1	B	638	ALA	3.2
1	B	310	GLY	3.2
1	B	297	ASP	3.1
1	A	309	ASP	3.0
1	A	297	ASP	3.0
1	H	417	LYS	3.0
1	B	528	GLY	2.9
1	B	536	LYS	2.9
1	F	526	LYS	2.9
1	A	207	VAL	2.8
1	B	308	LYS	2.8
1	A	60	ILE	2.8
1	A	415	GLY	2.7
1	A	638	ALA	2.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	419	ASN	2.7
1	A	208	PHE	2.6
1	G	309	ASP	2.5
1	B	537	VAL	2.5
1	A	289	ALA	2.5
1	D	415	GLY	2.4
1	A	365	ASP	2.4
1	A	417	LYS	2.4
1	B	59	LYS	2.3
1	B	309	ASP	2.3
1	B	415	GLY	2.3
1	B	545	ARG	2.3
1	A	291	ASP	2.2
1	A	206	LYS	2.2
1	F	297	ASP	2.2
1	B	526	LYS	2.2
1	A	295	LEU	2.1
1	A	308	LYS	2.1
1	A	311	LYS	2.0
1	B	60	ILE	2.0
1	E	638	ALA	2.0
1	G	310	GLY	2.0
1	A	526	LYS	2.0
1	G	59	LYS	2.0
1	A	418	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no 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(\AA^2)	Q<0.9
3	CUK	B	702	6/6	0.83	0.12	57,61,62,62	6
6	K	A	705	1/1	0.86	0.10	54,54,54,54	0
7	IMD	D	639	5/5	0.89	0.16	46,46,47,47	0
7	IMD	F	639	5/5	0.89	0.17	47,47,48,48	0
4	CA	A	703	1/1	0.91	0.10	47,47,47,47	0
6	K	E	705	1/1	0.91	0.08	46,46,46,46	0
7	IMD	G	639	5/5	0.91	0.16	45,45,45,46	0
6	K	C	705	1/1	0.92	0.07	41,41,41,41	0
6	K	G	705	1/1	0.95	0.08	44,44,44,44	0
6	K	H	705	1/1	0.95	0.08	37,37,37,37	0
3	CUK	G	702	6/6	0.95	0.07	34,41,44,45	6
3	CUK	H	702	6/6	0.95	0.09	34,37,39,40	6
3	CUK	F	702	6/6	0.95	0.07	26,32,34,36	6
3	CUK	E	702	6/6	0.96	0.07	31,37,40,41	6
6	K	D	705	1/1	0.96	0.05	31,31,31,31	0
7	IMD	E	640	5/5	0.96	0.12	24,24,25,25	0
3	CUK	A	702	6/6	0.96	0.07	49,53,53,54	6
2	CUA	B	701	2/2	0.96	0.04	52,52,52,54	0
5	CL	A	704	1/1	0.97	0.06	46,46,46,46	0
7	IMD	E	639	5/5	0.97	0.12	37,37,38,38	0
3	CUK	C	702	6/6	0.97	0.05	29,36,38,39	6
6	K	B	705	1/1	0.97	0.06	48,48,48,48	0
2	CUA	A	701	2/2	0.97	0.04	31,31,31,34	0
7	IMD	H	639	5/5	0.97	0.08	22,22,23,24	0
2	CUA	F	701	2/2	0.98	0.07	22,22,22,33	0
5	CL	B	704	1/1	0.98	0.11	50,50,50,50	0
2	CUA	G	701	2/2	0.98	0.06	19,19,19,27	0
3	CUK	D	702	6/6	0.98	0.06	27,34,36,38	6
2	CUA	C	701	2/2	0.98	0.03	27,27,27,33	0
4	CA	E	703	1/1	0.99	0.06	18,18,18,18	0
4	CA	G	703	1/1	0.99	0.06	26,26,26,26	0
2	CUA	D	701	2/2	0.99	0.04	21,21,21,23	0
6	K	F	705	1/1	0.99	0.03	26,26,26,26	0
2	CUA	E	701	2/2	0.99	0.04	18,18,18,24	0
5	CL	C	704	1/1	0.99	0.07	26,26,26,26	0
5	CL	D	704	1/1	0.99	0.04	25,25,25,25	0
5	CL	F	704	1/1	0.99	0.07	24,24,24,24	0
5	CL	G	704	1/1	0.99	0.09	29,29,29,29	0
5	CL	H	704	1/1	0.99	0.05	29,29,29,29	0
2	CUA	H	701	2/2	0.99	0.03	33,33,33,35	0
4	CA	D	703	1/1	0.99	0.06	25,25,25,25	0
4	CA	B	703	1/1	1.00	0.05	27,27,27,27	0
4	CA	H	703	1/1	1.00	0.08	15,15,15,15	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	CL	E	704	1/1	1.00	0.07	23,23,23,23	0
4	CA	C	703	1/1	1.00	0.08	15,15,15,15	0
4	CA	F	703	1/1	1.00	0.04	17,17,17,17	0

6.5 Other polymers [i](#)

There are no such residues in this entry.