WORLDWIDE PDB

PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 04:37 AM GMT

PDB ID	:	2NM2
Title	:	Crystal structure of dihydroneopterin aldolase from S. aureus in complex with (1S,2R)-neopterin at 1.50 Angstrom resolution
Authors	:	Blaszczyk, J.; Ji, X.; Yan, H.
Deposited on	:	2006-10-20
Resolution	:	1.70 Å(reported)

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

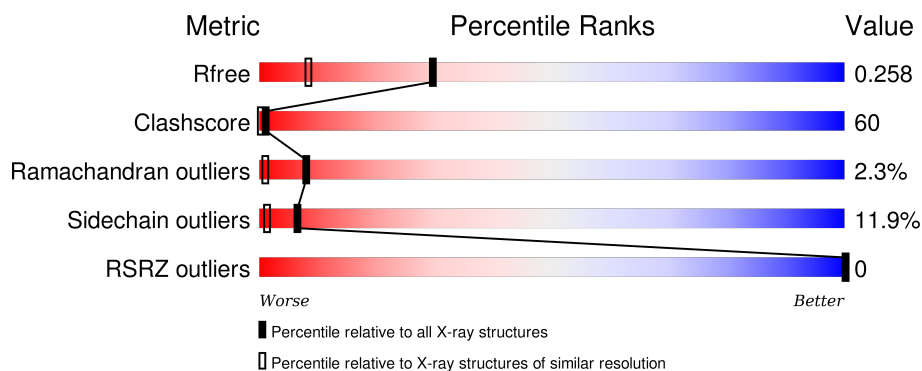|		
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.70 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	Percentile Ranks	Value
Rfree		0.258
Clashscore		60
Ramachandran outliers		2.3%
Sidechain outliers		11.9%
RSRZ outliers		0

Worse   *Better*

■ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R$_{free}$	91344	3190 (1.70-1.70)
Clashscore	102246	3585 (1.70-1.70)
Ramachandran outliers	100387	3527 (1.70-1.70)
Sidechain outliers	100360	3527 (1.70-1.70)
RSRZ outliers	91569	3200 (1.70-1.70)

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 <=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	121	31% / 58% / 11% •
1	B	121	24% / 67% / 8% •
1	C	121	20% / 70% / 10%
1	D	121	31% / 60% / 9%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 4582 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 Dihydroneopterin aldolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	121	Total	C	N	O	S	0	0	0
			967	608	169	186	4			
1	B	121	Total	C	N	O	S	0	0	0
			967	608	169	186	4			
1	C	121	Total	C	N	O	S	0	0	0
			967	608	169	186	4			
1	D	121	Total	C	N	O	S	0	0	0
			967	608	169	186	4			

- Molecule 2 is L-NEOPTERIN (three-letter code: NEU) (formula: $C_9H_{11}N_5O_4$).
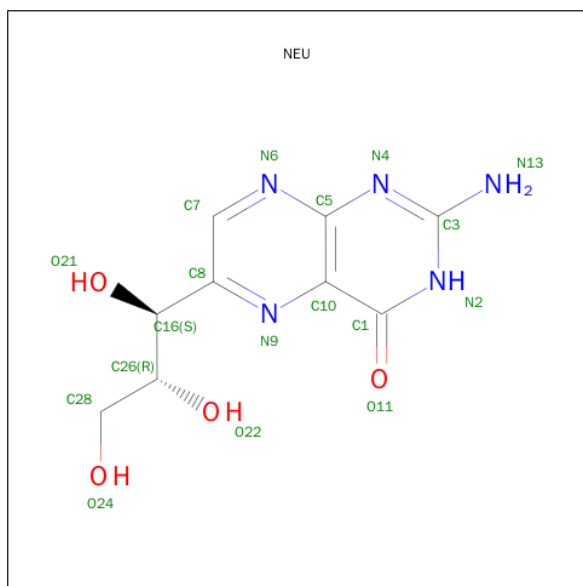
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			18	9	5	4		
2	B	1	Total	C	N	O	0	0
			18	9	5	4		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	C	1	Total	C	N	O	0	0
			18	9	5	4		
2	D	1	Total	C	N	O	0	0
			18	9	5	4		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	169	Total	O	0	0
			169	169		
3	B	166	Total	O	0	0
			166	166		
3	C	201	Total	O	0	0
			201	201		
3	D	106	Total	O	0	0
			106	106		

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.
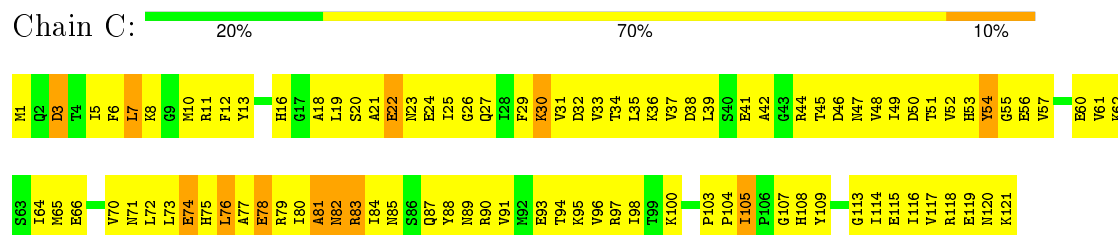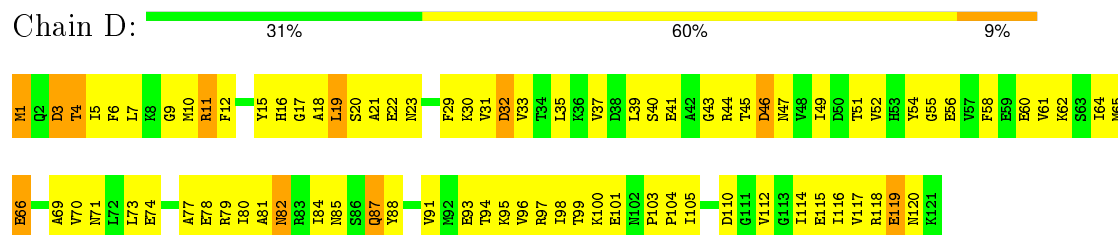
- Molecule 1: Dihydroneopterin aldolase
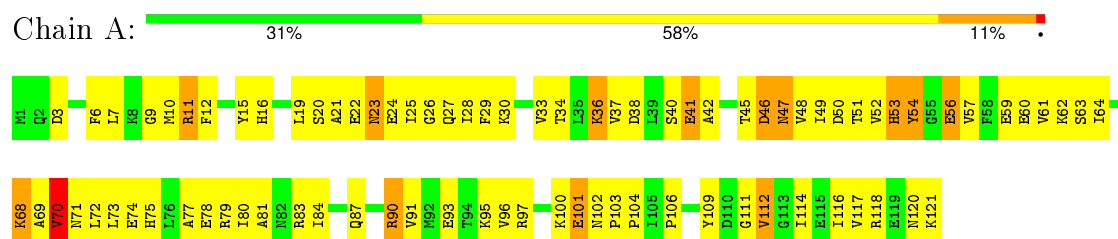
- Molecule 1: Dihydroneopterin aldolase
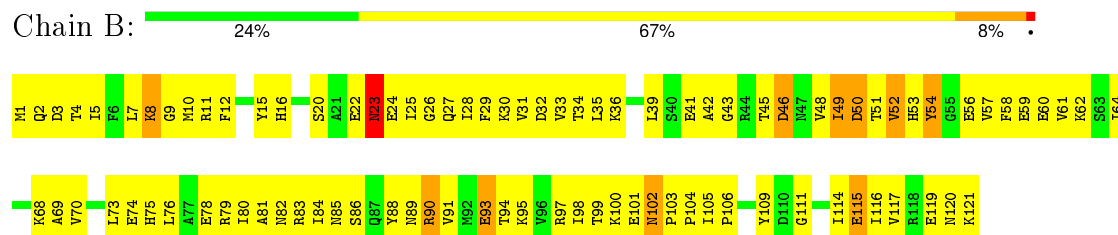
- Molecule 1: Dihydroneopterin aldolase

- Molecule 1: Dihydroneopterin aldolase

4   Data and refinement statistics (i)

Property	Value	Source
Space group	P 42	Depositor
Cell constants a, b, c, α, β, γ	60.03Å 60.03Å 123.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	22.46 – 1.70 22.46 – 1.70	Depositor EDS
% Data completeness (in resolution range)	88.0 (22.46-1.70) 61.3 (22.46-1.70)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.25 (at 1.71Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.220 , 0.262 0.207 , 0.258	Depositor DCC
R_{free} test set	1356 reflections (4.87%)	DCC
Wilson B-factor (Å^2)	17.7	Xtriage
Anisotropy	0.248	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 80.1	EDS
Estimated twinning fraction	0.499 for h,-k,-l	Xtriage
L-test for twinning[2]	$< |L| > = 0.44$, $< L^2 > = 0.26$	Xtriage
Outliers	0 of 29225 reflections	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	4582	wwPDB-VP
Average B, all atoms (Å^2)	27.0	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 62.73 % 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 1.0771e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: NEU

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	0.41	0/982	0.68	0/1321
1	B	0.38	0/982	0.68	0/1321
1	C	0.40	0/982	0.64	0/1321
1	D	0.40	0/982	0.73	0/1321
All	All	0.40	0/3928	0.68	0/5284

There are no bond length outliers.

There are no bond angle outliers.

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	967	0	965	136	0
1	B	967	0	965	120	0
1	C	967	0	965	142	0
1	D	967	0	965	108	0
2	A	18	0	10	3	0
2	B	18	0	10	4	0
2	C	18	0	10	1	0
2	D	18	0	10	4	0
3	A	169	0	0	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	166	0	0	13	0
3	C	201	0	0	14	0
3	D	106	0	0	13	0
All	All	4582	0	3900	469	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 60.

All (469) 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:D:41:GLU:HG3	1:D:44:ARG:HD3	1.31	1.10
1:A:104:PRO:HB3	1:C:25:ILE:HG23	1.39	1.02
1:B:90:ARG:HB3	1:B:90:ARG:HH11	1.20	1.02
1:A:112:VAL:HG11	1:B:7:LEU:HD23	1.44	0.97
1:A:36:LYS:HB3	1:A:36:LYS:HZ3	1.27	0.96
1:C:77:ALA:HB1	1:C:96:VAL:HG11	1.49	0.94
1:A:52:VAL:HG23	3:A:1079:HOH:O	1.73	0.89
1:C:53:HIS:CD2	1:C:56:GLU:HG3	2.08	0.88
1:A:61:VAL:HG13	1:A:80:ILE:HD13	1.54	0.87
1:A:41:GLU:HG3	1:A:50:ASP:HB3	1.57	0.86
1:C:33:VAL:HG22	1:C:96:VAL:HG23	1.58	0.85
1:B:100:LYS:HD2	1:B:103:PRO:HB3	1.58	0.83
1:A:112:VAL:CG1	1:B:7:LEU:HD23	2.10	0.81
1:A:37:VAL:HG22	1:A:91:VAL:HA	1.62	0.80
1:B:78:GLU:HB3	3:B:1101:HOH:O	1.80	0.80
1:A:75:HIS:HB2	1:B:46:ASP:OD1	1.82	0.80
1:D:45:THR:O	1:D:46:ASP:HB2	1.80	0.79
1:A:112:VAL:HG12	1:B:7:LEU:HA	1.64	0.78
1:C:77:ALA:HB1	1:C:96:VAL:CG1	2.14	0.78
1:C:107:GLY:HA3	1:D:58:PHE:CZ	2.18	0.77
1:D:78:GLU:HA	1:D:78:GLU:OE1	1.84	0.77
1:D:104:PRO:C	1:D:105:ILE:HD12	2.04	0.77
1:B:90:ARG:CB	1:B:90:ARG:HH11	1.96	0.77
1:D:5:ILE:HD12	1:D:37:VAL:HG21	1.66	0.77
1:B:70:VAL:HG21	1:B:76:LEU:HG	1.66	0.77
1:D:66:GLU:HG2	3:D:1021:HOH:O	1.84	0.77
1:A:114:ILE:HG22	1:B:5:ILE:HG12	1.66	0.77
1:B:41:GLU:HG3	1:B:50:ASP:OD2	1.84	0.77
1:A:24:GLU:OE2	1:C:21:ALA:HB2	1.85	0.76
1:A:27:GLN:NE2	1:A:100:LYS:HE2	2.00	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:74:GLU:N	1:B:74:GLU:OE1	2.19	0.76
1:A:11:ARG:HG2	1:A:11:ARG:HH11	1.50	0.76
1:D:70:VAL:HG12	3:D:1151:HOH:O	1.85	0.75
1:A:70:VAL:HG21	1:A:75:HIS:CD2	2.22	0.75
1:C:105:ILE:HG21	1:D:55:GLY:HA2	1.66	0.75
1:C:82:ASN:HB3	3:C:1129:HOH:O	1.86	0.75
1:D:11:ARG:HH12	1:D:30:LYS:HD2	1.52	0.75
1:B:90:ARG:NH1	1:B:90:ARG:HB3	1.98	0.75
1:C:118:ARG:HA	3:C:1062:HOH:O	1.86	0.75
1:A:36:LYS:HB3	1:A:36:LYS:NZ	2.02	0.74
1:C:88:TYR:HD2	1:C:90:ARG:HD2	1.51	0.74
1:B:100:LYS:O	1:B:103:PRO:HD3	1.88	0.73
1:D:19:LEU:HD12	1:D:20:SER:N	2.03	0.73
1:C:45:THR:HB	1:C:47:ASN:HD22	1.52	0.73
1:A:70:VAL:HG21	1:A:75:HIS:HD2	1.52	0.73
1:A:9:GLY:O	1:A:11:ARG:HG3	1.89	0.72
1:D:18:ALA:HA	1:D:71:ASN:HD22	1.55	0.72
1:C:44:ARG:NH1	1:C:44:ARG:HB3	2.03	0.72
1:B:34:THR:HB	1:B:95:LYS:HE2	1.71	0.72
1:C:5:ILE:HD12	1:C:37:VAL:HG21	1.70	0.72
1:A:103:PRO:HB2	2:A:122:NEU:H281	1.70	0.72
1:D:74:GLU:HG3	1:D:114:ILE:HD13	1.71	0.70
1:D:65:MET:HB2	3:D:1021:HOH:O	1.92	0.70
1:A:104:PRO:HB2	3:A:1380:HOH:O	1.91	0.70
1:C:25:ILE:HG22	1:C:26:GLY:O	1.92	0.69
1:D:87:GLN:HB3	1:D:88:TYR:CE1	2.27	0.69
1:C:62:LYS:HG3	1:C:66:GLU:HG3	1.74	0.69
1:C:6:PHE:HB3	1:C:34:THR:HG23	1.73	0.69
1:B:15:TYR:HA	1:B:26:GLY:HA2	1.74	0.69
1:D:12:PHE:CD2	1:D:65:MET:HG3	2.28	0.69
1:B:15:TYR:O	1:B:23:ASN:HA	1.93	0.69
1:A:36:LYS:HZ2	1:A:93:GLU:HB2	1.57	0.69
1:D:16:HIS:ND1	1:D:69:ALA:HA	2.08	0.69
1:C:118:ARG:HB3	3:C:1150:HOH:O	1.91	0.69
1:D:18:ALA:HA	1:D:71:ASN:ND2	2.08	0.68
1:D:97:ARG:HG2	3:D:1098:HOH:O	1.91	0.68
1:B:16:HIS:ND1	1:B:69:ALA:HA	2.09	0.68
1:D:64:ILE:HG21	1:D:80:ILE:HG13	1.76	0.68
1:C:78:GLU:OE2	1:D:43:GLY:HA3	1.93	0.67
1:B:42:ALA:HA	1:B:50:ASP:HB2	1.77	0.67
1:C:5:ILE:HG22	3:C:1107:HOH:O	1.93	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:100:LYS:O	1:C:103:PRO:HD3	1.94	0.67
1:C:53:HIS:HD2	1:C:56:GLU:N	1.92	0.67
1:B:79:ARG:HG3	3:B:1101:HOH:O	1.94	0.67
1:C:37:VAL:HG22	1:C:91:VAL:HG22	1.76	0.66
1:B:60:GLU:OE1	1:B:83:ARG:HD2	1.95	0.66
1:A:100:LYS:O	1:A:103:PRO:HD3	1.96	0.66
1:B:1:MET:HG3	1:B:36:LYS:HE2	1.78	0.66
1:B:81:ALA:HB2	1:B:116:ILE:HD11	1.79	0.65
1:A:77:ALA:HA	1:A:96:VAL:HG11	1.77	0.65
1:C:66:GLU:HB3	3:C:1095:HOH:O	1.95	0.65
1:C:19:LEU:HB3	1:C:22:GLU:CG	2.26	0.65
1:C:73:LEU:HG	3:C:1054:HOH:O	1.97	0.64
1:C:10:MET:HB3	1:C:12:PHE:CE1	2.32	0.64
1:C:75:HIS:HA	1:C:78:GLU:HB2	1.77	0.64
1:C:82:ASN:HA	1:C:85:ASN:HB2	1.80	0.64
1:A:104:PRO:HG2	2:A:122:NEU:O24	1.97	0.64
1:D:5:ILE:CD1	1:D:52:VAL:HB	2.28	0.64
1:A:22:GLU:OE1	1:A:100:LYS:NZ	2.30	0.64
1:A:104:PRO:HB3	1:C:25:ILE:CG2	2.22	0.64
1:B:76:LEU:O	1:B:80:ILE:HG13	1.97	0.64
1:C:119:GLU:HG2	3:C:1039:HOH:O	1.98	0.64
1:A:59:GLU:HG3	3:A:1063:HOH:O	1.96	0.64
1:A:27:GLN:NE2	1:A:100:LYS:CE	2.61	0.63
1:D:116:ILE:HG21	3:D:1050:HOH:O	1.97	0.63
1:C:96:VAL:HG12	1:C:116:ILE:CG1	2.29	0.63
1:C:53:HIS:HD2	1:C:56:GLU:H	1.46	0.63
1:D:116:ILE:HD13	3:D:1050:HOH:O	1.98	0.63
1:C:19:LEU:O	1:C:22:GLU:HG3	1.98	0.63
1:C:105:ILE:HG22	3:D:1016:HOH:O	1.98	0.63
1:B:49:ILE:HG23	1:B:50:ASP:OD1	1.98	0.62
1:B:45:THR:O	1:B:46:ASP:HB3	2.00	0.62
1:D:103:PRO:HG2	1:D:105:ILE:HD13	1.82	0.62
1:C:33:VAL:CG2	1:C:96:VAL:HG23	2.27	0.62
1:A:36:LYS:HB2	1:A:93:GLU:HB3	1.82	0.62
1:B:25:ILE:HA	3:B:1153:HOH:O	1.98	0.62
1:A:104:PRO:HD3	3:A:1099:HOH:O	1.99	0.62
1:B:64:ILE:CD1	1:B:80:ILE:HA	2.29	0.62
1:A:48:VAL:HA	1:A:51:THR:HG22	1.82	0.61
1:D:119:GLU:HB3	3:D:1032:HOH:O	2.01	0.61
1:A:60:GLU:HB2	1:A:84:ILE:HD11	1.81	0.61
1:A:70:VAL:HG12	3:B:1357:HOH:O	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:52:VAL:HG13	1:C:88:TYR:CD2	2.35	0.61
1:D:74:GLU:CG	1:D:114:ILE:HD13	2.30	0.61
1:C:18:ALA:HA	1:C:71:ASN:OD1	2.01	0.61
1:D:18:ALA:H	2:D:422:NEU:H16	1.66	0.61
1:A:41:GLU:CG	1:A:50:ASP:HB3	2.30	0.60
1:C:61:VAL:O	1:C:65:MET:HG2	2.02	0.60
1:A:114:ILE:CG2	1:B:5:ILE:HG12	2.30	0.60
1:A:106:PRO:HA	1:C:13:TYR:CD2	2.36	0.60
1:C:107:GLY:HA3	1:D:58:PHE:HZ	1.66	0.60
1:D:15:TYR:HD2	1:D:23:ASN:O	1.83	0.60
1:A:101:GLU:HA	1:A:111:GLY:HA2	1.83	0.60
1:D:41:GLU:HA	1:D:44:ARG:CB	2.32	0.60
1:B:10:MET:HE3	1:B:58:PHE:CD1	2.37	0.60
1:D:54:TYR:CD1	1:D:55:GLY:N	2.70	0.60
1:C:74:GLU:OE2	1:D:39:LEU:HD22	2.01	0.60
1:A:7:LEU:HB2	1:A:33:VAL:HG22	1.83	0.59
1:D:35:LEU:CD2	1:D:94:THR:HG23	2.32	0.59
1:C:103:PRO:HG2	1:C:105:ILE:HG13	1.84	0.59
1:C:45:THR:HB	1:C:47:ASN:ND2	2.16	0.59
1:B:31:VAL:HG22	1:B:98:ILE:HG12	1.84	0.59
1:D:5:ILE:HD13	1:D:52:VAL:HB	1.83	0.59
1:A:53:HIS:HB3	1:A:56:GLU:HB2	1.85	0.59
1:D:18:ALA:HB3	2:D:422:NEU:H16	1.83	0.59
1:D:41:GLU:HA	1:D:44:ARG:HB2	1.85	0.59
1:B:73:LEU:H	2:B:222:NEU:HN2	1.49	0.59
1:A:11:ARG:HG2	1:A:11:ARG:NH1	2.17	0.59
1:C:49:ILE:HD12	1:C:90:ARG:NH2	2.18	0.59
1:D:88:TYR:HB2	1:D:91:VAL:HG23	1.84	0.59
1:A:53:HIS:HA	3:A:1028:HOH:O	2.02	0.59
1:D:19:LEU:HD12	1:D:21:ALA:H	1.68	0.59
1:B:85:ASN:HB3	1:B:120:ASN:OD1	2.03	0.59
1:D:19:LEU:HG	1:D:21:ALA:HB3	1.85	0.59
1:B:41:GLU:HA	1:B:41:GLU:OE1	2.03	0.58
1:A:74:GLU:CG	1:B:39:LEU:HD13	2.33	0.58
1:A:90:ARG:CB	1:A:90:ARG:HH11	2.16	0.58
1:C:103:PRO:HD2	1:C:109:TYR:HE1	1.67	0.58
1:A:21:ALA:O	1:A:24:GLU:HB3	2.03	0.58
1:B:22:GLU:C	1:B:24:GLU:H	2.06	0.58
1:B:56:GLU:HB3	3:B:1140:HOH:O	2.02	0.58
1:A:73:LEU:HG	2:A:122:NEU:O11	2.03	0.58
1:B:45:THR:O	1:B:46:ASP:CB	2.52	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:90:ARG:HB3	1:A:90:ARG:HH11	1.67	0.58
1:A:10:MET:HB3	1:A:12:PHE:CE2	2.39	0.58
1:D:3:ASP:O	1:D:4:THR:HG23	2.03	0.58
1:A:69:ALA:O	1:A:70:VAL:HG13	2.03	0.57
1:C:49:ILE:HD12	1:C:90:ARG:HH22	1.69	0.57
1:C:93:GLU:HA	1:C:119:GLU:HA	1.85	0.57
1:C:93:GLU:CD	1:C:117:VAL:HG13	2.24	0.57
1:A:27:GLN:HE21	1:A:100:LYS:CE	2.16	0.57
1:A:27:GLN:HE21	1:A:100:LYS:HE2	1.69	0.57
1:C:64:ILE:HA	3:C:1409:HOH:O	2.05	0.57
1:C:62:LYS:CG	1:C:66:GLU:HG3	2.35	0.57
1:A:7:LEU:HB2	1:A:33:VAL:CG2	2.35	0.56
1:D:73:LEU:HD11	1:D:100:LYS:HD2	1.86	0.56
1:D:78:GLU:OE1	1:D:81:ALA:HB3	2.05	0.56
1:D:19:LEU:CD1	1:D:21:ALA:H	2.18	0.56
1:A:64:ILE:HG21	1:A:79:ARG:HB3	1.86	0.56
1:C:74:GLU:OE1	1:C:114:ILE:HG12	2.06	0.56
1:C:97:ARG:HB2	1:C:115:GLU:HG3	1.88	0.56
1:D:60:GLU:O	1:D:64:ILE:HG12	2.05	0.56
1:C:96:VAL:HG12	1:C:116:ILE:HG13	1.88	0.56
1:A:75:HIS:HA	3:B:1051:HOH:O	2.05	0.56
1:D:56:GLU:O	1:D:60:GLU:HG2	2.05	0.56
1:B:64:ILE:HD12	1:B:80:ILE:HA	1.87	0.55
1:C:37:VAL:HG12	1:C:38:ASP:H	1.72	0.55
1:C:5:ILE:HD11	1:C:39:LEU:HD21	1.89	0.55
1:A:57:VAL:O	1:A:61:VAL:HG23	2.06	0.55
1:C:121:LYS:HD2	1:C:121:LYS:N	2.22	0.55
1:A:19:LEU:HG	1:A:21:ALA:H	1.72	0.54
1:A:37:VAL:HG13	1:A:90:ARG:O	2.07	0.54
1:D:35:LEU:HB3	1:D:91:VAL:HG13	1.88	0.54
1:D:62:LYS:HG2	1:D:66:GLU:HG3	1.88	0.54
1:D:11:ARG:HH11	1:D:11:ARG:HG2	1.73	0.54
1:A:68:LYS:HE3	1:A:79:ARG:NH1	2.23	0.54
1:C:87:GLN:HG3	1:C:88:TYR:CE1	2.43	0.54
1:A:71:ASN:ND2	3:A:1001:HOH:O	2.41	0.54
1:A:57:VAL:HG13	1:A:84:ILE:HD12	1.89	0.54
1:B:88:TYR:HB2	1:B:91:VAL:HG23	1.89	0.53
1:A:49:ILE:O	1:A:90:ARG:NH2	2.41	0.53
1:C:46:ASP:OD1	1:C:46:ASP:O	2.27	0.53
1:D:15:TYR:O	1:D:23:ASN:HA	2.09	0.53
1:A:15:TYR:O	1:A:23:ASN:HB3	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:33:VAL:HA	1:C:95:LYS:O	2.08	0.53
1:A:36:LYS:HZ2	1:A:93:GLU:CB	2.21	0.53
1:A:61:VAL:HG22	1:A:80:ILE:CG2	2.38	0.53
1:B:68:LYS:HA	3:B:1091:HOH:O	2.08	0.53
1:B:101:GLU:HA	1:B:111:GLY:HA2	1.91	0.53
1:B:102:ASN:N	1:B:103:PRO:CD	2.72	0.52
1:C:76:LEU:O	1:C:80:ILE:HG13	2.09	0.52
1:B:42:ALA:HA	1:B:50:ASP:CB	2.39	0.52
1:A:74:GLU:HG2	1:B:39:LEU:HD13	1.90	0.52
1:B:121:LYS:HD2	1:B:121:LYS:N	2.25	0.52
1:A:33:VAL:HG11	1:A:61:VAL:HG21	1.91	0.52
1:A:15:TYR:O	1:A:23:ASN:HA	2.09	0.52
1:C:120:ASN:C	1:C:121:LYS:HD2	2.29	0.52
1:A:116:ILE:HG22	1:B:39:LEU:HD12	1.91	0.52
1:B:80:ILE:O	1:B:84:ILE:HG12	2.10	0.52
1:C:27:GLN:OE1	1:C:100:LYS:HG3	2.10	0.52
1:D:74:GLU:HG3	1:D:114:ILE:CD1	2.40	0.52
1:B:35:LEU:HD22	1:B:94:THR:OG1	2.10	0.51
1:C:54:TYR:HD1	1:C:55:GLY:N	2.08	0.51
1:B:83:ARG:HG2	1:B:83:ARG:HH11	1.76	0.51
1:C:16:HIS:HB2	1:C:29:PHE:CZ	2.45	0.51
1:C:16:HIS:ND1	1:C:70:VAL:HG22	2.24	0.51
1:A:72:LEU:HG	1:A:74:GLU:OE1	2.10	0.51
1:A:15:TYR:HB3	1:A:23:ASN:HA	1.91	0.51
1:A:33:VAL:O	1:A:33:VAL:HG23	2.10	0.51
1:B:73:LEU:N	2:B:222:NEU:HN2	2.08	0.51
1:C:79:ARG:O	1:C:83:ARG:HB2	2.10	0.51
1:D:3:ASP:OD2	1:D:39:LEU:HB2	2.10	0.51
1:B:53:HIS:HB3	1:B:56:GLU:HG3	1.91	0.51
1:B:51:THR:OG1	1:B:52:VAL:N	2.43	0.51
1:A:49:ILE:O	1:A:49:ILE:HG13	2.10	0.51
1:B:64:ILE:HD12	1:B:80:ILE:HG12	1.93	0.51
1:D:62:LYS:HA	3:D:1021:HOH:O	2.10	0.51
1:A:37:VAL:HG11	3:A:1079:HOH:O	2.11	0.51
1:A:101:GLU:HG3	3:A:1037:HOH:O	2.10	0.51
1:D:41:GLU:O	1:D:41:GLU:HG2	2.11	0.51
1:C:85:ASN:ND2	1:C:119:GLU:O	2.44	0.51
1:C:44:ARG:HH11	1:C:44:ARG:HB3	1.76	0.51
1:D:101:GLU:HG2	1:D:110:ASP:O	2.11	0.50
1:A:74:GLU:HG3	1:B:39:LEU:HD13	1.94	0.50
1:B:4:THR:HB	1:B:34:THR:CG2	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:37:VAL:HG12	1:C:38:ASP:N	2.26	0.50
1:B:27:GLN:HB2	1:B:102:ASN:HD22	1.76	0.50
1:C:109:TYR:HA	1:D:9:GLY:O	2.11	0.50
1:D:35:LEU:HD13	1:D:84:ILE:HG21	1.93	0.50
1:B:12:PHE:O	1:B:28:ILE:HA	2.11	0.50
1:A:45:THR:O	1:A:46:ASP:CB	2.60	0.50
1:A:47:ASN:HB3	1:A:49:ILE:HG22	1.92	0.50
1:A:42:ALA:HA	1:A:50:ASP:HB2	1.94	0.50
1:C:53:HIS:CD2	1:C:56:GLU:H	2.29	0.49
1:A:73:LEU:HD21	1:A:100:LYS:HD2	1.94	0.49
1:B:85:ASN:HB3	1:B:120:ASN:CG	2.33	0.49
1:D:45:THR:HB	1:D:47:ASN:ND2	2.27	0.49
1:D:74:GLU:OE1	1:D:114:ILE:HD13	2.12	0.49
1:A:34:THR:HB	1:A:95:LYS:HD3	1.94	0.49
1:C:96:VAL:HG12	1:C:116:ILE:HG12	1.95	0.49
1:D:45:THR:O	1:D:46:ASP:CB	2.56	0.49
1:D:97:ARG:HB2	1:D:115:GLU:HG3	1.94	0.49
1:D:97:ARG:NH1	3:D:1072:HOH:O	2.45	0.49
1:B:12:PHE:O	1:B:29:PHE:N	2.38	0.49
1:A:40:SER:HB3	3:A:1048:HOH:O	2.12	0.49
1:A:56:GLU:O	1:A:60:GLU:HG2	2.12	0.49
1:D:32:ASP:HB2	1:D:97:ARG:HB3	1.93	0.49
1:B:30:LYS:HB3	1:B:99:THR:HB	1.94	0.49
1:B:114:ILE:HD12	1:B:115:GLU:N	2.28	0.49
1:A:78:GLU:OE1	1:A:78:GLU:HA	2.12	0.49
1:C:11:ARG:HH11	1:C:11:ARG:HG2	1.77	0.49
1:B:70:VAL:HB	1:B:75:HIS:CD2	2.48	0.49
1:C:44:ARG:HH11	1:C:44:ARG:CB	2.26	0.49
1:C:97:ARG:CB	1:C:115:GLU:HG3	2.43	0.49
1:B:49:ILE:HG13	1:B:49:ILE:O	2.13	0.49
1:D:10:MET:HE1	1:D:61:VAL:HG21	1.94	0.49
1:D:49:ILE:HD11	3:D:1348:HOH:O	2.11	0.49
1:C:72:LEU:HB3	2:C:322:NEU:O11	2.13	0.48
1:B:73:LEU:HB2	1:B:114:ILE:HG12	1.94	0.48
1:C:19:LEU:HB3	1:C:22:GLU:HG3	1.95	0.48
1:D:73:LEU:HD13	1:D:98:ILE:O	2.14	0.48
1:D:104:PRO:O	1:D:105:ILE:HD12	2.12	0.48
1:C:48:VAL:O	1:C:51:THR:HG22	2.12	0.48
1:C:98:ILE:O	1:C:113:GLY:HA3	2.12	0.48
1:B:70:VAL:CG1	1:B:75:HIS:HD2	2.27	0.48
1:D:10:MET:HE2	1:D:61:VAL:HG11	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:20:SER:HB2	3:B:1601:HOH:O	2.13	0.48
1:B:48:VAL:C	1:B:50:ASP:H	2.17	0.48
1:C:36:LYS:HG3	3:C:1065:HOH:O	2.13	0.48
1:A:7:LEU:HD11	1:A:54:TYR:HB2	1.94	0.48
1:A:19:LEU:HG	1:A:20:SER:N	2.29	0.48
1:A:81:ALA:HB1	3:A:1064:HOH:O	2.14	0.48
1:B:9:GLY:O	1:B:11:ARG:HG3	2.14	0.48
1:A:25:ILE:HD11	1:C:21:ALA:HB3	1.95	0.47
1:C:93:GLU:HG2	1:C:94:THR:N	2.28	0.47
1:C:114:ILE:HD12	1:C:114:ILE:C	2.34	0.47
1:C:8:LYS:HE3	3:C:1100:HOH:O	2.13	0.47
1:D:94:THR:HG22	1:D:95:LYS:N	2.29	0.47
1:B:1:MET:O	1:B:2:GLN:HG3	2.14	0.47
1:D:6:PHE:C	1:D:7:LEU:HD12	2.34	0.47
1:B:7:LEU:CD1	1:B:57:VAL:HG12	2.44	0.47
1:C:31:VAL:HG22	1:C:98:ILE:HG12	1.96	0.47
1:D:49:ILE:HD12	1:D:49:ILE:C	2.34	0.47
1:C:75:HIS:NE2	1:C:79:ARG:HD2	2.30	0.47
1:B:32:ASP:HB2	1:B:97:ARG:HB3	1.97	0.47
1:D:81:ALA:O	1:D:85:ASN:ND2	2.48	0.47
1:C:73:LEU:HD21	1:C:100:LYS:HE3	1.96	0.47
1:A:12:PHE:CE1	1:A:62:LYS:HB2	2.48	0.47
1:C:30:LYS:HE2	1:C:32:ASP:OD2	2.15	0.47
1:B:49:ILE:O	1:B:90:ARG:NH2	2.48	0.47
1:A:64:ILE:CG2	1:A:79:ARG:HB3	2.43	0.47
1:D:31:VAL:HG22	1:D:98:ILE:HG12	1.97	0.47
1:B:33:VAL:CG1	1:B:35:LEU:HD21	2.45	0.47
1:C:3:ASP:OD1	1:C:3:ASP:N	2.46	0.47
1:B:93:GLU:HA	1:B:119:GLU:HA	1.96	0.47
1:A:72:LEU:O	1:A:75:HIS:HB3	2.16	0.46
1:B:74:GLU:OE1	2:B:222:NEU:N13	2.45	0.46
1:A:81:ALA:HB1	1:A:118:ARG:HG3	1.97	0.46
1:D:41:GLU:HA	1:D:44:ARG:HB3	1.97	0.46
1:B:104:PRO:HG2	2:B:222:NEU:O24	2.16	0.46
1:A:112:VAL:HG11	1:B:7:LEU:CD2	2.30	0.46
1:A:114:ILE:HG22	1:B:5:ILE:HA	1.98	0.46
1:C:49:ILE:CD1	1:C:90:ARG:HH22	2.28	0.46
1:A:91:VAL:O	1:A:120:ASN:HB2	2.16	0.46
1:A:70:VAL:HG11	1:A:75:HIS:CD2	2.50	0.46
1:D:78:GLU:OE1	1:D:78:GLU:CA	2.60	0.46
1:C:42:ALA:HB2	1:C:50:ASP:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:96:VAL:CG1	1:C:116:ILE:HG12	2.46	0.46
1:B:100:LYS:HD2	1:B:103:PRO:CB	2.40	0.46
1:B:1:MET:HE1	1:B:3:ASP:HB2	1.96	0.46
1:C:105:ILE:HD13	1:D:54:TYR:CD1	2.51	0.46
1:C:12:PHE:CE2	1:C:62:LYS:HA	2.51	0.46
1:C:54:TYR:O	1:C:57:VAL:HB	2.15	0.46
1:D:64:ILE:HG23	1:D:79:ARG:NH1	2.31	0.46
1:B:83:ARG:HG2	1:B:83:ARG:NH1	2.31	0.46
1:C:20:SER:HA	1:C:23:ASN:HB2	1.97	0.46
1:C:8:LYS:HB3	3:C:1100:HOH:O	2.16	0.46
1:A:74:GLU:HG3	1:A:114:ILE:HG12	1.97	0.45
1:C:108:HIS:O	1:D:10:MET:HA	2.16	0.45
1:C:7:LEU:HD21	1:C:57:VAL:HG11	1.99	0.45
1:B:35:LEU:HD11	1:B:57:VAL:HG11	1.98	0.45
1:A:70:VAL:HG11	1:A:75:HIS:NE2	2.31	0.45
1:A:36:LYS:NZ	1:A:36:LYS:CB	2.76	0.45
1:D:64:ILE:HG13	1:D:80:ILE:HG12	1.98	0.45
1:A:73:LEU:HD11	1:A:100:LYS:CD	2.46	0.45
1:D:78:GLU:OE2	1:D:118:ARG:NE	2.49	0.45
1:D:77:ALA:HA	1:D:96:VAL:HG11	1.99	0.45
1:D:99:THR:HG22	1:D:100:LYS:N	2.32	0.45
1:B:22:GLU:C	1:B:24:GLU:N	2.70	0.45
1:A:78:GLU:HG2	1:B:43:GLY:O	2.16	0.45
1:A:100:LYS:HD3	1:B:54:TYR:OH	2.16	0.45
1:B:35:LEU:HB3	1:B:91:VAL:HG13	1.97	0.45
1:A:21:ALA:HA	1:A:24:GLU:HB3	1.98	0.45
1:B:7:LEU:HB3	1:B:10:MET:SD	2.57	0.45
1:A:116:ILE:CG2	1:B:39:LEU:HD12	2.47	0.45
1:C:62:LYS:O	1:C:66:GLU:HG2	2.17	0.45
1:B:70:VAL:HB	1:B:75:HIS:HD2	1.80	0.44
1:D:103:PRO:CG	1:D:105:ILE:HD13	2.46	0.44
1:C:81:ALA:HA	1:C:94:THR:HG21	1.98	0.44
1:D:23:ASN:ND2	1:D:23:ASN:N	2.65	0.44
1:A:121:LYS:HD2	1:A:121:LYS:N	2.32	0.44
1:C:89:ASN:O	1:C:89:ASN:ND2	2.51	0.44
1:B:16:HIS:HB3	1:B:70:VAL:HG22	1.99	0.44
1:A:51:THR:OG1	1:A:52:VAL:N	2.49	0.44
1:A:6:PHE:C	1:A:7:LEU:HD12	2.38	0.44
1:D:87:GLN:HB3	1:D:88:TYR:CD1	2.52	0.44
1:A:60:GLU:O	1:A:64:ILE:HG12	2.18	0.44
1:C:51:THR:O	1:C:90:ARG:HD3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:19:LEU:C	1:D:19:LEU:HD12	2.38	0.44
1:D:17:GLY:HA2	3:D:1047:HOH:O	2.18	0.44
1:B:35:LEU:HD22	1:B:84:ILE:HG21	2.00	0.44
1:C:105:ILE:HD13	1:D:54:TYR:CE1	2.53	0.44
1:A:19:LEU:HD21	1:A:21:ALA:HB3	1.99	0.43
1:B:48:VAL:O	1:B:50:ASP:N	2.51	0.43
1:A:59:GLU:OE2	1:A:62:LYS:HD2	2.18	0.43
1:D:93:GLU:HA	1:D:119:GLU:HA	2.01	0.43
1:D:95:LYS:HG3	1:D:117:VAL:HG22	2.00	0.43
1:D:1:MET:SD	1:D:3:ASP:HB2	2.58	0.43
1:B:79:ARG:N	3:B:1101:HOH:O	2.50	0.43
1:D:18:ALA:CB	2:D:422:NEU:H16	2.48	0.43
1:C:10:MET:HB3	1:C:12:PHE:HE1	1.81	0.43
1:D:120:ASN:HB2	3:D:1114:HOH:O	2.19	0.43
1:A:109:TYR:N	1:A:109:TYR:CD1	2.86	0.43
1:A:25:ILE:CD1	1:C:21:ALA:HB3	2.47	0.43
1:C:37:VAL:CG2	1:C:91:VAL:HG22	2.47	0.43
1:C:60:GLU:HB3	1:C:83:ARG:CG	2.49	0.43
1:B:48:VAL:C	1:B:50:ASP:N	2.71	0.43
1:C:45:THR:O	1:C:46:ASP:HB3	2.19	0.43
1:C:47:ASN:HB2	1:C:50:ASP:OD2	2.18	0.43
1:A:19:LEU:HD11	1:C:24:GLU:OE2	2.17	0.43
1:B:2:GLN:HE21	1:B:2:GLN:HB2	1.56	0.43
1:D:7:LEU:HB2	1:D:33:VAL:HB	2.01	0.43
1:B:75:HIS:HE1	3:B:1243:HOH:O	2.02	0.43
1:D:12:PHE:CE2	1:D:61:VAL:HG12	2.53	0.43
1:C:62:LYS:O	1:C:66:GLU:CG	2.67	0.43
1:C:7:LEU:HD11	1:C:54:TYR:HB2	2.00	0.43
1:A:95:LYS:HG2	1:A:117:VAL:HG22	2.01	0.43
1:A:19:LEU:HD23	1:C:25:ILE:HD11	2.01	0.43
1:A:64:ILE:HG23	1:A:79:ARG:HG2	2.01	0.43
1:C:85:ASN:O	1:C:120:ASN:ND2	2.42	0.43
1:D:73:LEU:N	2:D:422:NEU:O11	2.49	0.43
1:A:37:VAL:CG2	1:A:91:VAL:HA	2.41	0.43
1:D:62:LYS:O	1:D:66:GLU:HG2	2.18	0.43
1:C:49:ILE:HG13	1:C:49:ILE:O	2.19	0.43
1:D:100:LYS:N	1:D:112:VAL:O	2.48	0.43
1:C:60:GLU:OE1	1:C:60:GLU:HA	2.19	0.43
1:A:97:ARG:NH2	1:B:8:LYS:HD3	2.34	0.43
1:A:22:GLU:O	1:A:26:GLY:N	2.34	0.42
1:B:94:THR:HG22	1:B:94:THR:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:1003:HOH:O	1:D:4:THR:N	2.44	0.42
1:A:83:ARG:NH2	3:A:1160:HOH:O	2.52	0.42
1:C:88:TYR:C	1:C:90:ARG:H	2.22	0.42
1:B:101:GLU:HG2	1:B:111:GLY:HA3	2.00	0.42
1:B:10:MET:HE2	1:B:61:VAL:HG11	2.02	0.42
1:A:49:ILE:HG23	1:A:50:ASP:OD1	2.19	0.42
1:A:62:LYS:NZ	3:A:1584:HOH:O	2.51	0.42
1:B:16:HIS:CE1	1:B:69:ALA:HA	2.54	0.42
1:A:36:LYS:NZ	1:A:93:GLU:HB2	2.32	0.42
1:D:78:GLU:O	1:D:82:ASN:HB2	2.19	0.42
1:C:121:LYS:HG2	3:C:1469:HOH:O	2.18	0.42
1:D:74:GLU:CD	1:D:114:ILE:HD13	2.39	0.42
1:A:25:ILE:HD13	1:C:104:PRO:HB3	2.01	0.42
1:A:104:PRO:CB	1:C:25:ILE:HG23	2.27	0.42
1:D:19:LEU:HB3	1:D:22:GLU:HG3	2.01	0.42
1:C:96:VAL:O	1:C:96:VAL:HG13	2.19	0.42
1:C:45:THR:O	1:C:46:ASP:CB	2.68	0.42
1:C:7:LEU:O	1:C:10:MET:HG3	2.19	0.42
1:C:64:ILE:HD11	1:C:83:ARG:CZ	2.49	0.42
1:C:74:GLU:HB3	1:D:43:GLY:CA	2.50	0.42
1:C:79:ARG:HG2	1:C:79:ARG:HH11	1.85	0.42
1:B:27:GLN:CG	1:B:102:ASN:HD22	2.33	0.42
1:B:1:MET:CE	1:B:3:ASP:H	2.33	0.42
1:B:22:GLU:O	1:B:24:GLU:N	2.53	0.42
1:A:74:GLU:OE2	1:B:51:THR:HG21	2.19	0.41
1:A:34:THR:HB	1:A:95:LYS:HB2	2.02	0.41
1:A:30:LYS:HB3	1:A:30:LYS:HE2	1.73	0.41
1:B:59:GLU:HB3	3:B:1158:HOH:O	2.19	0.41
1:A:61:VAL:HG22	1:A:80:ILE:HG23	2.00	0.41
1:B:68:LYS:NZ	3:B:1057:HOH:O	2.52	0.41
1:A:16:HIS:HB2	1:A:29:PHE:CZ	2.55	0.41
1:A:73:LEU:HD11	1:A:100:LYS:HD2	2.01	0.41
1:C:82:ASN:HD22	1:C:82:ASN:HA	1.59	0.41
1:D:16:HIS:CE1	1:D:69:ALA:HA	2.55	0.41
1:C:65:MET:SD	1:C:76:LEU:HD13	2.60	0.41
1:C:30:LYS:C	1:C:30:LYS:HD3	2.41	0.41
1:B:4:THR:HB	1:B:34:THR:HG23	2.03	0.41
1:B:95:LYS:HB2	1:B:117:VAL:HG22	2.03	0.41
1:A:45:THR:OG1	1:A:46:ASP:N	2.53	0.41
1:C:73:LEU:HD13	1:C:98:ILE:HG22	2.03	0.41
1:C:5:ILE:O	1:C:35:LEU:N	2.47	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:60:GLU:HB2	1:C:84:ILE:HD11	2.01	0.41
1:B:30:LYS:O	1:B:98:ILE:HA	2.20	0.41
1:B:31:VAL:HA	1:B:97:ARG:O	2.20	0.41
1:B:105:ILE:HB	1:B:109:TYR:OH	2.20	0.41
1:D:49:ILE:O	1:D:49:ILE:HD12	2.21	0.41
1:A:97:ARG:NH1	3:A:1041:HOH:O	2.53	0.41
1:A:48:VAL:C	1:A:50:ASP:H	2.22	0.41
1:B:3:ASP:OD2	1:B:39:LEU:HB2	2.20	0.41
1:C:44:ARG:NH1	1:C:44:ARG:CB	2.77	0.41
1:C:79:ARG:O	1:C:83:ARG:CB	2.69	0.41
1:B:58:PHE:HD2	1:B:59:GLU:OE2	2.04	0.41
1:D:51:THR:OG1	1:D:52:VAL:N	2.54	0.41
1:C:35:LEU:HD22	1:C:91:VAL:HG11	2.02	0.41
1:C:11:ARG:NH1	1:C:11:ARG:HG2	2.35	0.41
1:B:33:VAL:N	3:B:1120:HOH:O	2.54	0.40
1:A:11:ARG:NH1	1:A:11:ARG:CG	2.84	0.40
1:B:1:MET:HE1	1:B:3:ASP:H	1.86	0.40
1:D:64:ILE:CG2	1:D:79:ARG:NH1	2.85	0.40
1:A:28:ILE:HG12	3:C:1049:HOH:O	2.20	0.40
1:A:3:ASP:O	1:A:36:LYS:HG2	2.20	0.40
1:C:96:VAL:CG1	1:C:116:ILE:CG1	2.99	0.40
1:C:60:GLU:HB3	1:C:83:ARG:HG2	2.03	0.40
1:A:36:LYS:CB	1:A:93:GLU:HB3	2.50	0.40
1:D:12:PHE:O	1:D:29:PHE:N	2.48	0.40
1:C:54:TYR:CD1	1:C:55:GLY:N	2.88	0.40
1:C:7:LEU:HD22	1:C:7:LEU:N	2.36	0.40
1:B:59:GLU:O	1:B:62:LYS:HB3	2.21	0.40
1:B:27:GLN:HB2	1:B:102:ASN:ND2	2.36	0.40
1:B:85:ASN:O	1:B:120:ASN:ND2	2.50	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	119/121 (98%)	95 (80%)	20 (17%)	4 (3%)	5	0
1	B	119/121 (98%)	106 (89%)	9 (8%)	4 (3%)	5	0
1	C	119/121 (98%)	105 (88%)	13 (11%)	1 (1%)	24	7
1	D	119/121 (98%)	99 (83%)	18 (15%)	2 (2%)	11	1
All	All	476/484 (98%)	405 (85%)	60 (13%)	11 (2%)	8	1

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	46	ASP
1	B	46	ASP
1	C	81	ALA
1	D	3	ASP
1	D	46	ASP
1	A	53	HIS
1	B	23	ASN
1	B	106	PRO
1	B	49	ILE
1	A	70	VAL
1	A	87	GLN

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	105/105 (100%)	90 (86%)	15 (14%)	4	0
1	B	105/105 (100%)	93 (89%)	12 (11%)	7	1
1	C	105/105 (100%)	92 (88%)	13 (12%)	6	1
1	D	105/105 (100%)	95 (90%)	10 (10%)	11	2
All	All	420/420 (100%)	370 (88%)	50 (12%)	6	1

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	ARG
1	A	23	ASN
1	A	36	LYS
1	A	38	ASP
1	A	41	GLU
1	A	47	ASN
1	A	54	TYR
1	A	56	GLU
1	A	63	SER
1	A	68	LYS
1	A	70	VAL
1	A	90	ARG
1	A	101	GLU
1	A	102	ASN
1	A	112	VAL
1	B	8	LYS
1	B	23	ASN
1	B	50	ASP
1	B	52	VAL
1	B	54	TYR
1	B	82	ASN
1	B	86	SER
1	B	89	ASN
1	B	90	ARG
1	B	93	GLU
1	B	102	ASN
1	B	115	GLU
1	C	1	MET
1	C	3	ASP
1	C	7	LEU
1	C	22	GLU
1	C	30	LYS
1	C	41	GLU
1	C	54	TYR
1	C	74	GLU
1	C	76	LEU
1	C	78	GLU
1	C	82	ASN
1	C	83	ARG
1	C	105	ILE
1	D	1	MET
1	D	4	THR
1	D	11	ARG

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Mol	Chain	Res	Type
1	D	19	LEU
1	D	32	ASP
1	D	40	SER
1	D	66	GLU
1	D	82	ASN
1	D	87	GLN
1	D	119	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	27	GLN
1	A	47	ASN
1	A	53	HIS
1	A	71	ASN
1	A	82	ASN
1	B	2	GLN
1	B	47	ASN
1	B	75	HIS
1	B	85	ASN
1	C	23	ASN
1	C	47	ASN
1	C	53	HIS
1	C	82	ASN
1	C	89	ASN
1	C	102	ASN
1	D	23	ASN
1	D	47	ASN
1	D	82	ASN

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)

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
2	NEU	A	122	-	18,19,19	5.85	9 (50%)	15,27,27	4.41	10 (66%)
2	NEU	B	222	-	18,19,19	5.50	9 (50%)	15,27,27	3.95	10 (66%)
2	NEU	C	322	-	18,19,19	6.05	11 (61%)	15,27,27	4.21	8 (53%)
2	NEU	D	422	-	18,19,19	5.71	10 (55%)	15,27,27	4.28	10 (66%)

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	NEU	A	122	-	-	0/10/10/10	0/2/2/2
2	NEU	B	222	-	-	0/10/10/10	0/2/2/2
2	NEU	C	322	-	-	0/10/10/10	0/2/2/2
2	NEU	D	422	-	-	0/10/10/10	0/2/2/2

All (39) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	322	NEU	C26-C16	-8.78	1.45	1.53
2	B	222	NEU	C26-C16	-7.68	1.46	1.53
2	A	122	NEU	C26-C16	-7.50	1.46	1.53
2	D	422	NEU	C26-C16	-6.98	1.47	1.53
2	B	222	NEU	C3-N13	-2.67	1.28	1.34
2	C	322	NEU	C3-N13	-2.28	1.29	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	422	NEU	C3-N13	-2.12	1.29	1.34
2	A	122	NEU	C8-C16	2.39	1.54	1.52
2	D	422	NEU	O11-C1	2.45	1.30	1.24
2	C	322	NEU	C5-N6	2.52	1.41	1.37
2	A	122	NEU	O11-C1	2.64	1.31	1.24
2	C	322	NEU	O11-C1	2.66	1.31	1.24
2	B	222	NEU	O11-C1	2.68	1.31	1.24
2	C	322	NEU	O21-C16	3.07	1.48	1.42
2	A	122	NEU	O21-C16	3.15	1.49	1.42
2	D	422	NEU	O21-C16	3.24	1.49	1.42
2	B	222	NEU	O21-C16	3.26	1.49	1.42
2	D	422	NEU	C1-N2	3.74	1.40	1.33
2	A	122	NEU	C1-N2	4.26	1.41	1.33
2	B	222	NEU	C1-N2	4.28	1.41	1.33
2	C	322	NEU	C1-N2	4.45	1.41	1.33
2	C	322	NEU	C8-C16	4.47	1.56	1.52
2	D	422	NEU	C8-C16	4.83	1.56	1.52
2	B	222	NEU	C10-N9	5.13	1.41	1.33
2	D	422	NEU	C10-N9	5.87	1.42	1.33
2	B	222	NEU	C7-N6	6.01	1.42	1.31
2	C	322	NEU	C10-N9	6.35	1.43	1.33
2	D	422	NEU	C7-N6	6.35	1.42	1.31
2	C	322	NEU	C7-N6	6.41	1.42	1.31
2	A	122	NEU	C7-N6	6.49	1.42	1.31
2	A	122	NEU	C10-N9	6.62	1.43	1.33
2	D	422	NEU	C3-N2	7.62	1.48	1.35
2	A	122	NEU	C3-N2	8.00	1.49	1.35
2	C	322	NEU	C3-N2	8.26	1.50	1.35
2	B	222	NEU	C3-N2	8.33	1.50	1.35
2	B	222	NEU	C8-N9	17.32	1.50	1.32
2	D	422	NEU	C8-N9	18.37	1.51	1.32
2	A	122	NEU	C8-N9	18.85	1.52	1.32
2	C	322	NEU	C8-N9	18.90	1.52	1.32

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	122	NEU	C1-C10-C5	-11.40	112.64	119.94
2	D	422	NEU	C1-C10-C5	-10.80	113.03	119.94
2	C	322	NEU	C1-C10-C5	-10.68	113.10	119.94
2	B	222	NEU	C1-C10-C5	-10.02	113.53	119.94
2	A	122	NEU	O22-C26-C28	-5.06	97.41	109.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	222	NEU	O22-C26-C28	-4.85	97.90	109.22
2	D	422	NEU	C7-C8-N9	-4.83	117.75	121.42
2	C	322	NEU	O22-C26-C28	-4.78	98.07	109.22
2	D	422	NEU	O22-C26-C28	-4.70	98.26	109.22
2	C	322	NEU	C7-C8-N9	-4.46	118.03	121.42
2	A	122	NEU	N4-C3-N2	-4.40	120.75	127.44
2	C	322	NEU	N4-C3-N2	-4.25	120.97	127.44
2	D	422	NEU	N4-C3-N2	-4.24	120.98	127.44
2	B	222	NEU	N4-C3-N2	-4.17	121.09	127.44
2	A	122	NEU	C7-C8-N9	-3.65	118.65	121.42
2	B	222	NEU	C7-C8-N9	-3.15	119.03	121.42
2	C	322	NEU	C10-C5-N6	-2.89	116.55	121.81
2	A	122	NEU	C10-C5-N6	-2.86	116.60	121.81
2	D	422	NEU	C10-C5-N6	-2.82	116.68	121.81
2	B	222	NEU	C10-C5-N6	-2.79	116.73	121.81
2	D	422	NEU	C1-N2-C3	2.02	118.74	115.94
2	B	222	NEU	N13-C3-N4	2.02	121.68	117.80
2	B	222	NEU	C1-N2-C3	2.14	118.91	115.94
2	A	122	NEU	N13-C3-N4	2.24	122.10	117.80
2	D	422	NEU	N13-C3-N4	2.25	122.12	117.80
2	A	122	NEU	C1-N2-C3	2.42	119.30	115.94
2	B	222	NEU	C1-C10-N9	3.70	123.20	118.72
2	B	222	NEU	C7-N6-C5	3.70	121.29	116.93
2	C	322	NEU	C7-N6-C5	4.21	121.89	116.93
2	C	322	NEU	C1-C10-N9	4.38	124.03	118.72
2	D	422	NEU	C7-N6-C5	4.39	122.10	116.93
2	D	422	NEU	C1-C10-N9	4.49	124.17	118.72
2	A	122	NEU	C7-N6-C5	4.60	122.35	116.93
2	A	122	NEU	C1-C10-N9	5.07	124.87	118.72
2	A	122	NEU	C28-C26-C16	5.42	120.96	111.94
2	C	322	NEU	C28-C26-C16	5.52	121.13	111.94
2	D	422	NEU	C28-C26-C16	5.59	121.24	111.94
2	B	222	NEU	C28-C26-C16	5.61	121.28	111.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	122	NEU	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	222	NEU	4	0
2	C	322	NEU	1	0
2	D	422	NEU	4	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å^2)	Q<0.9
1	A	121/121 (100%)	-0.09	0	100 · 100	15, 27, 38, 43	0
1	B	121/121 (100%)	-0.04	0	100 · 100	15, 27, 36, 44	0
1	C	121/121 (100%)	-0.02	0	100 · 100	12, 29, 37, 44	0
1	D	121/121 (100%)	-0.07	0	100 · 100	13, 28, 36, 43	0
All	All	484/484 (100%)	-0.05	0	100 · 100	12, 28, 37, 44	0

There are no RSRZ outliers to report.

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	NEU	B	222	18/18	0.90	0.12	1.51	23,26,41,42	0
2	NEU	C	322	18/18	0.92	0.09	-0.50	23,26,32,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
2	NEU	D	422	18/18	0.94	0.08	-0.74	24,26,40,44	0
2	NEU	A	122	18/18	0.94	0.08	-1.09	16,25,26,27	0

6.5 Other polymers (i)

There are no such residues in this entry.