Full wwPDB X-ray Structure Validation Report (i)

Sep 10, 2023 – 01:21 PM EDT

PDB ID	:	4JRE
Title	:	Crystal structure of nitrate/nitrite exchanger NarK with nitrite bound
Authors	:	Zheng, H.; Wisedchaisri, G.; Gonen, T.
Deposited on	:	2013-03-21
Resolution	:	2.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

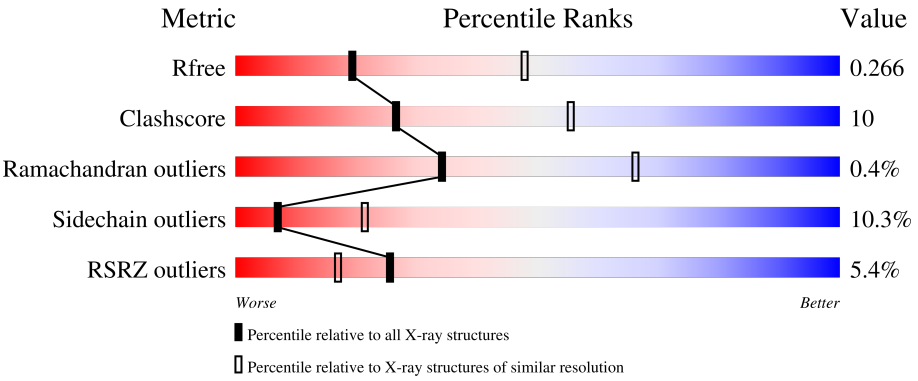
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	466	8% 67% 17% • 12%
1	D	466	11% 67% 17% • 14%
2	B	217	71% 22% 5% • •
2	H	217	69% 25% • • •
3	C	211	% 73% 22% •

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Mol	Chain	Length	Quality of chain
3	L	211	

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 12589 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 Nitrite extrusion protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	409	Total	C	N	O	S	0	0	0
			3088	2055	492	521	20			
1	D	402	Total	C	N	O	S	0	0	0
			3054	2040	484	510	20			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP P10903
A	-1	SER	-	expression tag	UNP P10903
A	0	HIS	-	expression tag	UNP P10903
D	-2	GLY	-	expression tag	UNP P10903
D	-1	SER	-	expression tag	UNP P10903
D	0	HIS	-	expression tag	UNP P10903

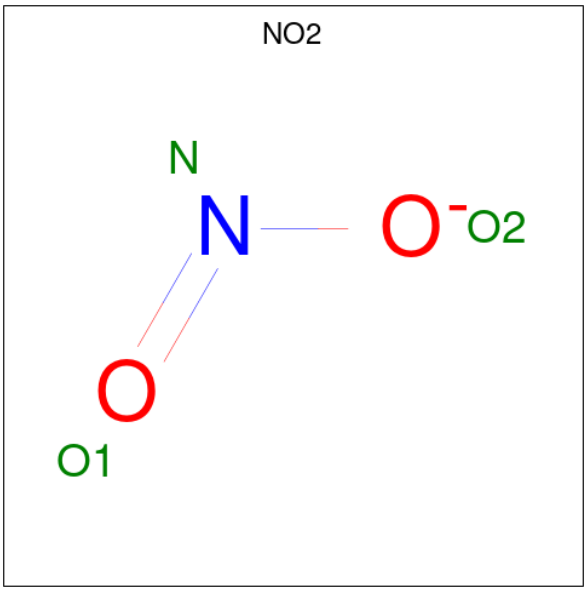
- Molecule 2 is a protein called Immunoglobulin Gamma-2a, Heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	213	Total	C	N	O	S	0	0	0
			1594	1017	261	309	7			
2	H	213	Total	C	N	O	S	0	0	0
			1592	1016	261	308	7			

- Molecule 3 is a protein called Immunoglobulin Kappa, Light chain.

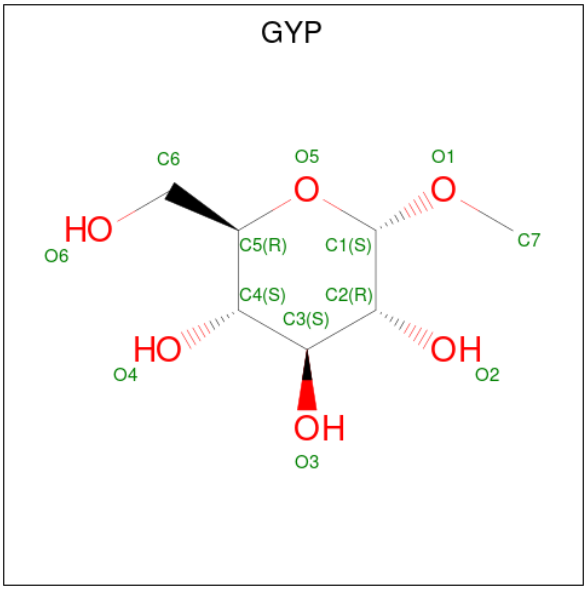
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	211	Total	C	N	O	S	0	0	0
			1597	1002	263	326	6			
3	L	211	Total	C	N	O	S	0	0	0
			1597	1002	262	327	6			

- Molecule 4 is NITRITE ION (three-letter code: NO2) (formula: NO_2).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total N O 3 1 2	0	0
4	D	1	Total N O 3 1 2	0	0

- Molecule 5 is methyl alpha-D-glucopyranoside (three-letter code: GYP) (formula: $C_7H_{14}O_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 13 7 6	0	0
5	D	1	Total C O 13 7 6	0	0

- Molecule 6 is water.

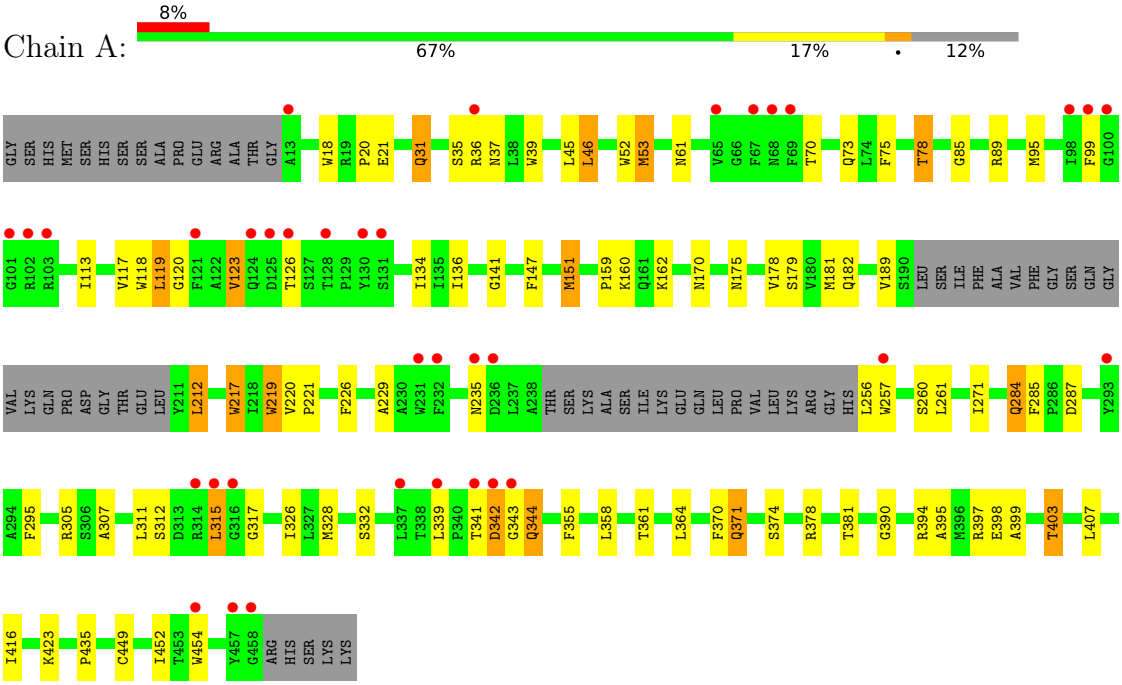
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total O 1 1	0	0
6	B	9	Total O 9 9	0	0
6	C	6	Total O 6 6	0	0
6	D	1	Total O 1 1	0	0
6	H	11	Total O 11 11	0	0
6	L	7	Total O 7 7	0	0

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.

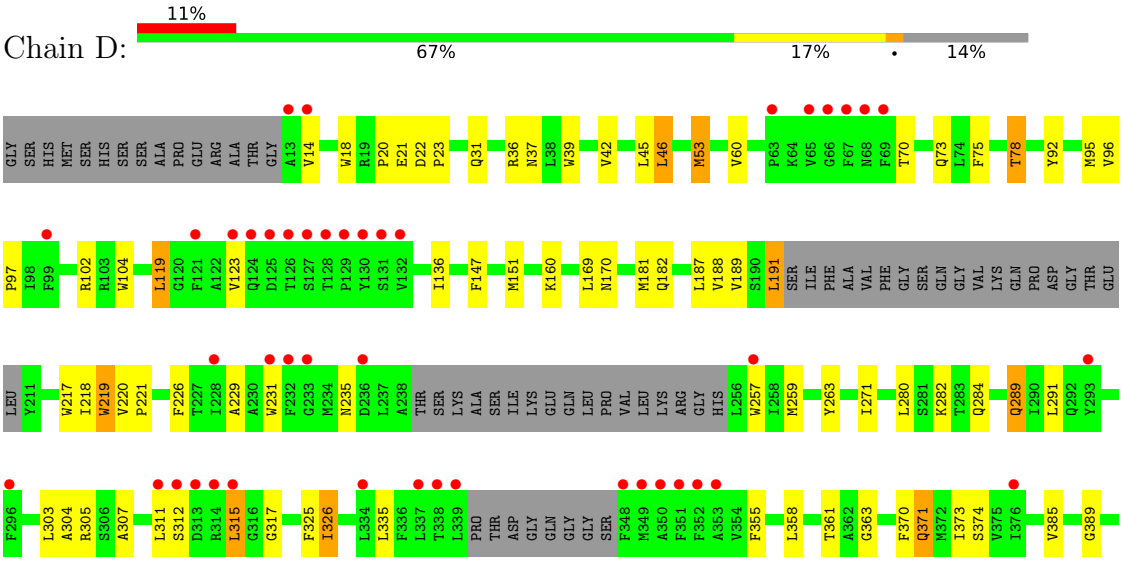
• Molecule 1: Nitrite extrusion protein 1

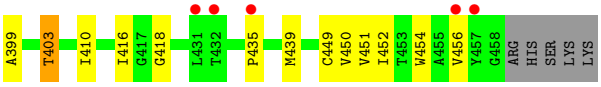
Chain A:



• Molecule 1: Nitrite extrusion protein 1

Chain D:



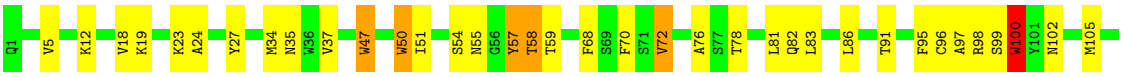


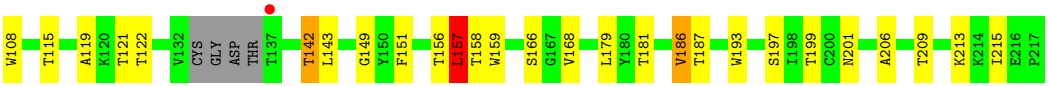
• Molecule 2: Immunoglobulin Gamma-2a, Heavy chain

Chain B:

• Molecule 2: Immunoglobulin Gamma-2a, Heavy chain

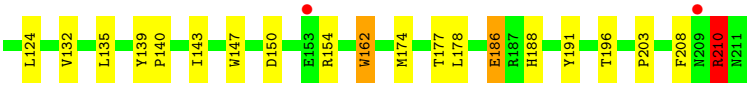
Chain H:





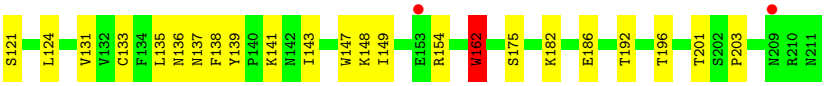
• Molecule 3: Immunoglobulin Kappa, Light chain

Chain C:



• Molecule 3: Immunoglobulin Kappa, Light chain

Chain L:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	81.91Å 81.41Å 138.49Å 100.07° 96.38° 115.92°	Depositor
Resolution (Å)	50.00 – 2.80 47.04 – 2.80	Depositor EDS
% Data completeness (in resolution range)	94.5 (50.00-2.80) 94.6 (47.04-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.16	Depositor
$< I/\sigma(I) >$ [1]	1.55 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.223 , 0.269 0.223 , 0.266	Depositor DCC
R_{free} test set	3641 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å^2)	50.7	Xtriage
Anisotropy	0.182	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 46.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.001 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.88	EDS
Total number of atoms	12589	wwPDB-VP
Average B, all atoms (Å^2)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.15% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GYP, NO2

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	0.53	6/3173 (0.2%)	0.56	2/4312 (0.0%)
1	D	0.53	5/3138 (0.2%)	0.57	2/4263 (0.0%)
2	B	0.65	4/1638 (0.2%)	0.74	2/2237 (0.1%)
2	H	0.65	6/1636 (0.4%)	0.73	1/2234 (0.0%)
3	C	0.54	2/1633 (0.1%)	0.64	1/2230 (0.0%)
3	L	0.54	2/1633 (0.1%)	0.63	1/2230 (0.0%)
All	All	0.56	25/12851 (0.2%)	0.63	9/17506 (0.1%)

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L	162	TRP	CD2-CE2	6.91	1.49	1.41
3	C	162	TRP	CD2-CE2	6.50	1.49	1.41
2	B	100	TRP	CD2-CE2	5.99	1.48	1.41
2	H	100	TRP	CD2-CE2	5.84	1.48	1.41
2	B	159	TRP	CD2-CE2	5.79	1.48	1.41
1	D	39	TRP	CD2-CE2	5.65	1.48	1.41
2	H	159	TRP	CD2-CE2	5.55	1.48	1.41
2	H	50	TRP	CD2-CE2	5.49	1.48	1.41
1	A	39	TRP	CD2-CE2	5.49	1.48	1.41
1	D	217	TRP	CD2-CE2	5.48	1.48	1.41
1	A	454	TRP	CD2-CE2	5.40	1.47	1.41
1	A	219	TRP	CD2-CE2	5.37	1.47	1.41
2	H	108	TRP	CD2-CE2	5.37	1.47	1.41
1	D	454	TRP	CD2-CE2	5.26	1.47	1.41
1	A	217	TRP	CD2-CE2	5.24	1.47	1.41
3	L	147	TRP	CD2-CE2	5.24	1.47	1.41
3	C	147	TRP	CD2-CE2	5.21	1.47	1.41
1	A	52	TRP	CD2-CE2	5.20	1.47	1.41
1	A	257	TRP	CD2-CE2	5.18	1.47	1.41
1	D	219	TRP	CD2-CE2	5.16	1.47	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	47	TRP	CD2-CE2	5.13	1.47	1.41
2	B	50	TRP	CD2-CE2	5.13	1.47	1.41
2	H	193	TRP	CD2-CE2	5.12	1.47	1.41
1	D	257	TRP	CD2-CE2	5.09	1.47	1.41
2	B	36	TRP	CD2-CE2	5.07	1.47	1.41

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	315	LEU	CA-CB-CG	6.06	129.23	115.30
2	B	157	LEU	CA-CB-CG	6.00	129.09	115.30
2	H	157	LEU	CA-CB-CG	5.75	128.53	115.30
1	D	46	LEU	CA-CB-CG	5.60	128.17	115.30
1	A	315	LEU	CA-CB-CG	5.47	127.89	115.30
1	A	46	LEU	CA-CB-CG	5.37	127.66	115.30
3	L	95	LEU	CA-CB-CG	5.30	127.49	115.30
3	C	95	LEU	CA-CB-CG	5.24	127.35	115.30
2	B	100	TRP	CA-CB-CG	5.06	123.31	113.70

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	A	3088	0	3119	49	0
1	D	3054	0	3096	50	0
2	B	1594	0	1546	45	0
2	H	1592	0	1541	47	0
3	C	1597	0	1500	39	0
3	L	1597	0	1498	35	0
4	A	3	0	0	0	0
4	D	3	0	0	0	0
5	A	13	0	14	0	0
5	D	13	0	14	0	0
6	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	9	0	0	0	0
6	C	6	0	0	0	0
6	D	1	0	0	0	0
6	H	11	0	0	1	0
6	L	7	0	0	1	0
All	All	12589	0	12328	257	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

All (257) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:100:TRP:HE3	2:B:100:TRP:O	1.39	1.05
2:H:18:VAL:HG23	2:H:86:LEU:HD11	1.43	1.01
1:A:37:ASN:HD21	1:A:235:ASN:HD22	1.04	0.99
2:H:142:THR:HB	2:H:187:THR:HG22	1.47	0.96
2:H:35:ASN:HD22	2:H:47:TRP:HE1	1.13	0.96
2:H:50:TRP:CE2	2:H:100:TRP:HD1	1.84	0.94
1:A:36:ARG:NH2	1:A:235:ASN:HD21	1.64	0.94
2:H:37:VAL:HG21	2:H:105:MET:HE1	1.47	0.93
2:B:50:TRP:CE2	2:B:100:TRP:HD1	1.88	0.92
2:H:100:TRP:HE3	2:H:100:TRP:O	1.52	0.90
1:D:37:ASN:HD21	1:D:235:ASN:HD22	1.20	0.88
1:D:181:MET:HG3	1:D:219:TRP:HH2	1.39	0.86
2:B:37:VAL:CG2	2:B:105:MET:HE1	2.05	0.86
2:H:50:TRP:CE2	2:H:100:TRP:CD1	2.64	0.85
2:B:37:VAL:HG21	2:B:105:MET:HE1	1.56	0.84
2:H:37:VAL:CG2	2:H:105:MET:HE1	2.06	0.84
2:B:100:TRP:O	2:B:100:TRP:CE3	2.28	0.83
2:B:35:ASN:HD22	2:B:47:TRP:HE1	1.27	0.83
2:H:18:VAL:CG2	2:H:86:LEU:HD11	2.08	0.83
1:D:36:ARG:HH21	1:D:235:ASN:HD21	1.25	0.82
1:A:181:MET:HG3	1:A:219:TRP:CH2	2.14	0.81
2:B:34:MET:HE1	2:B:96:CYS:HB2	1.64	0.80
2:B:34:MET:CE	2:B:96:CYS:HB2	2.12	0.79
2:H:76:ALA:O	2:H:78:THR:HG23	1.82	0.79
2:H:50:TRP:CD2	2:H:100:TRP:HD1	2.02	0.78
1:A:399:ALA:O	1:A:403:THR:HG23	1.83	0.77
1:D:36:ARG:NH2	1:D:235:ASN:HD21	1.83	0.76
1:D:326:ILE:HD12	1:D:450:VAL:HG21	1.68	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:50:TRP:CE2	2:B:100:TRP:CD1	2.72	0.76
2:B:35:ASN:ND2	2:B:47:TRP:HE1	1.84	0.75
2:B:100:TRP:HZ3	3:C:91:TYR:O	1.70	0.75
1:A:36:ARG:HH21	1:A:235:ASN:HD21	1.33	0.75
2:H:100:TRP:O	2:H:100:TRP:CE3	2.39	0.75
2:H:142:THR:HB	2:H:187:THR:CG2	2.20	0.72
1:D:312:SER:OG	1:D:317:GLY:HA2	1.91	0.70
1:A:37:ASN:ND2	1:A:235:ASN:HD22	1.86	0.70
1:D:119:LEU:HB3	1:D:136:ILE:HG21	1.74	0.69
2:B:50:TRP:CD2	2:B:100:TRP:HD1	2.11	0.69
2:B:51:ILE:HD13	2:B:72:VAL:HG23	1.75	0.69
2:B:76:ALA:O	2:B:78:THR:HG23	1.93	0.68
1:A:119:LEU:HB3	1:A:136:ILE:HG21	1.76	0.68
1:D:181:MET:HG3	1:D:219:TRP:CH2	2.26	0.68
1:D:399:ALA:O	1:D:403:THR:HG23	1.94	0.66
3:L:148:LYS:HB2	3:L:192:THR:HB	1.78	0.66
3:C:196:THR:HG22	3:C:203:PRO:HB3	1.78	0.65
2:H:100:TRP:HZ3	3:L:91:TYR:O	1.79	0.65
2:B:100:TRP:CZ3	3:C:91:TYR:O	2.49	0.65
3:L:34:VAL:HG23	3:L:89:LEU:HB3	1.77	0.64
2:H:35:ASN:ND2	2:H:47:TRP:HE1	1.90	0.64
3:C:106:LYS:HE3	2:H:206:ALA:O	1.99	0.62
2:H:55:ASN:HB3	2:H:57:TYR:HB2	1.81	0.62
1:D:18:TRP:NE1	1:D:20:PRO:HG3	2.15	0.62
3:C:38:GLN:HG3	3:C:44:PRO:HG3	1.82	0.61
2:B:97:ALA:HB3	2:B:105:MET:HE2	1.82	0.61
2:B:58:THR:HG22	2:B:70:PHE:HB2	1.83	0.61
3:C:112:PRO:HG3	3:C:143:ILE:HD11	1.83	0.60
3:L:38:GLN:HG3	3:L:44:PRO:HG3	1.85	0.59
1:D:191:LEU:HD22	1:D:191:LEU:H	1.67	0.59
1:D:358:LEU:HA	1:D:361:THR:HG22	1.82	0.59
2:H:34:MET:CE	2:H:96:CYS:HB2	2.32	0.59
1:A:182:GLN:HE21	1:A:295:PHE:HA	1.66	0.59
2:B:37:VAL:HG23	2:B:105:MET:HE1	1.84	0.59
3:L:33:ILE:HG22	3:L:51:THR:HA	1.84	0.58
2:B:142:THR:HG22	2:B:187:THR:HB	1.84	0.58
2:H:98:ARG:O	2:H:105:MET:HA	2.03	0.58
1:A:358:LEU:HA	1:A:361:THR:HG22	1.85	0.58
3:L:35:TRP:CH2	3:L:88:CYS:HB3	2.38	0.58
3:L:162:TRP:CD1	3:L:162:TRP:N	2.72	0.58
1:A:123:VAL:HG21	1:A:212:LEU:HD12	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:29:ILE:HG21	3:C:90:GLN:HG3	1.87	0.57
2:H:143:LEU:HD22	2:H:215:ILE:HG21	1.86	0.57
2:B:18:VAL:HG22	2:B:86:LEU:HD11	1.85	0.57
1:D:53:MET:HA	1:D:53:MET:CE	2.34	0.56
2:H:168:VAL:HG22	2:H:186:VAL:CG1	2.35	0.56
1:D:21:GLU:OE2	1:D:160:LYS:HG2	2.05	0.56
1:A:18:TRP:NE1	1:A:20:PRO:HG3	2.21	0.56
1:A:307:ALA:O	1:A:311:LEU:HB2	2.05	0.56
1:D:188:VAL:HG21	1:D:218:ILE:HD12	1.88	0.56
2:H:91:THR:HG23	2:H:115:THR:HA	1.88	0.56
3:L:34:VAL:HG13	3:L:91:TYR:CE1	2.41	0.56
3:C:34:VAL:HG12	3:C:49:TYR:HA	1.88	0.56
1:D:181:MET:HE2	1:D:182:GLN:HG3	1.88	0.55
3:C:94:LEU:O	3:C:95:LEU:HD23	2.05	0.55
2:H:157:LEU:HD12	2:H:158:THR:N	2.22	0.55
3:C:35:TRP:CZ3	3:C:88:CYS:HB3	2.42	0.55
2:H:100:TRP:CZ3	3:L:91:TYR:O	2.58	0.55
2:H:50:TRP:CD2	2:H:100:TRP:CD1	2.89	0.55
2:B:175:LEU:HB2	2:B:180:TYR:CE1	2.42	0.55
2:H:34:MET:HE1	2:H:96:CYS:HB2	1.89	0.55
3:C:33:ILE:HG22	3:C:51:THR:HA	1.89	0.55
1:A:75:PHE:O	1:A:78:THR:HG22	2.07	0.54
3:L:196:THR:HG22	3:L:203:PRO:HB3	1.90	0.54
1:D:325:PHE:CE2	1:D:449:CYS:HB3	2.43	0.54
2:B:159:TRP:CE2	2:B:186:VAL:HG22	2.43	0.54
3:C:143:ILE:HG22	3:C:162:TRP:CZ3	2.43	0.54
3:C:35:TRP:CE2	3:C:73:PHE:HB2	2.43	0.54
3:C:35:TRP:CH2	3:C:88:CYS:HB3	2.43	0.53
3:L:107:ARG:HD2	3:L:139:TYR:CB	2.38	0.53
1:A:181:MET:CG	1:A:219:TRP:CH2	2.90	0.53
1:A:312:SER:OG	1:A:317:GLY:HA2	2.09	0.53
2:B:34:MET:HE1	2:B:96:CYS:CB	2.37	0.53
2:B:97:ALA:HB3	2:B:105:MET:CE	2.39	0.53
3:L:106:LYS:HA	3:L:139:TYR:OH	2.09	0.53
2:B:91:THR:HG23	2:B:115:THR:HA	1.90	0.52
2:B:157:LEU:C	2:B:157:LEU:HD12	2.30	0.52
3:C:34:VAL:HG13	3:C:91:TYR:CE1	2.44	0.52
3:L:143:ILE:HG22	3:L:162:TRP:CZ3	2.45	0.52
1:A:381:THR:HG21	1:A:398:GLU:HB2	1.92	0.52
1:D:147:PHE:O	1:D:151:MET:HB2	2.09	0.52
3:L:143:ILE:HG22	3:L:162:TRP:CH2	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:312:SER:HG	1:D:317:GLY:HA2	1.75	0.52
2:H:50:TRP:CZ2	2:H:100:TRP:CD1	2.98	0.51
1:A:181:MET:CE	1:A:182:GLN:HG3	2.41	0.51
2:B:168:VAL:HG22	2:B:186:VAL:HG13	1.91	0.51
1:D:60:VAL:HG11	1:D:291:LEU:HD11	1.92	0.51
1:A:151:MET:HG2	1:A:407:LEU:HD21	1.92	0.51
2:B:68:PHE:CE2	2:B:83:LEU:HD21	2.45	0.51
3:C:12:SER:HB2	3:C:106:LYS:HE2	1.93	0.51
3:C:154:ARG:HG2	3:C:178:LEU:HD11	1.93	0.51
1:D:75:PHE:O	1:D:78:THR:HG22	2.11	0.51
1:D:325:PHE:CD2	1:D:449:CYS:HB3	2.47	0.50
3:C:12:SER:HA	3:C:104:GLU:O	2.11	0.50
1:A:449:CYS:HA	1:A:452:ILE:HG22	1.94	0.50
3:L:35:TRP:CZ3	3:L:88:CYS:HB3	2.46	0.50
3:C:91:TYR:HA	3:C:95:LEU:HD22	1.93	0.50
1:A:312:SER:HB3	1:A:371:GLN:HG2	1.94	0.50
2:H:37:VAL:CG2	2:H:105:MET:CE	2.85	0.50
3:L:182:LYS:O	3:L:186:GLU:HB2	2.12	0.50
1:A:118:TRP:CE3	1:A:136:ILE:HG12	2.46	0.50
2:H:68:PHE:CE2	2:H:83:LEU:HD23	2.47	0.50
3:C:143:ILE:HG22	3:C:162:TRP:CH2	2.47	0.49
1:D:373:ILE:HD13	1:D:410:ILE:HD13	1.94	0.49
2:H:58:THR:HG22	2:H:70:PHE:HB2	1.94	0.49
3:C:186:GLU:O	3:C:210:ARG:NH2	2.45	0.49
3:L:112:PRO:HG3	3:L:143:ILE:HD11	1.93	0.49
1:D:263:TYR:OH	1:D:305:ARG:NH2	2.46	0.49
3:L:107:ARG:HD3	3:L:108:ALA:O	2.12	0.49
3:C:89:LEU:HD21	3:C:95:LEU:HD13	1.95	0.49
1:D:37:ASN:ND2	1:D:235:ASN:HD22	2.00	0.49
2:H:157:LEU:HD12	2:H:157:LEU:C	2.32	0.49
1:A:160:LYS:HG3	1:A:397:ARG:HG2	1.94	0.49
3:L:89:LEU:HD21	3:L:95:LEU:HD13	1.94	0.49
3:L:94:LEU:O	3:L:95:LEU:HD23	2.13	0.49
2:H:51:ILE:HD13	2:H:72:VAL:HG23	1.95	0.48
1:D:271:ILE:HG22	1:D:418:GLY:HA3	1.94	0.48
1:A:120:GLY:HA3	1:A:217:TRP:NE1	2.27	0.48
1:A:159:PRO:HG2	1:A:162:LYS:HB2	1.96	0.48
3:C:150:ASP:OD2	3:C:188:HIS:HB3	2.14	0.48
2:H:12:LYS:HG3	2:H:18:VAL:HG22	1.95	0.48
3:C:34:VAL:HG21	3:C:36:TYR:OH	2.13	0.48
2:H:55:ASN:HB3	2:H:57:TYR:H	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:226:PHE:HA	1:A:229:ALA:HB3	1.94	0.48
2:B:13:LYS:HG3	2:B:16:GLN:NE2	2.29	0.47
1:A:31:GLN:O	1:A:35:SER:HB3	2.13	0.47
2:B:119:ALA:HB3	2:B:151:PHE:CZ	2.50	0.47
3:L:83:VAL:HG21	6:L:302:HOH:O	2.12	0.47
1:A:175:ASN:ND2	1:A:305:ARG:HH11	2.12	0.47
3:C:107:ARG:HD3	3:C:108:ALA:O	2.15	0.47
2:H:50:TRP:CZ2	2:H:100:TRP:HD1	2.28	0.47
2:B:128:PRO:HD3	2:B:213:LYS:HG2	1.96	0.47
1:D:181:MET:CG	1:D:219:TRP:HH2	2.20	0.47
1:D:70:THR:HB	1:D:73:GLN:H	1.79	0.47
3:C:34:VAL:CG2	3:C:89:LEU:HD23	2.44	0.47
1:D:449:CYS:HA	1:D:452:ILE:HG22	1.97	0.47
1:D:53:MET:HA	1:D:53:MET:HE3	1.97	0.47
2:H:37:VAL:HB	2:H:95:PHE:HB2	1.96	0.47
3:L:34:VAL:HG21	3:L:36:TYR:OH	2.15	0.47
3:L:35:TRP:CE2	3:L:73:PHE:HB2	2.49	0.47
2:H:97:ALA:HB3	2:H:105:MET:HE2	1.97	0.46
1:D:96:VAL:HB	1:D:97:PRO:HD3	1.98	0.46
2:H:119:ALA:HB3	2:H:151:PHE:CE2	2.50	0.46
1:A:45:LEU:HD23	1:A:170:ASN:O	2.15	0.46
1:A:371:GLN:HA	1:A:374:SER:HB3	1.96	0.46
3:C:47:LEU:HA	3:C:58:ILE:HG13	1.96	0.46
1:D:226:PHE:HA	1:D:229:ALA:HB3	1.98	0.46
2:B:48:MET:HG2	2:B:64:PHE:CE1	2.51	0.46
1:A:343:GLY:HA2	1:A:344:GLN:HA	1.69	0.46
1:A:390:GLY:HA3	1:A:394:ARG:NH2	2.31	0.46
2:B:37:VAL:HG23	2:B:105:MET:CE	2.45	0.46
2:H:50:TRP:CD1	2:H:59:THR:HB	2.50	0.46
1:A:381:THR:HG22	1:A:395:ALA:HA	1.98	0.46
2:B:52:ASN:HB3	2:B:55:ASN:OD1	2.16	0.46
2:B:39:GLN:HE22	3:C:38:GLN:HE22	1.64	0.45
3:L:91:TYR:CB	3:L:95:LEU:HD22	2.45	0.45
3:L:138:PHE:HE2	3:L:141:LYS:O	1.99	0.45
2:B:48:MET:HA	2:B:64:PHE:CD2	2.52	0.45
2:B:152:PRO:HD2	2:B:206:ALA:CB	2.46	0.45
2:B:212:ASP:O	2:B:213:LYS:HD2	2.17	0.45
2:H:68:PHE:HE2	2:H:83:LEU:HD23	1.81	0.45
2:H:142:THR:CB	2:H:187:THR:HG22	2.31	0.45
1:A:339:LEU:HD13	1:A:435:PRO:HG2	1.99	0.44
3:L:91:TYR:HA	3:L:95:LEU:HD22	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:55:GLU:HA	3:C:55:GLU:OE1	2.18	0.44
1:D:312:SER:HB3	1:D:371:GLN:HG2	1.99	0.44
2:H:47:TRP:CE2	3:L:95:LEU:HG	2.53	0.44
1:A:21:GLU:OE2	1:A:160:LYS:HG2	2.18	0.44
3:C:132:VAL:HG22	3:C:177:THR:HG22	2.00	0.44
1:A:378:ARG:HG3	1:A:399:ALA:HB1	1.98	0.44
2:B:50:TRP:CD1	2:B:59:THR:HB	2.53	0.44
2:H:149:GLY:HA2	2:H:179:LEU:HB3	1.99	0.44
2:B:34:MET:HE2	2:B:96:CYS:HB2	1.95	0.44
1:A:85:GLY:O	1:A:89:ARG:HG3	2.18	0.43
2:B:51:ILE:CD1	2:B:72:VAL:HG23	2.46	0.43
3:C:191:TYR:HB2	3:C:208:PHE:CE2	2.53	0.43
2:H:23:LYS:HA	2:H:78:THR:HG22	2.01	0.43
2:B:175:LEU:HD13	2:B:180:TYR:CE2	2.53	0.43
1:D:307:ALA:O	1:D:311:LEU:HB2	2.19	0.43
1:A:147:PHE:O	1:A:151:MET:HB2	2.19	0.43
3:C:94:LEU:C	3:C:95:LEU:HD23	2.39	0.43
2:B:189:THR:OG1	2:B:192:THR:HG22	2.18	0.42
3:L:34:VAL:HA	3:L:48:ILE:O	2.19	0.42
1:D:385:VAL:O	1:D:389:GLY:N	2.48	0.42
1:D:102:ARG:HD2	1:D:231:TRP:O	2.19	0.42
2:H:19:LYS:HA	2:H:81:LEU:O	2.19	0.42
1:A:220:VAL:N	1:A:221:PRO:HD2	2.35	0.42
3:C:33:ILE:CG2	3:C:51:THR:HA	2.50	0.42
1:D:335:LEU:HD23	1:D:439:MET:SD	2.59	0.42
2:H:70:PHE:HB3	6:H:303:HOH:O	2.19	0.42
1:D:435:PRO:O	1:D:439:MET:HB2	2.19	0.42
3:L:149:ILE:HD12	3:L:154:ARG:HD3	2.00	0.42
1:A:36:ARG:HH21	1:A:235:ASN:ND2	2.10	0.42
1:A:85:GLY:HA2	1:A:141:GLY:O	2.20	0.42
1:D:220:VAL:N	1:D:221:PRO:HD2	2.35	0.42
1:A:341:THR:O	1:A:343:GLY:HA2	2.20	0.42
1:A:423:LYS:HA	1:A:423:LYS:HD2	1.86	0.42
2:B:48:MET:HG2	2:B:64:PHE:CZ	2.54	0.42
1:D:280:LEU:C	1:D:282:LYS:H	2.23	0.42
1:D:304:ALA:HB3	1:D:363:GLY:HA3	2.02	0.42
3:L:34:VAL:CG2	3:L:89:LEU:HB3	2.46	0.42
1:A:53:MET:HG2	1:A:178:VAL:HG13	2.02	0.41
1:A:284:GLN:HB3	1:A:285:PHE:CD1	2.55	0.41
3:L:89:LEU:HG	3:L:90:GLN:N	2.35	0.41
1:D:92:TYR:HA	1:D:95:MET:HG2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:259:MET:HA	1:D:259:MET:CE	2.50	0.41
1:D:95:MET:HG3	1:D:104:TRP:CZ2	2.56	0.41
3:L:29:ILE:HG21	3:L:90:GLN:HG3	2.01	0.41
3:L:136:ASN:HB3	3:L:137:ASN:OD1	2.20	0.41
3:C:29:ILE:CG2	3:C:90:GLN:HG3	2.50	0.41
1:A:70:THR:HB	1:A:73:GLN:H	1.86	0.41
1:A:95:MET:HE3	1:A:99:PHE:HE2	1.85	0.41
1:A:342:ASP:HA	1:A:343:GLY:HA3	1.94	0.41
3:C:139:TYR:CD1	3:C:140:PRO:HA	2.55	0.41
1:D:271:ILE:HD13	1:D:271:ILE:HA	1.91	0.41
1:D:289:GLN:HE21	1:D:289:GLN:HB3	1.75	0.41
1:D:456:VAL:O	1:D:456:VAL:HG12	2.21	0.41
3:L:13:VAL:CG1	3:L:17:SER:CB	2.99	0.41
3:L:38:GLN:CG	3:L:44:PRO:HG3	2.50	0.41
3:C:78:LEU:HD11	3:C:103:LEU:HD21	2.03	0.41
3:C:139:TYR:CG	3:C:140:PRO:HA	2.56	0.41
1:D:45:LEU:HD11	1:D:147:PHE:HA	2.03	0.41
2:H:24:ALA:HB1	2:H:27:TYR:CE1	2.56	0.41
1:D:22:ASP:HA	1:D:23:PRO:HD2	1.94	0.40
1:A:61:ASN:CB	1:A:212:LEU:HD21	2.51	0.40
1:A:113:ILE:O	1:A:117:VAL:HG23	2.22	0.40
1:D:42:VAL:HG22	1:D:170:ASN:HA	2.04	0.40
2:B:108:TRP:CE2	3:C:44:PRO:HB2	2.57	0.40
3:C:30:THR:O	3:C:31:ASN:HB2	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	403/466 (86%)	384 (95%)	18 (4%)	1 (0%)	47 78

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	394/466 (84%)	377 (96%)	17 (4%)	0	100	100
2	B	209/217 (96%)	197 (94%)	10 (5%)	2 (1%)	15	44
2	H	209/217 (96%)	200 (96%)	8 (4%)	1 (0%)	29	61
3	C	209/211 (99%)	193 (92%)	15 (7%)	1 (0%)	29	61
3	L	209/211 (99%)	197 (94%)	11 (5%)	1 (0%)	29	61
All	All	1633/1788 (91%)	1548 (95%)	79 (5%)	6 (0%)	34	66

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	99	SER
1	A	342	ASP
3	C	210	ARG
2	H	99	SER
3	L	92	ASN
2	B	55	ASN

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	314/364 (86%)	285 (91%)	29 (9%)	9	27
1	D	311/364 (85%)	288 (93%)	23 (7%)	13	37
2	B	175/182 (96%)	155 (89%)	20 (11%)	5	18
2	H	174/182 (96%)	153 (88%)	21 (12%)	5	15
3	C	178/190 (94%)	159 (89%)	19 (11%)	6	20
3	L	178/190 (94%)	153 (86%)	25 (14%)	3	11
All	All	1330/1472 (90%)	1193 (90%)	137 (10%)	7	21

All (137) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	GLN
1	A	46	LEU
1	A	53	MET
1	A	78	THR
1	A	119	LEU
1	A	123	VAL
1	A	126	THR
1	A	134	ILE
1	A	151	MET
1	A	179	SER
1	A	189	VAL
1	A	212	LEU
1	A	256	LEU
1	A	260	SER
1	A	261	LEU
1	A	271	ILE
1	A	284	GLN
1	A	287	ASP
1	A	315	LEU
1	A	326	ILE
1	A	328	MET
1	A	332	SER
1	A	344	GLN
1	A	355	PHE
1	A	364	LEU
1	A	370	PHE
1	A	371	GLN
1	A	403	THR
1	A	416	ILE
2	B	18	VAL
2	B	57	TYR
2	B	58	THR
2	B	83	LEU
2	B	98	ARG
2	B	100	TRP
2	B	102	ASN
2	B	113	SER
2	B	121	THR
2	B	142	THR
2	B	148	LYS
2	B	157	LEU
2	B	181	THR
2	B	185	SER

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Mol	Chain	Res	Type
2	B	186	VAL
2	B	187	THR
2	B	192	THR
2	B	195	SER
2	B	201	ASN
2	B	209	THR
3	C	3	LEU
3	C	7	SER
3	C	12	SER
3	C	15	VAL
3	C	30	THR
3	C	38	GLN
3	C	60	SER
3	C	69	ARG
3	C	83	VAL
3	C	89	LEU
3	C	90	GLN
3	C	105	ILE
3	C	107	ARG
3	C	113	THR
3	C	124	LEU
3	C	135	LEU
3	C	174	MET
3	C	186	GLU
3	C	210	ARG
1	D	14	VAL
1	D	31	GLN
1	D	46	LEU
1	D	53	MET
1	D	78	THR
1	D	119	LEU
1	D	123	VAL
1	D	169	LEU
1	D	187	LEU
1	D	189	VAL
1	D	191	LEU
1	D	284	GLN
1	D	289	GLN
1	D	303	LEU
1	D	315	LEU
1	D	326	ILE
1	D	355	PHE

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Mol	Chain	Res	Type
1	D	370	PHE
1	D	371	GLN
1	D	374	SER
1	D	403	THR
1	D	416	ILE
1	D	451	VAL
2	H	5	VAL
2	H	54	SER
2	H	57	TYR
2	H	58	THR
2	H	72	VAL
2	H	82	GLN
2	H	100	TRP
2	H	102	ASN
2	H	121	THR
2	H	122	THR
2	H	142	THR
2	H	156	THR
2	H	157	LEU
2	H	166	SER
2	H	181	THR
2	H	186	VAL
2	H	197	SER
2	H	199	THR
2	H	201	ASN
2	H	209	THR
2	H	213	LYS
3	L	3	LEU
3	L	15	VAL
3	L	27	GLN
3	L	30	THR
3	L	33	ILE
3	L	38	GLN
3	L	56	SER
3	L	60	SER
3	L	61	ARG
3	L	69	ARG
3	L	79	GLN
3	L	81	GLU
3	L	89	LEU
3	L	90	GLN
3	L	105	ILE

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Mol	Chain	Res	Type
3	L	107	ARG
3	L	113	THR
3	L	121	SER
3	L	124	LEU
3	L	131	VAL
3	L	133	CYS
3	L	135	LEU
3	L	162	TRP
3	L	175	SER
3	L	201	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	163	GLN
1	A	175	ASN
1	A	182	GLN
1	A	235	ASN
2	B	35	ASN
2	B	39	GLN
3	C	38	GLN
3	C	197	HIS
1	D	163	GLN
1	D	182	GLN
1	D	235	ASN
1	D	284	GLN
1	D	289	GLN
2	H	35	ASN
2	H	39	GLN
3	L	38	GLN
3	L	197	HIS

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)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	GYP	A	502	-	13,13,13	0.77	1 (7%)	18,18,18	1.46	2 (11%)
4	NO2	A	501	-	1,2,2	0.19	0	0,1,1	-	-
4	NO2	D	501	-	1,2,2	0.15	0	0,1,1	-	-
5	GYP	D	502	-	13,13,13	0.81	1 (7%)	18,18,18	1.46	2 (11%)

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
5	GYP	A	502	-	-	2/4/24/24	0/1/1/1
5	GYP	D	502	-	-	2/4/24/24	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	502	GYP	O1-C1	2.37	1.44	1.40
5	A	502	GYP	O1-C1	2.33	1.44	1.40

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	502	GYP	O1-C1-C2	4.90	113.89	108.15
5	D	502	GYP	O1-C1-C2	4.58	113.52	108.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	D	502	GYP	C1-O5-C5	2.62	118.84	113.69
5	A	502	GYP	C1-C2-C3	2.48	115.17	110.00

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	D	502	GYP	C2-C1-O1-C7
5	D	502	GYP	O5-C1-O1-C7
5	A	502	GYP	C2-C1-O1-C7
5	A	502	GYP	O5-C1-O1-C7

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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	409/466 (87%)	0.22	36 (8%) 10 5	30, 73, 105, 139	0
1	D	402/466 (86%)	0.45	49 (12%) 4 2	30, 78, 105, 125	0
2	B	213/217 (98%)	-0.45	0 100 100	23, 36, 62, 112	0
2	H	213/217 (98%)	-0.51	1 (0%) 91 88	24, 35, 63, 94	0
3	C	211/211 (100%)	-0.35	2 (0%) 84 80	25, 41, 69, 84	0
3	L	211/211 (100%)	-0.34	2 (0%) 84 80	23, 40, 70, 84	0
All	All	1659/1788 (92%)	-0.05	90 (5%) 25 17	23, 53, 100, 139	0

All (90) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	315	LEU	6.5
1	D	126	THR	6.4
1	D	127	SER	6.2
1	D	431	LEU	5.9
1	A	65	VAL	5.6
1	D	314	ARG	5.4
1	D	13	ALA	5.3
1	A	315	LEU	4.7
1	A	343	GLY	4.7
1	A	131	SER	4.7
1	D	131	SER	4.6
1	D	350	ALA	4.5
1	D	311	LEU	4.4
1	D	353	ALA	4.3
1	D	349	MET	4.3
1	A	342	ASP	4.2
1	D	132	VAL	4.2
1	D	121	PHE	4.0
1	D	125	ASP	4.0

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Mol	Chain	Res	Type	RSRZ
1	D	352	PHE	3.9
1	D	68	ASN	3.8
1	D	457	TYR	3.8
1	D	236	ASP	3.7
1	D	67	PHE	3.7
1	D	69	PHE	3.7
1	D	124	GLN	3.6
1	D	65	VAL	3.6
1	A	101	GLY	3.6
1	D	313	ASP	3.6
1	D	128	THR	3.6
1	A	68	ASN	3.6
1	A	99	PHE	3.5
1	A	128	THR	3.5
1	A	67	PHE	3.5
1	A	13	ALA	3.4
1	D	293	TYR	3.4
1	D	348	PHE	3.4
1	A	457	TYR	3.3
1	D	337	LEU	3.3
1	D	130	TYR	3.2
1	D	339	LEU	3.2
1	A	316	GLY	3.1
1	A	121	PHE	3.1
1	D	296	PHE	3.1
1	A	124	GLN	3.0
1	A	341	THR	3.0
1	A	314	ARG	3.0
1	D	312	SER	3.0
1	A	235	ASN	3.0
1	D	257	TRP	2.9
1	A	102	ARG	2.9
1	D	231	TRP	2.9
1	A	125	ASP	2.9
1	D	99	PHE	2.8
1	D	456	VAL	2.8
1	A	458	GLY	2.8
1	D	232	PHE	2.7
3	C	209	ASN	2.7
1	A	130	TYR	2.7
1	D	14	VAL	2.7
1	A	126	THR	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	98	ILE	2.6
1	A	231	TRP	2.6
1	A	236	ASP	2.6
1	A	339	LEU	2.6
1	A	454	TRP	2.6
2	H	137	THR	2.6
1	D	233	GLY	2.5
1	A	36	ARG	2.4
1	A	293	TYR	2.4
1	D	334	LEU	2.4
1	D	432	THR	2.4
1	D	123	VAL	2.3
1	A	103	ARG	2.3
1	A	257	TRP	2.3
1	D	129	PRO	2.3
1	D	66	GLY	2.3
3	L	153	GLU	2.3
1	A	100	GLY	2.2
1	A	337	LEU	2.2
1	A	232	PHE	2.2
1	D	338	THR	2.2
1	D	376	ILE	2.2
3	C	153	GLU	2.1
3	L	209	ASN	2.1
1	D	63	PRO	2.1
1	D	228	ILE	2.1
1	D	435	PRO	2.1
1	D	351	PHE	2.0
1	A	69	PHE	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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	NO2	A	501	3/3	0.79	0.18	78,78,80,80	0
5	GYP	D	502	13/13	0.84	0.18	86,96,108,119	0
5	GYP	A	502	13/13	0.85	0.19	82,91,99,106	0
4	NO2	D	501	3/3	0.91	0.27	71,71,72,73	0

6.5 Other polymers

There are no such residues in this entry.