



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:04 PM GMT

PDB ID : 1ND0
Title : CATIONIC CYCLIZATION ANTIBODY 4C6 COMPLEX WITH TRANSITION STATE ANALOG
Authors : Zhu, X.; Wilson, I.A.
Deposited on : 2002-12-05
Resolution : 2.45 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

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

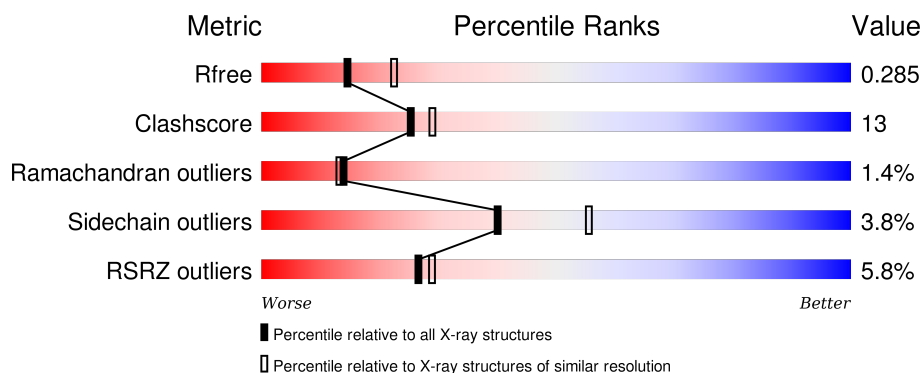
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	4776 (2.50-2.42)
Clashscore	102246	1030 (2.48-2.44)
Ramachandran outliers	100387	1024 (2.48-2.44)
Sidechain outliers	100360	1024 (2.48-2.44)
RSRZ outliers	91569	4787 (2.50-2.42)

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

Mol	Chain	Length	Quality of chain
1	A	219	<div> <div>4%</div> <div>78%</div> <div>21%</div> <div>.</div> </div>
1	C	219	<div> <div>3%</div> <div>77%</div> <div>23%</div> </div>
1	E	219	<div> <div>%</div> <div>75%</div> <div>24%</div> <div>.</div> </div>
1	G	219	<div> <div>4%</div> <div>76%</div> <div>23%</div> </div>
2	B	222	<div> <div>7%</div> <div>66%</div> <div>30%</div> <div>.</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	D	222	
2	F	222	
2	H	222	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SO4	B	503	-	X	-	-
3	SO4	D	504	-	X	-	-
3	SO4	F	501	-	X	-	X
3	SO4	H	502	-	X	-	X
4	DP4	A	401	-	-	-	X
4	DP4	C	402	-	-	-	X
4	DP4	E	403	-	-	-	X
4	DP4	G	404	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 14002 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 IMMUNOGLOBULIN IGG2A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	219	Total	C	N	O	S	0	0	0
			1702	1064	291	340	7			
1	C	219	Total	C	N	O	S	0	0	0
			1702	1064	291	340	7			
1	E	219	Total	C	N	O	S	0	0	0
			1702	1064	291	340	7			
1	G	219	Total	C	N	O	S	0	0	0
			1702	1064	291	340	7			

- Molecule 2 is a protein called IMMUNOGLOBULIN IGG2A.

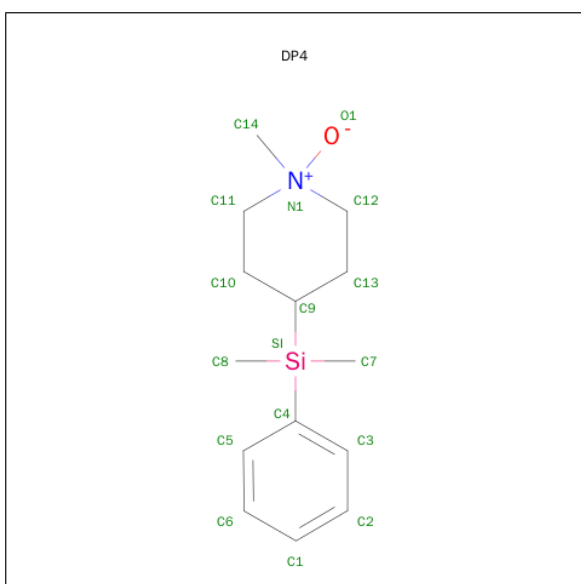
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	222	Total	C	N	O	S	0	0	0
			1678	1063	277	332	6			
2	D	222	Total	C	N	O	S	0	0	0
			1678	1063	277	332	6			
2	F	222	Total	C	N	O	S	0	0	0
			1678	1063	277	332	6			
2	H	222	Total	C	N	O	S	0	0	0
			1678	1063	277	332	6			

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	F	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is (1S,4S)-4-[DIMETHYL(PHENYL)SILYL]-1-METHYLPYPERIDINE 1-OXIDE (three-letter code: DP4) (formula: C₁₄H₂₃NOSi).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	Si	0	0
			17	14	1	1	1		
4	C	1	Total	C	N	O	Si	0	0
			17	14	1	1	1		
4	E	1	Total	C	N	O	Si	0	0
			17	14	1	1	1		
4	G	1	Total	C	N	O	Si	0	0
			17	14	1	1	1		

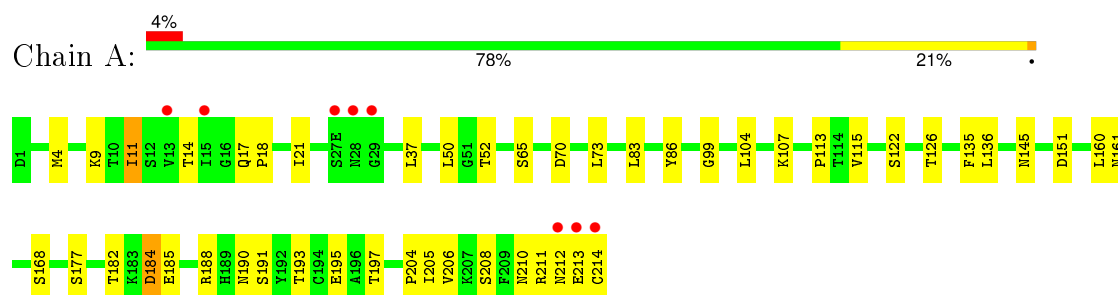
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	53	Total	O	0	0
			53	53		
5	B	48	Total	O	0	0
			48	48		
5	C	41	Total	O	0	0
			41	41		
5	D	49	Total	O	0	0
			49	49		
5	E	56	Total	O	0	0
			56	56		
5	F	52	Total	O	0	0
			52	52		
5	G	59	Total	O	0	0
			59	59		
5	H	36	Total	O	0	0
			36	36		

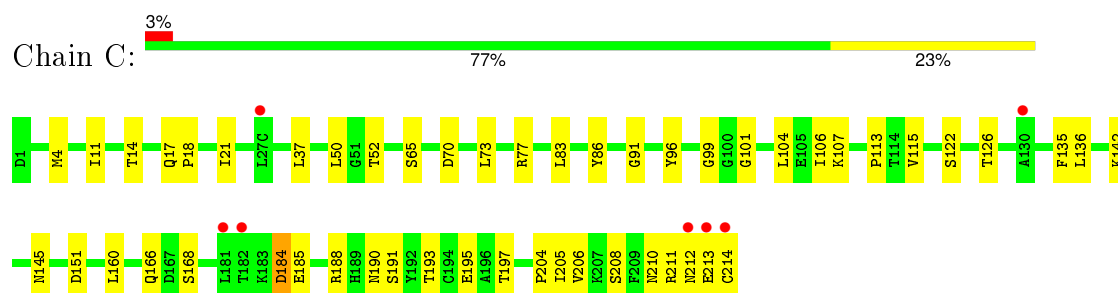
3 Residue-property plots [i](#)

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.

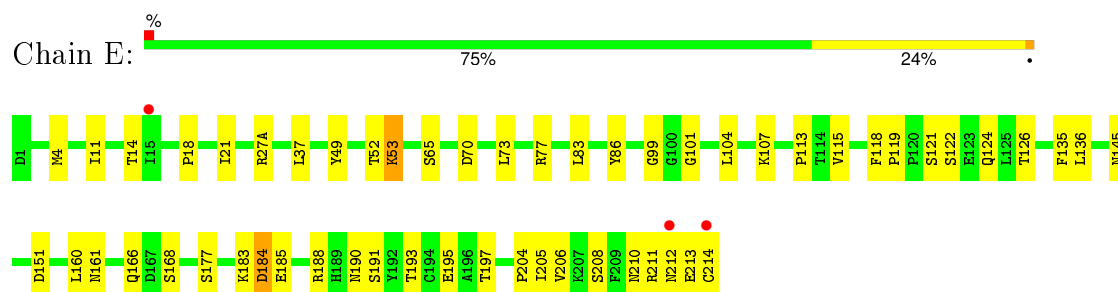
• Molecule 1: IMMUNOGLOBULIN IGG2A



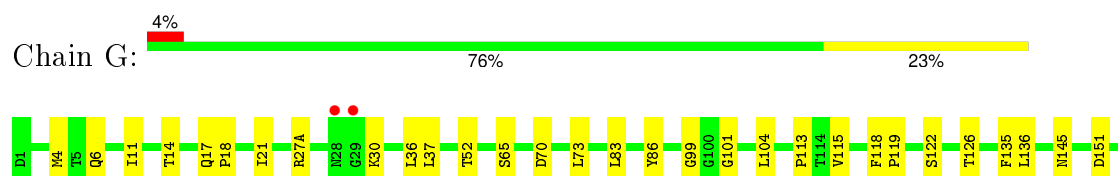
• Molecule 1: IMMUNOGLOBULIN IGG2A



• Molecule 1: IMMUNOGLOBULIN IGG2A

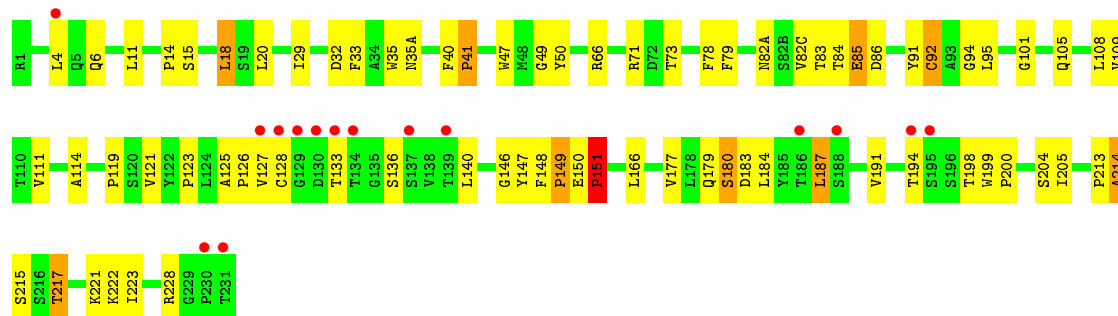


• Molecule 1: IMMUNOGLOBULIN IGG2A

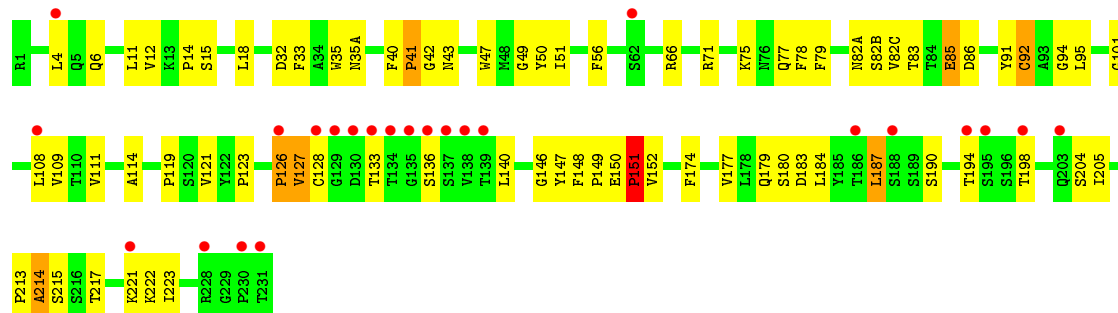




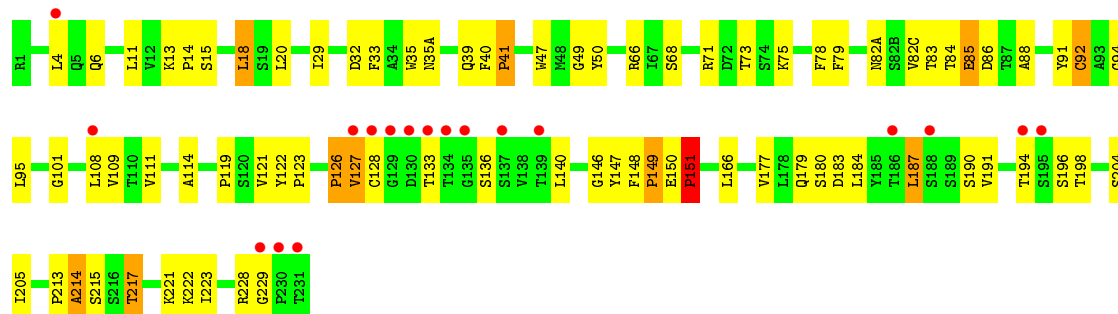
• Molecule 2: IMMUNOGLOBULIN IGG2A



• Molecule 2: IMMUNOGLOBULIN IGG2A

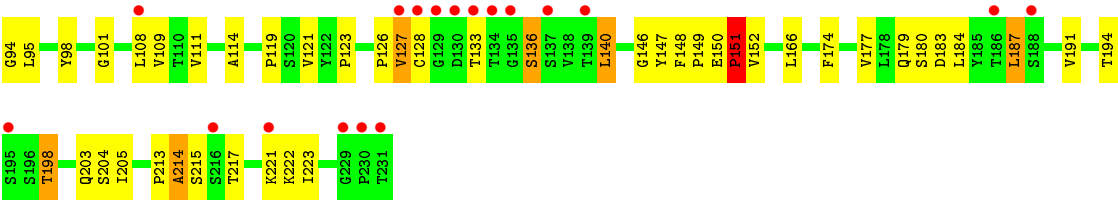


• Molecule 2: IMMUNOGLOBULIN IGG2A



• Molecule 2: IMMUNOGLOBULIN IGG2A





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	36.57Å 95.16Å 141.06Å 75.51° 88.64° 89.28°	Depositor
Resolution (Å)	50.00 – 2.45 36.56 – 2.45	Depositor EDS
% Data completeness (in resolution range)	72.9 (50.00-2.45) 67.2 (36.56-2.45)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.04 (at 2.45Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.242 , 0.286 0.243 , 0.285	Depositor DCC
R_{free} test set	2539 reflections (5.15%)	DCC
Wilson B-factor (Å ²)	29.4	Xtriage
Anisotropy	0.413	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 46.9	EDS
Estimated twinning fraction	0.044 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 54427 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	14002	wwPDB-VP
Average B, all atoms (Å ²)	34.0	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 55.65 % 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 3.0687e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: DP4, SO4

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	0.36	0/1740	0.62	0/2358
1	C	0.37	0/1740	0.62	0/2358
1	E	0.37	0/1740	0.63	0/2358
1	G	0.38	0/1740	0.63	0/2358
2	B	0.39	0/1724	0.70	2/2361 (0.1%)
2	D	0.41	0/1724	0.70	2/2361 (0.1%)
2	F	0.42	0/1724	0.71	2/2361 (0.1%)
2	H	0.42	0/1724	0.71	1/2361 (0.0%)
All	All	0.39	0/13856	0.67	7/18876 (0.0%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	92	CYS	CA-CB-SG	5.47	123.85	114.00
2	B	92	CYS	CA-CB-SG	5.46	123.83	114.00
2	D	32	ASP	N-CA-C	5.15	124.92	111.00
2	F	32	ASP	N-CA-C	5.13	124.86	111.00
2	H	92	CYS	CA-CB-SG	5.07	123.13	114.00
2	B	32	ASP	N-CA-C	5.06	124.65	111.00
2	D	92	CYS	CA-CB-SG	5.04	123.08	114.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1702	0	1657	32	0
1	C	1702	0	1657	36	0
1	E	1702	0	1657	40	0
1	G	1702	0	1657	33	0
2	B	1678	0	1633	49	0
2	D	1678	0	1633	51	0
2	F	1678	0	1633	63	0
2	H	1678	0	1633	54	0
3	B	5	0	0	0	0
3	D	5	0	0	0	0
3	F	5	0	0	0	0
3	H	5	0	0	0	0
4	A	17	0	16	0	0
4	C	17	0	16	0	0
4	E	17	0	16	0	0
4	G	17	0	16	0	0
5	A	53	0	0	3	0
5	B	48	0	0	3	0
5	C	41	0	0	2	0
5	D	49	0	0	3	0
5	E	56	0	0	4	0
5	F	52	0	0	7	0
5	G	59	0	0	4	0
5	H	36	0	0	2	0
All	All	14002	0	13224	339	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 13.

All (339) 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:G:160:LEU:HD11	2:H:179:GLN:HG3	1.46	0.98
2:D:204:SER:HB2	2:D:222:LYS:HE3	1.51	0.91
2:F:83:THR:OG1	2:F:85:GLU:HG2	1.72	0.89
2:D:83:THR:OG1	2:D:85:GLU:HG2	1.75	0.85
2:H:83:THR:OG1	2:H:85:GLU:HG2	1.77	0.85
2:B:83:THR:OG1	2:B:85:GLU:HG2	1.78	0.84
1:G:160:LEU:CD1	2:H:179:GLN:HG3	2.09	0.81

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:14:THR:HA	1:A:107:LYS:HB3	1.66	0.76
1:G:195:GLU:HG2	1:G:206:VAL:HG22	1.68	0.75
1:G:193:THR:HG23	1:G:208:SER:HB3	1.68	0.75
1:A:195:GLU:HG2	1:A:206:VAL:HG22	1.70	0.73
1:C:193:THR:HG23	1:C:208:SER:HB3	1.70	0.73
5:G:405:HOH:O	2:H:127:VAL:HG12	1.87	0.73
2:D:204:SER:CB	2:D:222:LYS:HE3	2.17	0.72
1:A:193:THR:HG23	1:A:208:SER:HB3	1.70	0.72
2:B:146:GLY:HA2	2:B:184:LEU:HB3	1.70	0.72
1:E:193:THR:HG23	1:E:208:SER:HB3	1.72	0.72
1:E:195:GLU:HG2	1:E:206:VAL:HG22	1.72	0.72
2:D:146:GLY:HA2	2:D:184:LEU:HB3	1.71	0.71
1:E:14:THR:HA	1:E:107:LYS:HB3	1.72	0.71
2:H:146:GLY:HA2	2:H:184:LEU:HB3	1.71	0.71
2:B:180:SER:HB2	5:B:523:HOH:O	1.90	0.71
2:H:6:GLN:HE21	2:H:91:TYR:HA	1.54	0.71
2:F:146:GLY:HA2	2:F:184:LEU:HB3	1.71	0.71
1:C:195:GLU:HG2	1:C:206:VAL:HG22	1.72	0.70
2:F:6:GLN:HE21	2:F:91:TYR:HA	1.55	0.69
1:C:14:THR:HA	1:C:107:LYS:HB3	1.73	0.69
2:D:75:LYS:HD2	5:D:530:HOH:O	1.93	0.69
1:E:83:LEU:HD21	1:E:168:SER:HA	1.73	0.68
2:D:6:GLN:HE21	2:D:91:TYR:HA	1.57	0.68
2:B:6:GLN:HE21	2:B:91:TYR:HA	1.59	0.66
2:H:136:SER:HA	5:H:513:HOH:O	1.96	0.66
2:F:6:GLN:HG3	2:F:92:CYS:SG	2.36	0.65
2:H:119:PRO:HB3	2:H:147:TYR:HB3	1.79	0.64
1:A:83:LEU:HD21	1:A:168:SER:HA	1.78	0.64
2:D:140:LEU:HG	2:D:223:ILE:HG21	1.78	0.64
2:B:179:GLN:HB3	5:B:523:HOH:O	1.98	0.64
2:F:119:PRO:HB3	2:F:147:TYR:HB3	1.79	0.63
2:D:119:PRO:HB3	2:D:147:TYR:HB3	1.79	0.62
1:E:21:ILE:HD11	1:E:73:LEU:HD23	1.82	0.62
2:B:140:LEU:HG	2:B:223:ILE:HG21	1.81	0.61
2:H:6:GLN:HG3	2:H:92:CYS:SG	2.40	0.61
1:G:52:THR:HG22	1:G:65:SER:HA	1.82	0.61
2:F:4:LEU:N	2:F:4:LEU:HD12	2.16	0.61
2:H:140:LEU:HG	2:H:223:ILE:HG21	1.81	0.61
2:B:4:LEU:N	2:B:4:LEU:HD12	2.16	0.61
2:F:140:LEU:HG	2:F:223:ILE:HG21	1.83	0.60
1:C:21:ILE:HD11	1:C:73:LEU:HD23	1.82	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:4:LEU:N	2:D:4:LEU:HD12	2.17	0.60
1:A:17:GLN:HG2	5:A:423:HOH:O	2.02	0.60
2:F:13:LYS:NZ	5:F:506:HOH:O	2.34	0.60
2:D:6:GLN:HG3	2:D:92:CYS:SG	2.41	0.60
1:E:160:LEU:HD11	2:F:179:GLN:HG3	1.83	0.60
2:B:119:PRO:HB3	2:B:147:TYR:HB3	1.83	0.59
2:F:11:LEU:HB2	2:F:149:PRO:HG3	1.83	0.59
1:E:52:THR:HG22	1:E:65:SER:HA	1.85	0.59
1:A:52:THR:HG22	1:A:65:SER:HA	1.85	0.59
1:A:21:ILE:HD11	1:A:73:LEU:HD23	1.85	0.59
1:G:6:GLN:HB2	5:G:431:HOH:O	2.02	0.58
2:H:187:LEU:HD23	2:H:187:LEU:C	2.24	0.58
1:E:183:LYS:HD3	5:E:413:HOH:O	2.03	0.58
2:H:12:VAL:O	2:H:111:VAL:HA	2.03	0.58
2:H:140:LEU:CD2	2:H:205:ILE:HD12	2.34	0.58
1:C:151:ASP:HA	1:C:191:SER:HB3	1.86	0.58
1:G:21:ILE:HD11	1:G:73:LEU:HD23	1.85	0.58
1:C:160:LEU:HD11	2:D:179:GLN:HG3	1.86	0.57
1:C:52:THR:HG22	1:C:65:SER:HA	1.84	0.57
2:F:187:LEU:HD23	2:F:187:LEU:C	2.24	0.57
2:B:187:LEU:C	2:B:187:LEU:HD23	2.24	0.57
2:H:149:PRO:HD2	2:H:214:ALA:CB	2.34	0.57
2:F:83:THR:C	2:F:111:VAL:HG11	2.24	0.57
2:B:84:THR:HA	2:B:111:VAL:HB	1.85	0.57
2:H:4:LEU:N	2:H:4:LEU:HD12	2.20	0.57
2:H:123:PRO:HB3	2:H:221:LYS:HG3	1.86	0.57
1:C:214:CYS:OXT	2:D:127:VAL:HA	2.04	0.57
2:F:6:GLN:NE2	2:F:91:TYR:HA	2.18	0.57
2:B:140:LEU:CD2	2:B:205:ILE:HD12	2.35	0.57
2:F:47:TRP:CZ2	2:F:49:GLY:HA2	2.40	0.57
2:D:123:PRO:HD3	2:D:221:LYS:HD2	1.87	0.57
2:D:123:PRO:HB3	2:D:221:LYS:HG3	1.87	0.57
2:F:66:ARG:HD2	2:F:82(A):ASN:O	2.05	0.56
2:H:121:VAL:O	2:H:221:LYS:HE3	2.05	0.56
2:B:123:PRO:HD3	2:B:221:LYS:HD2	1.87	0.56
2:D:149:PRO:HD2	2:D:214:ALA:CB	2.35	0.56
1:G:151:ASP:HA	1:G:191:SER:HB3	1.86	0.56
2:B:123:PRO:HB3	2:B:221:LYS:HG3	1.86	0.56
2:H:198:THR:HG22	2:H:203:GLN:HE21	1.71	0.56
2:D:47:TRP:CZ2	2:D:49:GLY:HA2	2.41	0.56
2:F:123:PRO:HD3	2:F:221:LYS:HD2	1.87	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:121:VAL:O	2:F:221:LYS:HE3	2.05	0.55
2:B:66:ARG:HD2	2:B:82(A):ASN:O	2.06	0.55
2:D:187:LEU:HD23	2:D:187:LEU:C	2.26	0.55
2:H:6:GLN:NE2	2:H:91:TYR:HA	2.21	0.55
2:B:121:VAL:O	2:B:221:LYS:HE3	2.07	0.55
1:A:151:ASP:HA	1:A:191:SER:HB3	1.88	0.55
1:C:83:LEU:HB3	1:C:106:ILE:HG12	1.88	0.55
1:E:37:LEU:HD13	1:E:86:TYR:CZ	2.41	0.55
1:E:151:ASP:HA	1:E:191:SER:HB3	1.88	0.55
2:H:128:CYS:HA	2:H:133:THR:OG1	2.07	0.55
2:F:123:PRO:HB3	2:F:221:LYS:HG3	1.87	0.55
2:F:84:THR:HA	2:F:111:VAL:HB	1.89	0.54
2:H:123:PRO:HD3	2:H:221:LYS:HD2	1.90	0.54
1:E:145:ASN:HB2	1:E:197:THR:OG1	2.07	0.54
2:F:68:SER:HB2	5:F:531:HOH:O	2.07	0.54
2:B:149:PRO:HD2	2:B:214:ALA:CB	2.37	0.54
2:D:6:GLN:NE2	2:D:91:TYR:HA	2.21	0.54
1:C:83:LEU:HD21	1:C:168:SER:HA	1.88	0.54
1:G:83:LEU:HD21	1:G:168:SER:HA	1.90	0.54
1:C:37:LEU:HD13	1:C:86:TYR:CZ	2.43	0.54
2:F:140:LEU:CD2	2:F:205:ILE:HD12	2.38	0.54
2:F:149:PRO:HD2	2:F:214:ALA:CB	2.37	0.53
2:D:66:ARG:HD2	2:D:82(A):ASN:O	2.07	0.53
2:B:83:THR:C	2:B:111:VAL:HG11	2.27	0.53
2:H:94:GLY:C	2:H:95:LEU:HD12	2.29	0.53
2:H:108:LEU:HD12	2:H:109:VAL:H	1.73	0.53
2:H:47:TRP:CZ2	2:H:49:GLY:HA2	2.44	0.53
2:D:121:VAL:O	2:D:221:LYS:HE3	2.08	0.53
1:C:145:ASN:HB2	1:C:197:THR:OG1	2.07	0.53
2:D:128:CYS:HA	2:D:133:THR:OG1	2.09	0.53
1:A:113:PRO:HG2	1:A:205:ILE:HD12	1.90	0.53
2:B:94:GLY:C	2:B:95:LEU:HD12	2.30	0.52
1:A:190:ASN:O	1:A:210:ASN:HA	2.10	0.52
2:H:66:ARG:HD2	2:H:82(A):ASN:O	2.09	0.52
1:C:113:PRO:HG2	1:C:205:ILE:HD12	1.92	0.52
2:B:6:GLN:HG3	2:B:92:CYS:SG	2.49	0.52
2:D:140:LEU:CD2	2:D:205:ILE:HD12	2.39	0.52
1:G:145:ASN:HB2	1:G:197:THR:OG1	2.10	0.52
2:B:6:GLN:NE2	2:B:91:TYR:HA	2.24	0.52
1:G:4:MET:HB2	1:G:99:GLY:HA2	1.92	0.52
2:B:47:TRP:CZ2	2:B:49:GLY:HA2	2.45	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:160:LEU:CD1	2:F:179:GLN:HG3	2.40	0.52
1:A:37:LEU:HD13	1:A:86:TYR:CZ	2.44	0.52
2:F:229:GLY:N	5:F:545:HOH:O	2.43	0.51
1:G:11:ILE:HG23	1:G:104:LEU:HA	1.92	0.51
1:G:190:ASN:O	1:G:210:ASN:HA	2.09	0.51
2:F:128:CYS:HA	2:F:133:THR:OG1	2.10	0.51
2:F:228:ARG:HG3	2:F:228:ARG:HH11	1.74	0.51
2:F:204:SER:HA	5:F:504:HOH:O	2.10	0.51
2:F:33:PHE:HB2	2:F:35:TRP:CZ2	2.46	0.51
1:A:197:THR:HG22	1:A:204:PRO:HB3	1.91	0.51
1:E:4:MET:HB2	1:E:99:GLY:HA2	1.92	0.51
2:D:35:TRP:HB3	2:D:78:PHE:CZ	2.45	0.51
2:F:108:LEU:HD12	2:F:109:VAL:H	1.76	0.51
2:B:128:CYS:HA	2:B:133:THR:OG1	2.10	0.51
1:A:4:MET:HB2	1:A:99:GLY:HA2	1.93	0.51
1:A:145:ASN:HB2	1:A:197:THR:OG1	2.11	0.51
2:B:108:LEU:HD12	2:B:109:VAL:H	1.76	0.51
1:E:113:PRO:HG2	1:E:205:ILE:HD12	1.93	0.51
1:C:135:PHE:CE2	2:D:190:SER:HB3	2.46	0.50
1:E:77:ARG:NE	5:E:423:HOH:O	2.44	0.50
1:E:197:THR:HG22	1:E:204:PRO:HB3	1.93	0.50
1:A:211:ARG:O	1:A:212:ASN:HB2	2.11	0.50
1:E:190:ASN:O	1:E:210:ASN:HA	2.12	0.50
2:D:94:GLY:C	2:D:95:LEU:HD12	2.31	0.50
2:D:12:VAL:O	2:D:111:VAL:HA	2.10	0.50
1:C:4:MET:HB2	1:C:99:GLY:HA2	1.94	0.50
1:C:190:ASN:O	1:C:210:ASN:HA	2.11	0.50
2:D:126:PRO:HG2	5:D:537:HOH:O	2.12	0.49
2:F:6:GLN:HE21	2:F:92:CYS:H	1.59	0.49
1:E:211:ARG:O	1:E:212:ASN:HB2	2.11	0.49
1:E:121:SER:OG	2:F:122:TYR:HB3	2.13	0.49
2:B:35(A):ASN:OD1	2:B:50:TYR:HB3	2.12	0.49
1:C:11:ILE:HG23	1:C:104:LEU:HA	1.95	0.49
1:G:36:LEU:HD21	5:G:433:HOH:O	2.12	0.49
2:B:35:TRP:HB3	2:B:78:PHE:CZ	2.48	0.49
1:E:135:PHE:CE2	2:F:190:SER:HB3	2.48	0.49
1:A:136:LEU:HD12	1:A:136:LEU:N	2.27	0.49
1:G:211:ARG:O	1:G:212:ASN:HB2	2.13	0.49
2:B:150:GLU:OE1	2:B:151:PRO:HA	2.13	0.48
1:A:11:ILE:HG23	1:A:104:LEU:HA	1.95	0.48
1:C:197:THR:HG22	1:C:204:PRO:HB3	1.94	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:94:GLY:O	2:B:101:GLY:HA2	2.14	0.48
1:E:119:PRO:HD2	2:F:228:ARG:HH12	1.79	0.48
1:G:37:LEU:HD13	1:G:86:TYR:CZ	2.48	0.48
1:G:197:THR:HG22	1:G:204:PRO:HB3	1.95	0.48
1:E:184:ASP:O	1:E:188:ARG:HG3	2.13	0.48
2:B:11:LEU:HB2	2:B:149:PRO:HG3	1.94	0.48
2:F:108:LEU:HG	5:F:546:HOH:O	2.13	0.48
2:B:105:GLN:OE1	5:B:531:HOH:O	2.20	0.48
2:D:35(A):ASN:OD1	2:D:50:TYR:HB3	2.14	0.48
2:F:94:GLY:C	2:F:95:LEU:HD12	2.35	0.48
1:C:136:LEU:HD12	1:C:136:LEU:N	2.28	0.48
1:E:49:TYR:CZ	1:E:53:LYS:HE2	2.49	0.47
2:H:204:SER:HA	5:H:529:HOH:O	2.12	0.47
1:C:211:ARG:O	1:C:212:ASN:HB2	2.14	0.47
2:D:6:GLN:HE21	2:D:92:CYS:H	1.61	0.47
2:D:11:LEU:HB2	2:D:149:PRO:HG3	1.96	0.47
2:D:71:ARG:HA	2:D:78:PHE:HA	1.96	0.47
2:B:166:LEU:HD21	2:B:191:VAL:HG21	1.97	0.47
1:C:160:LEU:CD1	2:D:179:GLN:HG3	2.44	0.47
2:D:150:GLU:OE1	2:D:151:PRO:HA	2.15	0.47
2:B:6:GLN:HE21	2:B:92:CYS:H	1.62	0.47
2:F:35(A):ASN:OD1	2:F:50:TYR:HB3	2.14	0.47
2:H:108:LEU:HD12	2:H:109:VAL:N	2.29	0.47
2:B:215:SER:OG	2:B:217:THR:OG1	2.32	0.47
1:E:11:ILE:HG23	1:E:104:LEU:HA	1.96	0.47
2:H:71:ARG:HA	2:H:78:PHE:HA	1.97	0.47
2:B:50:TYR:CD1	2:B:50:TYR:C	2.89	0.47
2:D:50:TYR:CD1	2:D:50:TYR:C	2.88	0.47
2:H:35(A):ASN:OD1	2:H:50:TYR:HB3	2.15	0.47
2:B:125:ALA:O	2:B:228:ARG:NH1	2.48	0.47
1:C:115:VAL:HA	1:C:135:PHE:O	2.15	0.46
2:H:82(C):VAL:HA	2:H:86:ASP:OD2	2.14	0.46
2:F:71:ARG:HA	2:F:78:PHE:HA	1.97	0.46
2:H:198:THR:HG22	2:H:203:GLN:NE2	2.30	0.46
1:G:184:ASP:O	1:G:188:ARG:HG3	2.16	0.46
2:D:114:ALA:HB3	2:D:148:PHE:CE2	2.50	0.46
2:B:40:PHE:HB3	2:B:41:PRO:HD2	1.97	0.46
2:D:82(C):VAL:HA	2:D:86:ASP:OD2	2.16	0.46
1:A:214:CYS:SG	1:A:214:CYS:OXT	2.73	0.46
2:F:82(C):VAL:HA	2:F:86:ASP:OD2	2.15	0.46
1:G:113:PRO:HG2	1:G:205:ILE:HD12	1.96	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:185:GLU:HA	1:E:188:ARG:NH1	2.31	0.46
2:H:114:ALA:HB3	2:H:148:PHE:CE2	2.50	0.46
1:G:161:ASN:HD22	1:G:177:SER:HA	1.81	0.46
2:H:35:TRP:HB3	2:H:78:PHE:CZ	2.50	0.46
2:D:108:LEU:HD12	2:D:109:VAL:H	1.79	0.46
2:B:71:ARG:HA	2:B:78:PHE:HA	1.97	0.46
1:A:184:ASP:O	1:A:188:ARG:HG3	2.15	0.46
2:F:50:TYR:C	2:F:50:TYR:CD1	2.90	0.46
2:H:33:PHE:HB2	2:H:35:TRP:CZ2	2.50	0.46
2:F:79:PHE:N	2:F:79:PHE:CD1	2.83	0.46
1:G:136:LEU:HD12	1:G:136:LEU:N	2.31	0.45
2:H:94:GLY:O	2:H:101:GLY:HA2	2.16	0.45
1:E:27(A):ARG:NH2	5:E:425:HOH:O	2.41	0.45
2:D:42:GLY:O	2:D:43:ASN:HB2	2.16	0.45
1:A:83:LEU:C	1:A:83:LEU:HD12	2.37	0.45
1:E:115:VAL:HA	1:E:135:PHE:O	2.15	0.45
2:F:94:GLY:O	2:F:101:GLY:HA2	2.16	0.45
1:E:124:GLN:HB2	2:F:122:TYR:CD2	2.52	0.45
2:H:150:GLU:OE1	2:H:151:PRO:HA	2.16	0.45
2:H:6:GLN:HE21	2:H:92:CYS:H	1.64	0.45
2:H:50:TYR:CD1	2:H:50:TYR:C	2.89	0.45
1:G:118:PHE:HA	1:G:119:PRO:HD3	1.84	0.45
1:A:161:ASN:HD22	1:A:177:SER:HA	1.81	0.45
1:A:185:GLU:HA	1:A:188:ARG:NH1	2.31	0.45
2:F:114:ALA:HB3	2:F:148:PHE:CE2	2.51	0.45
1:C:184:ASP:O	1:C:188:ARG:HG3	2.16	0.45
1:A:115:VAL:HA	1:A:135:PHE:O	2.17	0.45
1:G:122:SER:O	1:G:126:THR:HG23	2.17	0.45
2:D:94:GLY:O	2:D:101:GLY:HA2	2.16	0.45
2:D:14:PRO:O	2:D:15:SER:OG	2.30	0.45
1:G:83:LEU:C	1:G:83:LEU:HD12	2.38	0.44
1:E:136:LEU:HD12	1:E:136:LEU:N	2.31	0.44
2:F:150:GLU:OE1	2:F:151:PRO:HA	2.17	0.44
1:G:86:TYR:O	1:G:101:GLY:HA2	2.17	0.44
1:C:185:GLU:HA	1:C:188:ARG:NH1	2.33	0.44
2:F:196:SER:N	5:F:507:HOH:O	2.49	0.44
1:E:118:PHE:HA	1:E:119:PRO:HD3	1.83	0.44
2:D:79:PHE:N	2:D:79:PHE:CD1	2.85	0.44
2:D:33:PHE:HB2	2:D:35:TRP:CZ2	2.52	0.44
2:F:108:LEU:HD12	2:F:109:VAL:N	2.32	0.44
2:F:166:LEU:HD21	2:F:191:VAL:HG21	2.00	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:18:PRO:HG2	1:C:18:PRO:HG2	2.00	0.44
2:H:14:PRO:O	2:H:15:SER:OG	2.34	0.44
1:E:161:ASN:HD22	1:E:177:SER:HA	1.82	0.44
1:G:115:VAL:HA	1:G:135:PHE:O	2.17	0.44
2:F:215:SER:OG	2:F:217:THR:OG1	2.36	0.44
2:D:40:PHE:HB3	2:D:41:PRO:HD2	2.00	0.44
1:E:86:TYR:O	1:E:101:GLY:HA2	2.17	0.44
2:B:33:PHE:HB2	2:B:35:TRP:CZ2	2.53	0.43
1:A:37:LEU:HD13	1:A:86:TYR:CE1	2.53	0.43
2:B:108:LEU:HD12	2:B:109:VAL:N	2.32	0.43
2:H:42:GLY:O	2:H:43:ASN:HB2	2.18	0.43
1:C:14:THR:O	1:C:17:GLN:HB2	2.18	0.43
2:H:204:SER:CB	2:H:222:LYS:HE2	2.48	0.43
2:F:40:PHE:HB3	2:F:41:PRO:HD2	2.00	0.43
2:B:29:ILE:HD11	2:B:73:THR:HA	1.99	0.43
1:C:122:SER:O	1:C:126:THR:HG23	2.18	0.43
1:G:185:GLU:HA	1:G:188:ARG:NH1	2.33	0.43
1:C:21:ILE:HB	5:C:409:HOH:O	2.19	0.43
1:C:83:LEU:HD22	1:C:166:GLN:HG2	1.99	0.43
2:F:39:GLN:O	2:F:88:ALA:HB1	2.18	0.43
1:G:30:LYS:HE2	2:H:98:TYR:CZ	2.54	0.43
2:B:82(C):VAL:HA	2:B:86:ASP:OD2	2.17	0.43
2:H:149:PRO:HD2	2:H:214:ALA:HB1	2.00	0.43
2:F:213:PRO:O	2:F:215:SER:N	2.52	0.43
2:H:79:PHE:CD1	2:H:79:PHE:N	2.86	0.43
2:H:11:LEU:HB2	2:H:149:PRO:HG3	2.01	0.43
2:B:204:SER:CB	2:B:222:LYS:HE2	2.49	0.43
2:D:108:LEU:HG	5:D:512:HOH:O	2.19	0.43
2:D:51:ILE:HA	2:D:56:PHE:O	2.19	0.43
2:D:149:PRO:HD2	2:D:214:ALA:HB1	2.00	0.42
2:H:18:LEU:HD22	2:H:20:LEU:HG	2.01	0.42
1:E:122:SER:O	1:E:126:THR:HG23	2.18	0.42
1:C:50:LEU:HA	1:C:50:LEU:HD23	1.92	0.42
1:C:77:ARG:HG2	1:C:77:ARG:HH11	1.84	0.42
1:E:37:LEU:HD13	1:E:86:TYR:CE1	2.55	0.42
1:E:49:TYR:CE1	1:E:53:LYS:HE2	2.53	0.42
1:E:83:LEU:HD22	1:E:166:GLN:HG2	2.01	0.42
2:F:228:ARG:HG3	2:F:228:ARG:NH1	2.33	0.42
2:H:39:GLN:O	2:H:88:ALA:HB1	2.19	0.42
1:G:14:THR:O	1:G:17:GLN:HB2	2.19	0.42
1:A:160:LEU:CD1	2:B:179:GLN:HG3	2.49	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:86:TYR:O	1:C:101:GLY:HA2	2.20	0.42
2:F:35:TRP:HB3	2:F:78:PHE:CZ	2.55	0.42
2:B:18:LEU:HD22	2:B:20:LEU:HG	2.00	0.42
1:E:83:LEU:C	1:E:83:LEU:HD12	2.40	0.42
1:C:37:LEU:HD13	1:C:86:TYR:CE1	2.54	0.42
1:A:182:THR:HG23	5:A:410:HOH:O	2.20	0.42
2:H:40:PHE:HB3	2:H:41:PRO:HD2	2.02	0.42
2:B:79:PHE:N	2:B:79:PHE:CD1	2.86	0.42
1:E:214:CYS:OXT	2:F:127:VAL:HA	2.20	0.42
2:H:51:ILE:HA	2:H:56:PHE:O	2.20	0.42
2:H:75:LYS:O	2:H:77:GLN:HG3	2.20	0.42
1:A:14:THR:O	1:A:17:GLN:HB2	2.19	0.42
1:G:27(A):ARG:NH2	5:G:460:HOH:O	2.52	0.42
1:C:91:GLY:HA2	1:C:96:TYR:CD1	2.55	0.42
2:B:114:ALA:HB3	2:B:148:PHE:CE2	2.55	0.42
1:C:142:LYS:NZ	5:C:420:HOH:O	2.53	0.41
1:A:50:LEU:HD23	1:A:50:LEU:HA	1.90	0.41
2:F:14:PRO:O	2:F:15:SER:OG	2.31	0.41
1:A:160:LEU:HD11	2:B:179:GLN:HG3	2.02	0.41
2:H:213:PRO:O	2:H:215:SER:N	2.53	0.41
1:C:83:LEU:C	1:C:83:LEU:HD12	2.41	0.41
2:F:140:LEU:HD22	2:F:205:ILE:HD12	2.03	0.41
2:D:213:PRO:O	2:D:215:SER:N	2.53	0.41
1:A:122:SER:O	1:A:126:THR:HG23	2.19	0.41
2:F:29:ILE:HD11	2:F:73:THR:HA	2.01	0.41
2:F:204:SER:CB	2:F:222:LYS:HE2	2.51	0.41
1:G:175:MET:N	2:H:174:PHE:HE2	2.19	0.41
2:H:166:LEU:HD21	2:H:191:VAL:HG21	2.03	0.41
2:D:174:PHE:CD1	2:D:174:PHE:N	2.88	0.41
2:D:75:LYS:O	2:D:77:GLN:HG3	2.21	0.41
2:D:108:LEU:HD12	2:D:109:VAL:N	2.34	0.41
2:B:14:PRO:O	2:B:15:SER:OG	2.29	0.41
2:F:75:LYS:NZ	5:F:534:HOH:O	2.47	0.41
2:B:199:TRP:CD1	2:B:200:PRO:HA	2.56	0.41
1:E:18:PRO:HG2	1:G:18:PRO:HG2	2.02	0.41
2:F:6:GLN:NE2	2:F:92:CYS:H	2.19	0.41
1:E:145:ASN:ND2	5:E:431:HOH:O	2.54	0.41
2:B:213:PRO:O	2:B:215:SER:N	2.55	0.41
2:F:18:LEU:HD22	2:F:20:LEU:HG	2.02	0.41
2:H:147:TYR:CE2	2:H:152:VAL:HG13	2.56	0.40
2:F:126:PRO:HB2	2:F:127:VAL:H	1.63	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:147:TYR:CE2	2:D:152:VAL:HG13	2.56	0.40
1:G:214:CYS:SG	1:G:214:CYS:OXT	2.80	0.40
2:F:4:LEU:CD1	2:F:4:LEU:N	2.84	0.40
1:A:9:LYS:HE3	5:A:416:HOH:O	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	217/219 (99%)	205 (94%)	11 (5%)	1 (0%)	34	41
1	C	217/219 (99%)	206 (95%)	10 (5%)	1 (0%)	34	41
1	E	217/219 (99%)	206 (95%)	10 (5%)	1 (0%)	34	41
1	G	217/219 (99%)	205 (94%)	11 (5%)	1 (0%)	34	41
2	B	220/222 (99%)	203 (92%)	12 (6%)	5 (2%)	8	5
2	D	220/222 (99%)	203 (92%)	12 (6%)	5 (2%)	8	5
2	F	220/222 (99%)	202 (92%)	13 (6%)	5 (2%)	8	5
2	H	220/222 (99%)	202 (92%)	13 (6%)	5 (2%)	8	5
All	All	1748/1764 (99%)	1632 (93%)	92 (5%)	24 (1%)	14	13

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	213	GLU
1	C	213	GLU
1	E	213	GLU
1	G	213	GLU
2	B	126	PRO
2	D	126	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	F	126	PRO
2	H	126	PRO
2	B	136	SER
2	B	214	ALA
2	D	214	ALA
2	F	214	ALA
2	H	136	SER
2	H	214	ALA
2	D	136	SER
2	F	136	SER
2	B	127	VAL
2	D	127	VAL
2	F	127	VAL
2	H	127	VAL
2	D	151	PRO
2	F	151	PRO
2	B	151	PRO
2	H	151	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	195/195 (100%)	192 (98%)	3 (2%)	72	84
1	C	195/195 (100%)	193 (99%)	2 (1%)	82	89
1	E	195/195 (100%)	192 (98%)	3 (2%)	72	84
1	G	195/195 (100%)	193 (99%)	2 (1%)	82	89
2	B	192/192 (100%)	180 (94%)	12 (6%)	22	30
2	D	192/192 (100%)	180 (94%)	12 (6%)	22	30
2	F	192/192 (100%)	180 (94%)	12 (6%)	22	30
2	H	192/192 (100%)	179 (93%)	13 (7%)	20	26
All	All	1548/1548 (100%)	1489 (96%)	59 (4%)	40	55

All (59) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	ILE
1	A	70	ASP
1	A	184	ASP
2	B	18	LEU
2	B	41	PRO
2	B	85	GLU
2	B	149	PRO
2	B	151	PRO
2	B	177	VAL
2	B	180	SER
2	B	183	ASP
2	B	187	LEU
2	B	194	THR
2	B	198	THR
2	B	217	THR
1	C	70	ASP
1	C	184	ASP
2	D	18	LEU
2	D	41	PRO
2	D	82(B)	SER
2	D	85	GLU
2	D	151	PRO
2	D	177	VAL
2	D	180	SER
2	D	183	ASP
2	D	187	LEU
2	D	194	THR
2	D	198	THR
2	D	217	THR
1	E	53	LYS
1	E	70	ASP
1	E	184	ASP
2	F	18	LEU
2	F	41	PRO
2	F	85	GLU
2	F	149	PRO
2	F	151	PRO
2	F	177	VAL
2	F	180	SER
2	F	183	ASP
2	F	187	LEU
2	F	194	THR
2	F	198	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	F	217	THR
1	G	70	ASP
1	G	184	ASP
2	H	18	LEU
2	H	41	PRO
2	H	82(B)	SER
2	H	85	GLU
2	H	140	LEU
2	H	151	PRO
2	H	177	VAL
2	H	180	SER
2	H	183	ASP
2	H	187	LEU
2	H	194	THR
2	H	198	THR
2	H	217	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	28	ASN
1	A	38	GLN
1	A	145	ASN
1	A	161	ASN
2	B	3	GLN
2	B	39	GLN
1	C	28	ASN
1	C	145	ASN
1	C	161	ASN
2	D	3	GLN
1	E	27	GLN
1	E	28	ASN
1	E	145	ASN
1	E	161	ASN
2	F	3	GLN
1	G	27	GLN
1	G	28	ASN
1	G	145	ASN
1	G	161	ASN
2	H	3	GLN
2	H	203	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

8 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	$\# Z > 2$
4	DP4	A	401	-	18,18,18	4.06	12 (66%)	21,27,27	1.35	3 (14%)
3	SO4	B	503	-	4,4,4	5.64	4 (100%)	6,6,6	0.09	0
4	DP4	C	402	-	18,18,18	3.98	12 (66%)	21,27,27	1.37	3 (14%)
3	SO4	D	504	-	4,4,4	5.75	4 (100%)	6,6,6	0.10	0
4	DP4	E	403	-	18,18,18	3.92	13 (72%)	21,27,27	1.34	3 (14%)
3	SO4	F	501	-	4,4,4	5.66	4 (100%)	6,6,6	0.14	0
4	DP4	G	404	-	18,18,18	3.93	12 (66%)	21,27,27	1.37	3 (14%)
3	SO4	H	502	-	4,4,4	5.82	4 (100%)	6,6,6	0.11	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	DP4	A	401	-	-	0/12/24/24	0/2/2/2
3	SO4	B	503	-	-	0/0/0/0	0/0/0/0
4	DP4	C	402	-	-	0/12/24/24	0/2/2/2
3	SO4	D	504	-	-	0/0/0/0	0/0/0/0
4	DP4	E	403	-	-	0/12/24/24	0/2/2/2
3	SO4	F	501	-	-	0/0/0/0	0/0/0/0
4	DP4	G	404	-	-	0/12/24/24	0/2/2/2
3	SO4	H	502	-	-	0/0/0/0	0/0/0/0

All (65) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	401	DP4	SI-C9	-10.78	1.82	1.89
4	C	402	DP4	SI-C9	-10.39	1.82	1.89
4	G	404	DP4	SI-C9	-9.60	1.83	1.89
4	E	403	DP4	SI-C9	-9.55	1.83	1.89
4	G	404	DP4	SI-C4	-7.77	1.80	1.88
4	E	403	DP4	SI-C4	-7.62	1.81	1.88
4	A	401	DP4	SI-C4	-7.35	1.81	1.88
4	C	402	DP4	SI-C4	-7.17	1.81	1.88
4	A	401	DP4	SI-C7	-3.38	1.81	1.86
4	E	403	DP4	SI-C8	-3.37	1.81	1.86
4	G	404	DP4	SI-C7	-3.34	1.81	1.86
4	E	403	DP4	SI-C7	-3.34	1.81	1.86
4	C	402	DP4	SI-C7	-3.32	1.81	1.86
4	G	404	DP4	SI-C8	-3.20	1.81	1.86
4	A	401	DP4	SI-C8	-3.13	1.81	1.86
4	C	402	DP4	SI-C8	-3.01	1.81	1.86
4	E	403	DP4	C11-N1	2.11	1.55	1.50
4	E	403	DP4	C6-C1	2.12	1.43	1.38
4	A	401	DP4	C6-C1	2.17	1.43	1.38
4	G	404	DP4	C6-C1	2.22	1.43	1.38
4	C	402	DP4	C6-C1	2.25	1.43	1.38
4	E	403	DP4	C2-C3	2.29	1.43	1.38
4	G	404	DP4	C2-C3	2.32	1.43	1.38
4	E	403	DP4	C12-N1	2.41	1.56	1.50
4	A	401	DP4	C2-C3	2.47	1.44	1.38
4	C	402	DP4	C2-C3	2.49	1.44	1.38
4	A	401	DP4	C2-C1	2.53	1.44	1.38
4	G	404	DP4	C2-C1	2.54	1.44	1.38
4	G	404	DP4	C12-N1	2.56	1.56	1.50
4	G	404	DP4	C5-C4	2.59	1.44	1.39
4	C	402	DP4	C12-N1	2.59	1.57	1.50

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	402	DP4	C2-C1	2.59	1.44	1.38
4	E	403	DP4	C2-C1	2.64	1.44	1.38
4	A	401	DP4	C12-N1	2.66	1.57	1.50
4	C	402	DP4	C5-C4	2.74	1.44	1.39
4	E	403	DP4	C5-C4	2.74	1.44	1.39
4	A	401	DP4	C6-C5	2.75	1.44	1.38
4	C	402	DP4	C6-C5	2.78	1.44	1.38
4	E	403	DP4	C6-C5	2.84	1.44	1.38
4	A	401	DP4	C5-C4	2.85	1.45	1.39
4	G	404	DP4	C6-C5	2.89	1.44	1.38
4	A	401	DP4	C3-C4	3.08	1.45	1.39
4	E	403	DP4	C3-C4	3.12	1.45	1.39
4	C	402	DP4	C3-C4	3.18	1.45	1.39
4	G	404	DP4	C3-C4	3.24	1.45	1.39
3	B	503	SO4	O3-S	5.31	1.66	1.47
3	B	503	SO4	O4-S	5.38	1.66	1.47
3	B	503	SO4	O2-S	5.47	1.65	1.47
3	F	501	SO4	O3-S	5.47	1.67	1.47
3	F	501	SO4	O4-S	5.57	1.67	1.47
3	D	504	SO4	O4-S	5.59	1.67	1.47
3	H	502	SO4	O4-S	5.60	1.67	1.47
3	D	504	SO4	O3-S	5.61	1.67	1.47
3	H	502	SO4	O3-S	5.62	1.67	1.47
3	F	501	SO4	O2-S	5.70	1.66	1.47
3	F	501	SO4	O1-S	5.87	1.67	1.47
3	D	504	SO4	O2-S	5.89	1.67	1.47
3	D	504	SO4	O1-S	5.90	1.67	1.47
3	H	502	SO4	O2-S	5.91	1.67	1.47
3	H	502	SO4	O1-S	6.14	1.68	1.47
3	B	503	SO4	O1-S	6.34	1.68	1.47
4	A	401	DP4	C14-N1	6.43	1.59	1.49
4	C	402	DP4	C14-N1	6.46	1.59	1.49
4	G	404	DP4	C14-N1	6.47	1.59	1.49
4	E	403	DP4	C14-N1	6.48	1.59	1.49

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	401	DP4	O1-N1-C11	-3.03	105.50	110.30
4	G	404	DP4	O1-N1-C11	-3.02	105.50	110.30
4	C	402	DP4	O1-N1-C11	-2.96	105.60	110.30
4	E	403	DP4	O1-N1-C11	-2.95	105.62	110.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	402	DP4	C8-SI-C7	-2.86	104.89	109.59
4	G	404	DP4	C8-SI-C7	-2.70	105.16	109.59
4	A	401	DP4	C8-SI-C7	-2.69	105.18	109.59
4	E	403	DP4	C8-SI-C7	-2.54	105.42	109.59
4	E	403	DP4	C14-N1-C12	2.38	113.92	110.22
4	A	401	DP4	C14-N1-C12	2.45	114.03	110.22
4	G	404	DP4	C14-N1-C12	2.49	114.09	110.22
4	C	402	DP4	C14-N1-C12	2.49	114.10	110.22

There are no chirality outliers.

There are no torsion outliers.

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, 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	219/219 (100%)	0.10	8 (3%) 45 49	14, 32, 54, 94	0
1	C	219/219 (100%)	0.20	7 (3%) 51 54	16, 33, 54, 95	0
1	E	219/219 (100%)	0.08	3 (1%) 78 80	15, 32, 52, 93	0
1	G	219/219 (100%)	0.17	8 (3%) 45 49	16, 33, 53, 94	0
2	B	222/222 (100%)	0.26	15 (6%) 20 22	10, 29, 66, 100	9 (4%)
2	D	222/222 (100%)	0.41	24 (10%) 8 7	12, 30, 67, 100	9 (4%)
2	F	222/222 (100%)	0.32	18 (8%) 15 15	14, 29, 64, 100	9 (4%)
2	H	222/222 (100%)	0.49	20 (9%) 12 12	11, 30, 68, 100	9 (4%)
All	All	1764/1764 (100%)	0.26	103 (5%) 26 29	10, 31, 59, 100	36 (2%)

All (103) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	231	THR	14.2
2	F	231	THR	9.7
2	D	231	THR	9.0
2	H	127	VAL	8.1
2	B	133	THR	7.9
2	B	231	THR	7.8
2	H	130	ASP	7.3
2	F	133	THR	7.0
2	H	129	GLY	6.6
2	H	230	PRO	6.6
2	B	195	SER	6.5
2	D	134	THR	6.4
2	H	128	CYS	5.9
2	D	137	SER	5.7
2	D	133	THR	5.6
1	C	214	CYS	5.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	D	135	GLY	5.2
2	H	137	SER	4.8
1	A	214	CYS	4.7
2	H	229	GLY	4.7
2	F	128	CYS	4.4
1	G	214	CYS	4.3
2	B	128	CYS	4.3
1	C	212	ASN	4.2
1	E	214	CYS	4.2
2	D	129	GLY	4.2
2	B	194	THR	4.1
2	H	134	THR	4.1
1	C	181	LEU	4.1
2	F	137	SER	3.9
2	B	130	ASP	3.8
2	F	188	SER	3.8
2	B	127	VAL	3.6
1	E	15	ILE	3.6
2	F	127	VAL	3.6
2	F	195	SER	3.6
2	F	130	ASP	3.5
2	F	135	GLY	3.5
2	B	129	GLY	3.5
1	G	213	GLU	3.4
2	B	137	SER	3.4
2	F	194	THR	3.3
2	D	4	LEU	3.3
2	B	139	THR	3.1
2	H	188	SER	3.1
2	H	108	LEU	3.1
2	B	186	THR	3.1
2	D	128	CYS	3.0
1	A	212	ASN	2.9
2	F	229	GLY	2.9
2	F	186	THR	2.9
2	F	230	PRO	2.9
2	D	195	SER	2.9
2	H	133	THR	2.9
2	B	188	SER	2.8
1	C	213	GLU	2.8
2	F	4	LEU	2.8
2	D	194	THR	2.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	D	136	SER	2.8
2	D	130	ASP	2.7
1	E	212	ASN	2.7
2	B	230	PRO	2.6
1	C	130	ALA	2.6
2	H	4	LEU	2.6
1	A	27(E)	SER	2.6
2	H	62	SER	2.5
2	H	195	SER	2.5
2	D	108	LEU	2.5
2	B	134	THR	2.5
2	D	230	PRO	2.5
2	F	134	THR	2.5
2	H	221	LYS	2.5
1	A	15	ILE	2.5
2	F	139	THR	2.5
2	D	188	SER	2.5
1	G	28	ASN	2.5
2	D	203	GLN	2.4
1	C	27(C)	LEU	2.4
1	A	28	ASN	2.4
2	H	139	THR	2.4
1	G	163	TRP	2.4
1	A	213	GLU	2.4
1	G	212	ASN	2.3
2	D	186	THR	2.3
2	H	186	THR	2.3
2	D	221	LYS	2.2
2	D	138	VAL	2.2
2	F	108	LEU	2.2
2	D	126	PRO	2.2
1	G	29	GLY	2.2
2	B	4	LEU	2.2
2	H	135	GLY	2.2
1	C	182	THR	2.2
1	A	13	VAL	2.1
2	D	139	THR	2.1
1	A	29	GLY	2.1
1	G	184	ASP	2.1
2	D	228	ARG	2.1
2	F	129	GLY	2.1
1	G	182	THR	2.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	D	198	THR	2.0
2	D	62	SER	2.0
2	H	216	SER	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	SO4	H	502	5/5	0.90	0.26	7.51	90,90,91,91	0
4	DP4	G	404	17/17	0.91	0.26	7.02	48,54,71,75	0
4	DP4	C	402	17/17	0.92	0.23	4.61	48,55,70,75	0
4	DP4	A	401	17/17	0.92	0.26	4.49	48,55,72,77	0
4	DP4	E	403	17/17	0.91	0.25	3.40	49,55,70,76	0
3	SO4	F	501	5/5	0.98	0.15	2.05	32,33,35,36	0
3	SO4	D	504	5/5	0.90	0.17	0.73	72,73,74,74	0
3	SO4	B	503	5/5	0.98	0.11	-1.97	22,25,28,29	0

6.5 Other polymers [i](#)

There are no such residues in this entry.