



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 10:28 am GMT

PDB ID : 1RIR  
Title : Crystal structure of meso-tetrasulphonatophenylporphyrin in complex with Peanut lectin.  
Authors : Goel, M.; Kaur, K.J.; Maiya, B.G.; Swamy, M.J.; Salunke, D.M.  
Deposited on : 2003-11-17  
Resolution : 2.90 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](mailto: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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : recalc28949

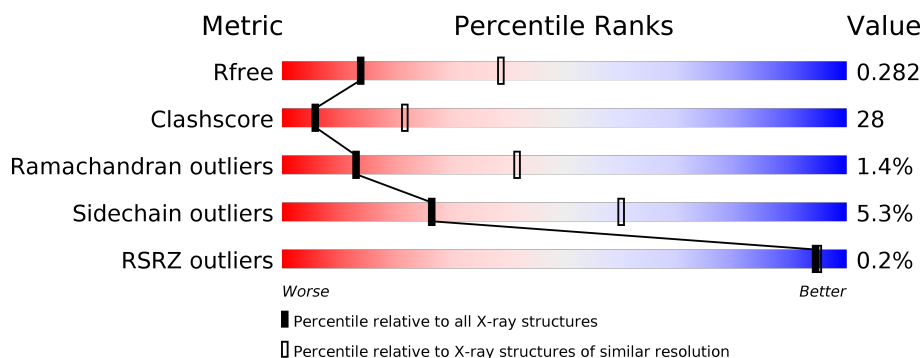
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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))
$R_{free}$	100719	1586 (2.90-2.90)
Clashscore	112137	1807 (2.90-2.90)
Ramachandran outliers	110173	1768 (2.90-2.90)
Sidechain outliers	110143	1770 (2.90-2.90)
RSRZ outliers	101464	1596 (2.90-2.90)

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  $\geq 3$ , 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	236	<div> <div>57%</div> <div>37%</div> <div>• •</div> </div>
1	B	236	<div> <div>56%</div> <div>39%</div> <div>• •</div> </div>
1	C	236	<div> <div>52%</div> <div>43%</div> <div>• •</div> </div>
1	D	236	<div> <div>52%</div> <div>42%</div> <div>• •</div> </div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7745 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 Galactose-binding lectin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	232	Total	C	N	O	S	0	0	0
			1743	1102	287	352	2			
1	B	232	Total	C	N	O	S	0	0	0
			1743	1102	287	352	2			
1	C	232	Total	C	N	O	S	0	0	0
			1743	1102	287	352	2			
1	D	232	Total	C	N	O	S	0	0	0
			1743	1102	287	352	2			

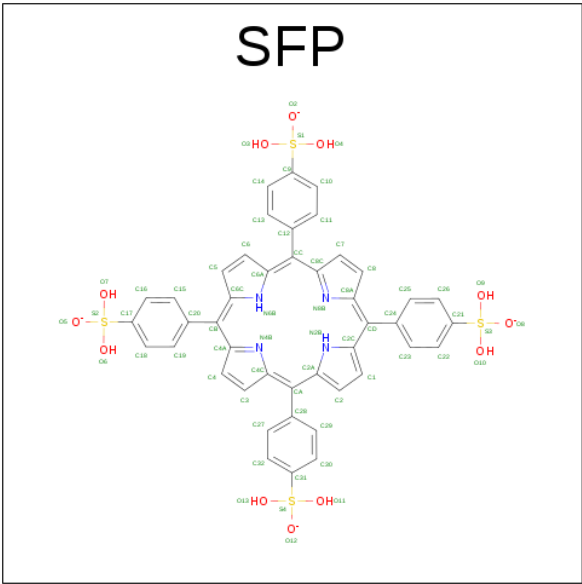
- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Mn	0	0
			1	1		
3	A	1	Total	Mn	0	0
			1	1		
3	D	1	Total	Mn	0	0
			1	1		
3	C	1	Total	Mn	0	0
			1	1		

- Molecule 4 is 5,10,15,20-TETRAKIS(4-SULPFONATOPHENYL)-21H,23H-PORPHINE (three-letter code: SFP) (formula: C<sub>44</sub>H<sub>34</sub>N<sub>4</sub>O<sub>12</sub>S<sub>4</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			64	44	4	12	4		
4	A	1	Total	C	N	O	S	0	0
			64	44	4	12	4		
4	B	1	Total	C	N	O	S	0	0
			64	44	4	12	4		
4	B	1	Total	C	N	O	S	0	0
			64	44	4	12	4		
4	C	1	Total	C	N	O	S	0	0
			64	44	4	12	4		
4	C	1	Total	C	N	O	S	0	0
			64	44	4	12	4		
4	D	1	Total	C	N	O	S	0	0
			64	44	4	12	4		
4	D	1	Total	C	N	O	S	0	0
			64	44	4	12	4		
4	B	1	Total	C	N	O	S	0	0
			64	44	4	12	4		
4	A	1	Total	C	N	O	S	0	0
			64	44	4	12	4		
4	A	1	Total	C	N	O	S	0	0
			64	44	4	12	4		

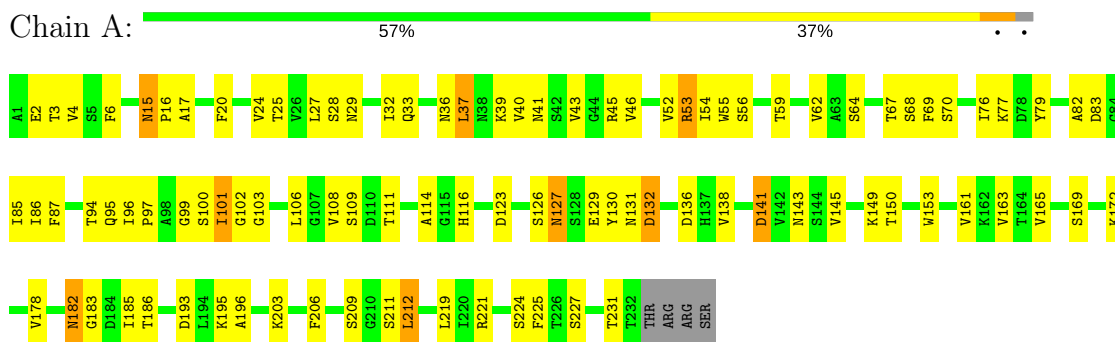
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	22	Total 22	O 22	0	0
5	B	15	Total 15	O 15	0	0
5	C	12	Total 12	O 12	0	0
5	D	12	Total 12	O 12	0	0

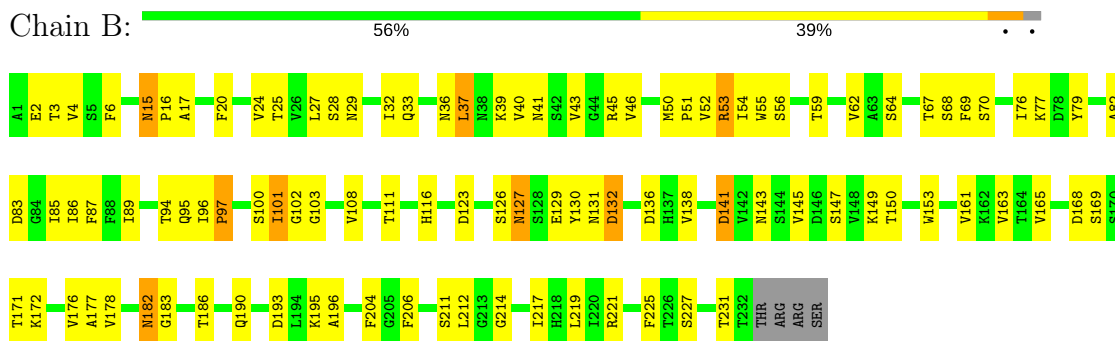
### 3 Residue-property plots

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

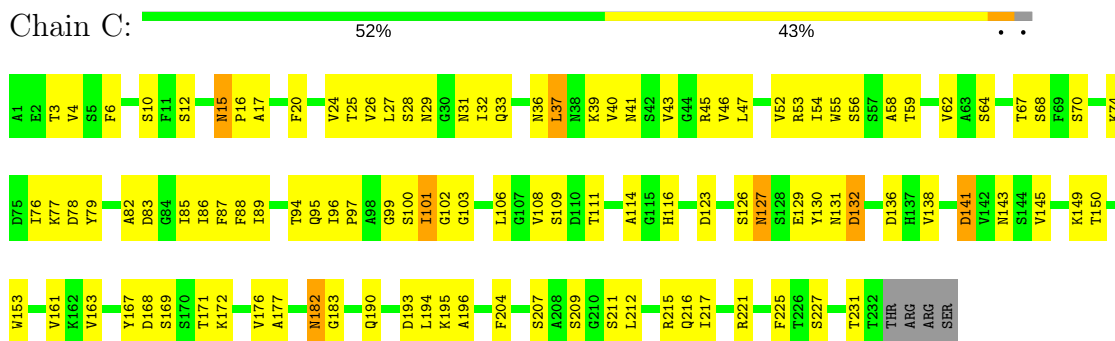
#### • Molecule 1: Galactose-binding lectin



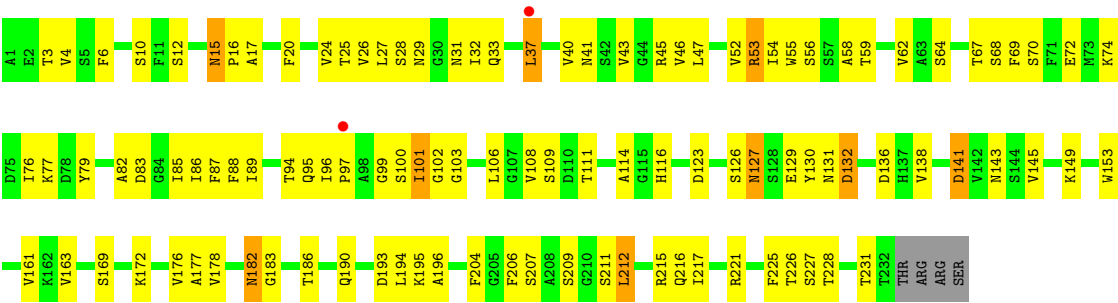
#### • Molecule 1: Galactose-binding lectin



#### • Molecule 1: Galactose-binding lectin



#### • Molecule 1: Galactose-binding lectin



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	94.80Å 94.80Å 144.00Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	100.00 – 2.90 33.73 – 2.90	Depositor EDS
% Data completeness (in resolution range)	(Not available) (100.00-2.90) 80.9 (33.73-2.90)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.42 (at 2.90Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.234 , 0.282 0.235 , 0.282	Depositor DCC
$R_{free}$ test set	2565 reflections (9.87%)	DCC
Wilson B-factor (Å <sup>2</sup> )	53.8	Xtriage
Anisotropy	0.029	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 49.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.021 for -h,-k,l 0.387 for h,-h-k,-l 0.030 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	7745	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.19% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

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



## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CA, MN, SFP

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	0.47	0/1779	0.74	0/2426
1	B	0.50	0/1779	0.75	0/2426
1	C	0.62	0/1779	0.79	0/2426
1	D	0.62	0/1779	0.78	0/2426
All	All	0.56	0/7116	0.77	0/9704

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	1743	0	1699	94	0
1	B	1743	0	1699	94	0
1	C	1743	0	1699	110	0
1	D	1743	0	1699	111	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	1	0	0	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	256	0	120	20	0
4	B	192	0	90	8	0
4	C	128	0	60	6	0
4	D	128	0	60	8	0
5	A	22	0	0	4	0
5	B	15	0	0	1	0
5	C	12	0	0	1	0
5	D	12	0	0	0	0
All	All	7745	0	7126	411	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 28.

All (411) 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:C:41:ASN:HB2	1:C:100:SER:O	1.53	1.07
1:B:41:ASN:HB2	1:B:100:SER:O	1.54	1.07
1:D:41:ASN:HB2	1:D:100:SER:O	1.55	1.05
1:A:41:ASN:HB2	1:A:100:SER:O	1.56	1.04
4:D:241:SFP:H15	4:D:242:SFP:H14	1.48	0.92
1:A:15:ASN:ND2	1:A:17:ALA:H	1.70	0.90
1:C:15:ASN:ND2	1:C:17:ALA:H	1.70	0.89
1:B:15:ASN:ND2	1:B:17:ALA:H	1.73	0.87
1:D:15:ASN:ND2	1:D:17:ALA:H	1.72	0.86
1:B:41:ASN:CB	1:B:100:SER:O	2.24	0.85
1:B:59:THR:HG21	1:B:231:THR:HG22	1.58	0.85
1:A:59:THR:HG21	1:A:231:THR:HG22	1.58	0.84
1:D:101:ILE:HG13	1:D:102:GLY:N	1.91	0.84
1:A:41:ASN:CB	1:A:100:SER:O	2.26	0.84
1:C:41:ASN:CB	1:C:100:SER:O	2.24	0.84
1:D:4:VAL:HG21	1:D:52:VAL:HG13	1.59	0.83
1:A:4:VAL:HG21	1:A:52:VAL:HG13	1.58	0.83
1:D:41:ASN:CB	1:D:100:SER:O	2.25	0.83
1:C:10:SER:HB3	1:D:74:LYS:HE2	1.60	0.82
1:C:74:LYS:HE2	1:D:10:SER:HB3	1.60	0.82
1:A:101:ILE:HG13	1:A:102:GLY:N	1.95	0.81
1:B:101:ILE:HG13	1:B:102:GLY:N	1.95	0.80

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:43:VAL:HG12	1:C:96:ILE:HD11	1.62	0.80
1:B:4:VAL:HG21	1:B:52:VAL:HG13	1.62	0.80
1:C:29:ASN:HA	1:D:217:ILE:CD1	2.12	0.79
1:C:101:ILE:HG13	1:C:102:GLY:N	1.96	0.79
1:C:4:VAL:HG21	1:C:52:VAL:HG13	1.64	0.79
1:D:231:THR:HB	4:D:241:SFP:H32	1.63	0.79
1:A:15:ASN:C	1:A:15:ASN:HD22	1.87	0.79
1:D:101:ILE:CG1	1:D:102:GLY:N	2.46	0.78
1:A:101:ILE:HG22	4:A:249:SFP:O6	1.84	0.78
1:D:43:VAL:HG12	1:D:96:ILE:HD11	1.64	0.78
1:C:217:ILE:CD1	1:D:29:ASN:HA	2.13	0.78
1:D:127:ASN:H	1:D:132:ASP:HB2	1.49	0.77
1:D:82:ALA:HB1	1:D:83:ASP:HA	1.66	0.77
1:C:127:ASN:H	1:C:132:ASP:HB2	1.51	0.76
1:A:127:ASN:H	1:A:132:ASP:HB2	1.49	0.75
1:B:127:ASN:H	1:B:132:ASP:HB2	1.49	0.75
1:A:101:ILE:CG1	1:A:102:GLY:N	2.49	0.75
1:D:15:ASN:C	1:D:15:ASN:HD22	1.90	0.74
1:C:101:ILE:CG1	1:C:102:GLY:N	2.51	0.74
1:A:52:VAL:HA	5:A:254:HOH:O	1.87	0.74
1:B:101:ILE:CG1	1:B:102:GLY:N	2.50	0.74
1:A:15:ASN:HD22	1:A:16:PRO:N	1.86	0.73
1:A:43:VAL:HG12	1:A:96:ILE:HD11	1.70	0.73
1:B:43:VAL:HG12	1:B:96:ILE:HD11	1.70	0.73
1:C:15:ASN:HD22	1:C:15:ASN:C	1.93	0.72
1:B:101:ILE:HG22	4:B:238:SFP:O9	1.91	0.71
1:D:59:THR:HG21	1:D:231:THR:HG22	1.71	0.70
1:B:15:ASN:C	1:B:15:ASN:HD22	1.93	0.70
1:B:219:LEU:HD11	4:B:243:SFP:H22	1.75	0.69
1:C:82:ALA:HB1	1:C:83:ASP:HA	1.73	0.69
1:B:15:ASN:HD22	1:B:16:PRO:N	1.91	0.69
1:C:15:ASN:HD22	1:C:16:PRO:N	1.89	0.69
1:D:15:ASN:HD22	1:D:16:PRO:N	1.90	0.69
1:A:203:LYS:HB3	5:A:269:HOH:O	1.93	0.69
1:B:24:VAL:HG21	1:B:45:ARG:O	1.93	0.68
4:A:244:SFP:H25	4:A:245:SFP:H26	1.76	0.68
1:A:101:ILE:CG2	4:A:249:SFP:S2	2.82	0.68
1:D:101:ILE:CG1	1:D:102:GLY:H	2.08	0.67
1:B:82:ALA:HB1	1:B:83:ASP:HA	1.77	0.67
1:C:59:THR:HG21	1:C:231:THR:HG22	1.74	0.67
1:C:231:THR:HB	4:C:239:SFP:H12	1.77	0.67

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:85:ILE:HG22	1:B:86:ILE:N	2.09	0.67
1:A:219:LEU:HD11	4:A:245:SFP:H22	1.75	0.66
1:A:82:ALA:HB1	1:A:83:ASP:HA	1.79	0.65
1:A:138:VAL:HG23	1:A:153:TRP:HB2	1.79	0.65
4:A:244:SFP:H25	4:A:245:SFP:C26	2.27	0.64
1:A:101:ILE:CG1	1:A:102:GLY:H	2.10	0.64
1:D:24:VAL:HG21	1:D:45:ARG:O	1.97	0.64
1:C:85:ILE:HG22	1:C:86:ILE:N	2.12	0.64
1:C:24:VAL:HG21	1:C:45:ARG:O	1.98	0.64
1:A:40:VAL:O	1:A:41:ASN:CG	2.36	0.63
1:D:138:VAL:HG23	1:D:153:TRP:HB2	1.79	0.63
1:B:25:THR:HG23	1:B:33:GLN:HB3	1.79	0.63
1:A:85:ILE:HG22	1:A:86:ILE:N	2.13	0.63
4:A:244:SFP:H27	4:A:244:SFP:C3	2.29	0.62
1:B:138:VAL:HG23	1:B:153:TRP:HB2	1.81	0.62
1:A:15:ASN:HD22	1:A:17:ALA:H	1.45	0.62
1:C:25:THR:HG23	1:C:33:GLN:HB3	1.80	0.62
1:A:56:SER:HB3	1:A:59:THR:OG1	1.99	0.62
4:A:244:SFP:H3	4:A:244:SFP:H27	1.82	0.62
1:B:40:VAL:O	1:B:41:ASN:CG	2.38	0.62
1:A:25:THR:HG23	1:A:33:GLN:HB3	1.81	0.62
4:A:244:SFP:H3	4:A:244:SFP:C27	2.31	0.61
1:B:56:SER:HB3	1:B:59:THR:OG1	2.00	0.61
1:C:101:ILE:CG1	1:C:102:GLY:H	2.14	0.61
1:C:10:SER:HB3	1:D:74:LYS:CE	2.29	0.61
1:B:101:ILE:CG1	1:B:102:GLY:H	2.13	0.61
1:D:25:THR:HG23	1:D:33:GLN:HB3	1.81	0.60
1:A:101:ILE:CG2	4:A:249:SFP:O5	2.48	0.60
1:C:138:VAL:HG23	1:C:153:TRP:HB2	1.83	0.60
1:C:74:LYS:CE	1:D:10:SER:HB3	2.31	0.60
1:D:56:SER:HB3	1:D:59:THR:OG1	2.00	0.59
1:D:85:ILE:HG22	1:D:86:ILE:N	2.17	0.59
1:A:94:THR:O	1:A:94:THR:HG23	2.01	0.59
4:A:244:SFP:C5	4:A:245:SFP:H9	2.33	0.58
1:B:85:ILE:HG22	1:B:86:ILE:H	1.69	0.58
4:C:239:SFP:H14	4:C:240:SFP:H15	1.85	0.58
1:C:85:ILE:HG22	1:C:86:ILE:H	1.67	0.58
1:A:24:VAL:HG21	1:A:45:ARG:O	2.02	0.58
1:B:32:ILE:HD13	1:B:46:VAL:HG21	1.85	0.58
1:B:15:ASN:HD22	1:B:17:ALA:H	1.49	0.58
1:C:15:ASN:HD22	1:C:17:ALA:H	1.48	0.58

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:56:SER:HB3	1:C:59:THR:OG1	2.03	0.57
1:C:27:LEU:HD13	1:D:27:LEU:HD13	1.87	0.57
4:C:239:SFP:H27	4:C:240:SFP:H32	1.85	0.57
1:D:4:VAL:HG21	1:D:52:VAL:CG1	2.33	0.57
1:A:101:ILE:CG2	4:A:249:SFP:O6	2.51	0.56
1:B:172:LYS:HE2	1:B:193:ASP:OD2	2.06	0.56
1:C:54:ILE:HG13	1:C:55:TRP:HD1	1.70	0.56
1:A:127:ASN:H	1:A:132:ASP:CB	2.18	0.56
1:C:32:ILE:HD13	1:C:46:VAL:HG21	1.88	0.56
1:B:182:ASN:HD22	1:B:183:GLY:N	2.03	0.56
1:A:85:ILE:HG22	1:A:86:ILE:H	1.71	0.56
1:A:62:VAL:O	1:A:169:SER:HB2	2.06	0.56
1:D:182:ASN:N	1:D:182:ASN:HD22	2.04	0.56
1:C:64:SER:OG	1:C:169:SER:HB3	2.06	0.56
1:B:101:ILE:CG2	4:B:238:SFP:S3	2.94	0.56
1:C:10:SER:HA	1:D:74:LYS:NZ	2.21	0.56
1:B:127:ASN:H	1:B:132:ASP:CB	2.19	0.55
1:B:6:PHE:CZ	1:B:225:PHE:HB3	2.41	0.55
1:A:212:LEU:O	1:A:212:LEU:HD23	2.06	0.55
1:B:182:ASN:HD22	1:B:183:GLY:H	1.53	0.55
1:D:15:ASN:C	1:D:15:ASN:ND2	2.59	0.55
1:C:182:ASN:HD22	1:C:183:GLY:N	2.03	0.55
1:D:54:ILE:HG13	1:D:55:TRP:HD1	1.72	0.55
1:D:6:PHE:CZ	1:D:225:PHE:HB3	2.41	0.55
1:B:217:ILE:HA	5:B:264:HOH:O	2.07	0.55
1:D:40:VAL:O	1:D:41:ASN:CG	2.45	0.55
1:B:54:ILE:HG13	1:B:55:TRP:HD1	1.71	0.55
1:D:15:ASN:HD22	1:D:17:ALA:H	1.51	0.55
1:D:67:THR:HG21	1:D:87:PHE:CZ	2.41	0.54
4:C:239:SFP:H27	4:C:240:SFP:C32	2.38	0.54
1:B:62:VAL:O	1:B:169:SER:HB2	2.07	0.54
1:D:53:ARG:NH2	4:D:241:SFP:O12	2.41	0.54
1:D:101:ILE:HG12	1:D:102:GLY:H	1.72	0.54
1:C:27:LEU:C	1:C:29:ASN:H	2.11	0.54
1:A:101:ILE:HG21	4:A:249:SFP:S2	2.47	0.53
1:C:182:ASN:HD22	1:C:183:GLY:H	1.56	0.53
1:C:67:THR:HG21	1:C:87:PHE:CZ	2.42	0.53
1:C:74:LYS:NZ	1:D:10:SER:HA	2.23	0.53
1:D:182:ASN:HD22	1:D:183:GLY:N	2.05	0.53
1:A:15:ASN:C	1:A:15:ASN:ND2	2.58	0.53
1:C:15:ASN:HD22	1:C:16:PRO:CD	2.21	0.53

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:182:ASN:HD22	1:A:183:GLY:N	2.06	0.53
1:B:68:SER:HA	1:B:163:VAL:O	2.07	0.53
1:A:54:ILE:HG13	1:A:55:TRP:HD1	1.73	0.53
1:B:193:ASP:HB3	1:B:196:ALA:HB3	1.91	0.53
1:C:4:VAL:HG21	1:C:52:VAL:CG1	2.38	0.53
1:A:68:SER:HA	1:A:163:VAL:O	2.08	0.53
1:C:15:ASN:C	1:C:15:ASN:ND2	2.61	0.53
1:C:6:PHE:CZ	1:C:225:PHE:HB3	2.44	0.53
1:C:95:GLN:HA	1:C:95:GLN:NE2	2.24	0.53
1:D:15:ASN:HD22	1:D:16:PRO:CD	2.22	0.53
1:D:172:LYS:HE2	1:D:193:ASP:OD2	2.09	0.53
1:A:224:SER:HB3	5:A:253:HOH:O	2.08	0.52
1:D:64:SER:OG	1:D:169:SER:HB3	2.09	0.52
1:A:2:GLU:OE1	1:A:53:ARG:NH1	2.43	0.52
1:D:127:ASN:H	1:D:132:ASP:CB	2.21	0.52
1:C:123:ASP:OD2	1:C:132:ASP:OD2	2.27	0.52
1:C:40:VAL:O	1:C:41:ASN:CG	2.48	0.52
1:D:85:ILE:HG22	1:D:86:ILE:H	1.74	0.52
4:A:244:SFP:H17	4:A:245:SFP:C6C	2.40	0.52
1:C:182:ASN:N	1:C:182:ASN:HD22	2.08	0.52
1:A:130:TYR:O	1:A:131:ASN:HB2	2.09	0.52
1:A:32:ILE:HD13	1:A:46:VAL:HG21	1.92	0.52
1:B:25:THR:CG2	1:B:33:GLN:HB3	2.39	0.52
1:C:54:ILE:HG13	1:C:55:TRP:CD1	2.45	0.52
1:D:62:VAL:O	1:D:169:SER:HB2	2.10	0.52
1:D:27:LEU:C	1:D:29:ASN:H	2.13	0.52
1:A:123:ASP:OD2	1:A:132:ASP:OD2	2.28	0.52
1:B:130:TYR:O	1:B:131:ASN:HB2	2.09	0.52
1:C:20:PHE:CD1	1:C:46:VAL:HG23	2.45	0.52
1:D:54:ILE:HG13	1:D:55:TRP:CD1	2.45	0.52
1:A:193:ASP:HB3	1:A:196:ALA:HB3	1.92	0.51
1:A:70:SER:HA	1:A:161:VAL:O	2.10	0.51
1:D:123:ASP:OD2	1:D:132:ASP:OD2	2.29	0.51
1:D:231:THR:HG21	4:D:241:SFP:O11	2.10	0.51
1:A:25:THR:CG2	1:A:33:GLN:HB3	2.40	0.51
1:A:3:THR:HG23	1:A:227:SER:O	2.11	0.51
1:A:20:PHE:CE1	1:A:46:VAL:HG23	2.45	0.51
1:A:67:THR:HG21	1:A:87:PHE:CZ	2.45	0.51
1:B:212:LEU:HD23	1:B:212:LEU:O	2.10	0.51
1:C:127:ASN:H	1:C:132:ASP:CB	2.22	0.51
1:D:193:ASP:HB3	1:D:196:ALA:HB3	1.92	0.51

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:172:LYS:HE2	1:A:193:ASP:OD2	2.11	0.51
1:C:20:PHE:CE1	1:C:46:VAL:HG23	2.45	0.51
1:C:193:ASP:HB3	1:C:196:ALA:HB3	1.92	0.51
1:D:20:PHE:CE1	1:D:46:VAL:HG23	2.46	0.51
1:D:97:PRO:HG2	1:D:108:VAL:HA	1.92	0.51
1:C:109:SER:HB2	1:C:114:ALA:O	2.11	0.51
1:C:176:VAL:HG12	1:C:177:ALA:N	2.26	0.51
1:D:182:ASN:HD22	1:D:183:GLY:H	1.59	0.51
1:D:32:ILE:HD13	1:D:46:VAL:HG21	1.92	0.51
4:A:244:SFP:C3	4:A:244:SFP:C27	2.87	0.51
1:B:15:ASN:C	1:B:15:ASN:ND2	2.64	0.51
1:C:70:SER:HA	1:C:161:VAL:O	2.10	0.51
1:A:116:HIS:HA	1:A:143:ASN:OD1	2.11	0.51
1:C:94:THR:O	1:C:94:THR:HG23	2.10	0.51
1:D:3:THR:HG23	1:D:227:SER:O	2.10	0.51
4:B:237:SFP:H25	4:B:238:SFP:C7	2.41	0.50
1:D:58:ALA:HB2	4:D:242:SFP:C3	2.41	0.50
1:A:4:VAL:HG21	1:A:52:VAL:CG1	2.33	0.50
1:D:47:LEU:HD21	1:D:88:PHE:HZ	1.77	0.50
1:D:95:GLN:NE2	1:D:95:GLN:HA	2.27	0.50
1:C:3:THR:HG23	1:C:227:SER:O	2.11	0.50
1:A:178:VAL:HB	1:A:186:THR:HB	1.94	0.50
1:B:70:SER:HA	1:B:161:VAL:O	2.12	0.50
1:C:89:ILE:HG12	1:C:204:PHE:CE1	2.47	0.50
1:A:101:ILE:HG12	1:A:102:GLY:H	1.76	0.50
1:B:94:THR:HG23	1:B:94:THR:O	2.10	0.50
1:C:97:PRO:HG2	1:C:108:VAL:HA	1.93	0.50
1:C:68:SER:HA	1:C:163:VAL:O	2.12	0.50
1:C:74:LYS:HE2	1:D:10:SER:CB	2.38	0.50
1:C:182:ASN:ND2	1:C:183:GLY:N	2.60	0.49
1:D:20:PHE:CD1	1:D:46:VAL:HG23	2.47	0.49
1:A:182:ASN:HD22	1:A:183:GLY:H	1.59	0.49
1:B:3:THR:HG23	1:B:227:SER:O	2.13	0.49
1:B:54:ILE:HG13	1:B:55:TRP:CD1	2.46	0.49
1:C:101:ILE:HG12	1:C:102:GLY:H	1.77	0.49
1:B:182:ASN:ND2	1:B:183:GLY:N	2.60	0.49
1:D:109:SER:HB2	1:D:114:ALA:O	2.13	0.49
1:D:130:TYR:O	1:D:131:ASN:HB2	2.12	0.49
1:D:182:ASN:ND2	1:D:183:GLY:N	2.61	0.48
1:D:221:ARG:HH11	1:D:221:ARG:HG2	1.78	0.48
1:A:54:ILE:HG13	1:A:55:TRP:CD1	2.47	0.48

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:101:ILE:HG12	1:B:102:GLY:H	1.77	0.48
1:B:178:VAL:HB	1:B:186:THR:HB	1.95	0.48
1:A:97:PRO:HG2	1:A:108:VAL:HA	1.95	0.48
1:B:123:ASP:OD2	1:B:132:ASP:OD2	2.32	0.48
1:D:70:SER:HA	1:D:161:VAL:O	2.12	0.48
1:D:95:GLN:O	1:D:97:PRO:HD3	2.13	0.48
1:B:126:SER:HA	1:B:132:ASP:HB3	1.95	0.48
1:C:10:SER:CB	1:D:74:LYS:HE2	2.39	0.48
1:B:101:ILE:CG2	4:B:238:SFP:O9	2.60	0.48
1:B:95:GLN:HA	1:B:95:GLN:NE2	2.29	0.48
1:C:126:SER:HA	1:C:132:ASP:HB3	1.94	0.48
1:C:101:ILE:O	1:C:211:SER:CB	2.61	0.48
1:C:29:ASN:HA	1:D:217:ILE:HD13	1.93	0.48
1:C:43:VAL:HG21	1:C:99:GLY:HA2	1.95	0.48
1:A:221:ARG:HH11	1:A:221:ARG:HG2	1.78	0.48
1:C:217:ILE:HD13	1:D:29:ASN:HA	1.92	0.48
1:A:95:GLN:HA	1:A:95:GLN:NE2	2.29	0.48
1:D:37:LEU:HG	1:D:76:ILE:HD13	1.95	0.48
1:D:43:VAL:HG21	1:D:99:GLY:HA2	1.95	0.48
1:A:126:SER:HA	1:A:132:ASP:HB3	1.95	0.48
1:B:55:TRP:HB3	1:B:62:VAL:HG22	1.96	0.48
1:C:172:LYS:HD3	1:C:193:ASP:HA	1.96	0.48
1:C:25:THR:CG2	1:C:33:GLN:HB3	2.44	0.48
4:A:248:SFP:H30	4:A:249:SFP:H29	1.95	0.48
1:B:20:PHE:CE1	1:B:46:VAL:HG23	2.48	0.48
1:C:212:LEU:HD23	1:C:212:LEU:O	2.14	0.48
1:D:172:LYS:HD3	1:D:193:ASP:HA	1.96	0.47
1:A:20:PHE:CD1	1:A:46:VAL:HG23	2.49	0.47
1:D:47:LEU:HD21	1:D:88:PHE:CZ	2.49	0.47
1:A:64:SER:OG	1:A:169:SER:HB3	2.14	0.47
1:A:37:LEU:HG	1:A:76:ILE:HD13	1.96	0.47
1:B:37:LEU:HG	1:B:76:ILE:HD13	1.96	0.47
1:B:64:SER:OG	1:B:169:SER:HB3	2.13	0.47
1:B:67:THR:HG21	1:B:87:PHE:CZ	2.49	0.47
1:D:68:SER:HA	1:D:163:VAL:O	2.14	0.47
1:D:82:ALA:CB	1:D:83:ASP:HA	2.32	0.47
1:B:97:PRO:HG2	1:B:108:VAL:HA	1.97	0.47
1:D:126:SER:HA	1:D:132:ASP:HB3	1.95	0.47
1:A:141:ASP:OD2	1:A:145:VAL:HA	2.15	0.47
1:B:116:HIS:HA	1:B:143:ASN:OD1	2.14	0.47
1:B:15:ASN:HD22	1:B:16:PRO:CD	2.27	0.47

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:47:LEU:HD21	1:C:88:PHE:HZ	1.80	0.47
1:A:182:ASN:HD22	1:A:182:ASN:N	2.12	0.47
1:B:4:VAL:HG21	1:B:52:VAL:CG1	2.38	0.47
1:D:221:ARG:NH1	1:D:221:ARG:HG2	2.29	0.47
1:C:55:TRP:HB3	1:C:62:VAL:HG22	1.97	0.47
1:A:182:ASN:ND2	1:A:183:GLY:N	2.63	0.46
1:B:41:ASN:O	1:B:41:ASN:OD1	2.33	0.46
1:B:32:ILE:CD1	1:B:46:VAL:HG21	2.45	0.46
1:D:127:ASN:HB3	1:D:129:GLU:CD	2.35	0.46
1:A:221:ARG:NH1	1:A:221:ARG:HG2	2.31	0.46
1:C:172:LYS:HE2	1:C:193:ASP:OD2	2.15	0.46
1:B:86:ILE:O	1:B:206:PHE:HA	2.15	0.46
1:D:25:THR:CG2	1:D:33:GLN:HB3	2.46	0.46
1:A:101:ILE:HG21	4:A:249:SFP:O5	2.15	0.46
1:D:46:VAL:O	1:D:47:LEU:HD23	2.15	0.46
4:A:244:SFP:C23	4:A:244:SFP:H8	2.45	0.46
1:A:6:PHE:CZ	1:A:225:PHE:HB3	2.49	0.46
1:B:149:LYS:HG2	1:B:150:THR:N	2.31	0.46
1:B:141:ASP:OD2	1:B:145:VAL:HA	2.16	0.46
1:C:141:ASP:OD2	1:C:145:VAL:HA	2.16	0.46
1:C:106:LEU:HA	1:C:209:SER:OG	2.16	0.46
1:D:138:VAL:HG23	1:D:153:TRP:CB	2.44	0.46
1:D:141:ASP:OD2	1:D:145:VAL:HA	2.15	0.46
1:A:149:LYS:HG2	1:A:150:THR:N	2.31	0.46
1:A:27:LEU:C	1:A:29:ASN:H	2.19	0.46
1:C:231:THR:CG2	4:C:239:SFP:O2	2.64	0.46
1:C:62:VAL:O	1:C:169:SER:HB2	2.16	0.45
1:D:76:ILE:HG13	1:D:76:ILE:O	2.16	0.45
1:A:109:SER:HB2	1:A:114:ALA:O	2.16	0.45
1:C:82:ALA:CB	1:C:83:ASP:HA	2.37	0.45
1:D:231:THR:CG2	4:D:241:SFP:O11	2.64	0.45
1:C:76:ILE:O	1:C:76:ILE:HG13	2.17	0.45
1:A:69:PHE:CE1	1:A:163:VAL:HB	2.52	0.45
1:A:172:LYS:HD3	1:A:193:ASP:HA	1.98	0.45
1:B:2:GLU:OE1	1:B:53:ARG:NH1	2.50	0.45
1:C:82:ALA:O	1:C:216:GLN:HG2	2.17	0.45
1:C:130:TYR:O	1:C:131:ASN:HB2	2.16	0.45
1:A:101:ILE:O	1:A:211:SER:CB	2.64	0.45
1:B:101:ILE:O	1:B:211:SER:CB	2.64	0.45
1:B:182:ASN:HD22	1:B:182:ASN:N	2.15	0.44
1:B:85:ILE:CG2	1:B:86:ILE:N	2.78	0.44

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:53:ARG:NH2	4:D:241:SFP:S4	2.90	0.44
1:B:101:ILE:CG2	4:B:238:SFP:O8	2.66	0.44
1:C:86:ILE:CG2	1:C:207:SER:HB3	2.47	0.44
1:D:101:ILE:O	1:D:211:SER:CB	2.65	0.44
1:D:89:ILE:HG12	1:D:204:PHE:CE1	2.52	0.44
1:C:221:ARG:NH2	1:D:72:GLU:OE1	2.50	0.44
1:B:127:ASN:HB3	1:B:129:GLU:CD	2.38	0.44
1:B:221:ARG:HG2	1:B:221:ARG:HH11	1.81	0.44
1:C:47:LEU:HD21	1:C:88:PHE:CZ	2.53	0.44
1:C:221:ARG:HG2	1:C:221:ARG:HH11	1.83	0.44
1:A:41:ASN:O	1:A:41:ASN:OD1	2.35	0.44
1:B:67:THR:HG22	1:B:165:VAL:HB	2.00	0.44
1:B:147:SER:HB2	1:B:150:THR:CG2	2.48	0.44
1:B:221:ARG:NH1	1:B:221:ARG:HG2	2.33	0.44
1:C:10:SER:HA	1:D:74:LYS:HZ1	1.83	0.44
1:C:85:ILE:CG2	1:C:86:ILE:N	2.80	0.44
1:D:176:VAL:HG12	1:D:177:ALA:N	2.33	0.44
1:B:89:ILE:HG12	1:B:204:PHE:CE1	2.53	0.43
1:B:149:LYS:HE3	1:B:190:GLN:OE1	2.18	0.43
1:C:36:ASN:HB3	1:C:39:LYS:HG3	1.99	0.43
1:B:193:ASP:OD1	1:B:195:LYS:HB3	2.18	0.43
1:B:20:PHE:CD1	1:B:46:VAL:HG23	2.54	0.43
1:A:15:ASN:HD22	1:A:16:PRO:CD	2.31	0.43
1:C:58:ALA:HB2	4:C:240:SFP:C7	2.49	0.43
1:A:36:ASN:HB3	1:A:39:LYS:HG3	2.00	0.43
1:A:43:VAL:HG21	1:A:99:GLY:HA2	2.01	0.43
1:B:27:LEU:C	1:B:29:ASN:H	2.22	0.43
1:C:78:ASP:N	5:C:257:HOH:O	2.29	0.43
1:A:127:ASN:HB3	1:A:129:GLU:CD	2.38	0.43
1:A:95:GLN:O	1:A:97:PRO:HD3	2.18	0.43
1:C:127:ASN:HB3	1:C:129:GLU:CD	2.38	0.43
1:A:185:ILE:HG12	1:D:228:THR:OG1	2.18	0.43
1:B:76:ILE:O	1:B:76:ILE:HG13	2.18	0.43
4:A:248:SFP:C6A	4:A:249:SFP:H9	2.48	0.43
1:C:149:LYS:HG2	1:C:150:THR:N	2.33	0.43
1:A:138:VAL:HG23	1:A:153:TRP:CB	2.48	0.42
1:A:76:ILE:O	1:A:79:TYR:HB2	2.19	0.42
1:B:69:PHE:CE1	1:B:163:VAL:HB	2.54	0.42
1:C:79:TYR:CE1	1:C:215:ARG:HD2	2.55	0.42
1:C:37:LEU:HG	1:C:76:ILE:HD13	2.00	0.42
1:B:172:LYS:HD3	1:B:193:ASP:HA	2.00	0.42

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:82:ALA:O	1:D:216:GLN:HG2	2.19	0.42
1:B:36:ASN:HB3	1:B:39:LYS:HG3	2.01	0.42
1:D:86:ILE:O	1:D:206:PHE:HA	2.20	0.42
4:B:237:SFP:C4	4:B:238:SFP:H19	2.50	0.42
1:C:25:THR:O	1:C:25:THR:HG23	2.20	0.42
1:D:212:LEU:O	1:D:212:LEU:HD23	2.20	0.42
1:D:94:THR:O	1:D:94:THR:HG23	2.19	0.42
1:A:25:THR:CG2	5:A:267:HOH:O	2.68	0.42
1:A:85:ILE:CG2	1:A:86:ILE:N	2.81	0.42
1:C:74:LYS:HZ3	1:D:10:SER:HA	1.84	0.42
1:C:95:GLN:O	1:C:97:PRO:HD3	2.20	0.42
1:D:55:TRP:CD2	1:D:195:LYS:HG3	2.54	0.42
1:C:168:ASP:HB3	1:C:171:THR:OG1	2.19	0.42
1:B:211:SER:OG	1:B:214:GLY:N	2.52	0.41
1:B:225:PHE:C	1:B:225:PHE:CD1	2.93	0.41
1:C:116:HIS:HA	1:C:143:ASN:OD1	2.20	0.41
1:D:178:VAL:HB	1:D:186:THR:HB	2.01	0.41
1:A:106:LEU:HA	1:A:209:SER:OG	2.20	0.41
1:A:67:THR:HG22	1:A:165:VAL:HB	2.01	0.41
1:B:101:ILE:O	1:B:211:SER:HA	2.19	0.41
1:B:176:VAL:HG12	1:B:177:ALA:N	2.35	0.41
1:C:167:TYR:CE2	1:C:194:LEU:HD12	2.55	0.41
1:D:116:HIS:HA	1:D:143:ASN:OD1	2.20	0.41
1:B:95:GLN:O	1:B:97:PRO:HD3	2.20	0.41
1:C:149:LYS:HE3	1:C:190:GLN:OE1	2.20	0.41
1:D:149:LYS:HE3	1:D:190:GLN:OE1	2.21	0.41
1:D:79:TYR:CE1	1:D:215:ARG:HD2	2.56	0.41
1:A:101:ILE:HG23	4:A:249:SFP:O5	2.20	0.41
1:C:221:ARG:HG2	1:C:221:ARG:NH1	2.35	0.41
1:B:168:ASP:HB3	1:B:171:THR:OG1	2.21	0.41
1:B:76:ILE:O	1:B:79:TYR:HB2	2.21	0.41
1:D:101:ILE:O	1:D:102:GLY:C	2.57	0.41
1:D:86:ILE:CG2	1:D:207:SER:HB3	2.50	0.41
1:D:31:ASN:HA	1:D:31:ASN:HD22	1.69	0.41
1:B:138:VAL:HG23	1:B:153:TRP:CB	2.49	0.41
1:B:193:ASP:HB3	1:B:196:ALA:CB	2.51	0.41
1:A:101:ILE:O	1:A:102:GLY:C	2.56	0.41
4:B:237:SFP:C8C	4:B:238:SFP:H9	2.51	0.41
1:C:12:SER:HA	1:C:26:VAL:HG11	2.03	0.41
1:C:55:TRP:CD2	1:C:195:LYS:HG3	2.56	0.41
1:D:69:PHE:CE1	1:D:163:VAL:HB	2.55	0.41

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:76:ILE:HG13	1:D:79:TYR:HB2	2.03	0.41
1:C:101:ILE:O	1:C:102:GLY:C	2.57	0.41
1:C:101:ILE:O	1:C:211:SER:HA	2.21	0.41
1:D:194:LEU:HA	1:D:194:LEU:HD23	1.86	0.41
1:A:29:ASN:ND2	4:A:245:SFP:O9	2.55	0.40
1:C:96:ILE:O	1:C:96:ILE:HG23	2.21	0.40
1:D:225:PHE:CD1	1:D:226:THR:N	2.89	0.40
1:A:86:ILE:O	1:A:206:PHE:HA	2.21	0.40
1:A:76:ILE:HG13	1:A:76:ILE:O	2.21	0.40
1:C:138:VAL:HG23	1:C:153:TRP:CB	2.50	0.40
1:D:12:SER:HA	1:D:26:VAL:HG11	2.03	0.40
1:B:50:MET:HA	1:B:51:PRO:HD3	1.97	0.40
1:D:106:LEU:HA	1:D:209:SER:OG	2.22	0.40
1:D:85:ILE:CG2	1:D:86:ILE:N	2.83	0.40
1:A:193:ASP:OD1	1:A:195:LYS:HB3	2.21	0.40
1:A:212:LEU:C	1:A:212:LEU:CD2	2.90	0.40
1:B:127:ASN:OD1	1:B:127:ASN:N	2.54	0.40
1:C:31:ASN:HD22	1:C:31:ASN:HA	1.73	0.40
1:C:41:ASN:O	1:C:43:VAL:HG23	2.21	0.40
4:D:241:SFP:H30	4:D:242:SFP:H27	2.04	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	230/236 (98%)	203 (88%)	24 (10%)	3 (1%)	14	43
1	B	230/236 (98%)	204 (89%)	22 (10%)	4 (2%)	11	36
1	C	230/236 (98%)	203 (88%)	24 (10%)	3 (1%)	14	43
1	D	230/236 (98%)	202 (88%)	25 (11%)	3 (1%)	14	43
All	All	920/944 (98%)	812 (88%)	95 (10%)	13 (1%)	13	41

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	103	GLY
1	B	103	GLY
1	C	103	GLY
1	D	103	GLY
1	D	28	SER
1	A	28	SER
1	C	28	SER
1	A	77	LYS
1	B	28	SER
1	B	77	LYS
1	C	77	LYS
1	D	77	LYS
1	B	97	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	197/201 (98%)	186 (94%)	11 (6%)	25	57
1	B	197/201 (98%)	187 (95%)	10 (5%)	28	62
1	C	197/201 (98%)	187 (95%)	10 (5%)	28	62
1	D	197/201 (98%)	186 (94%)	11 (6%)	25	57
All	All	788/804 (98%)	746 (95%)	42 (5%)	26	60

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	ASN
1	A	37	LEU
1	A	53	ARG
1	A	101	ILE
1	A	111	THR
1	A	127	ASN
1	A	132	ASP

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	136	ASP
1	A	141	ASP
1	A	182	ASN
1	A	212	LEU
1	B	15	ASN
1	B	37	LEU
1	B	53	ARG
1	B	101	ILE
1	B	111	THR
1	B	127	ASN
1	B	132	ASP
1	B	136	ASP
1	B	141	ASP
1	B	182	ASN
1	C	15	ASN
1	C	37	LEU
1	C	53	ARG
1	C	101	ILE
1	C	111	THR
1	C	127	ASN
1	C	132	ASP
1	C	136	ASP
1	C	141	ASP
1	C	182	ASN
1	D	15	ASN
1	D	37	LEU
1	D	53	ARG
1	D	101	ILE
1	D	111	THR
1	D	127	ASN
1	D	132	ASP
1	D	136	ASP
1	D	141	ASP
1	D	182	ASN
1	D	212	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	15	ASN
1	A	19	ASN
1	A	33	GLN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	61	ASN
1	A	95	GLN
1	A	182	ASN
1	A	216	GLN
1	B	15	ASN
1	B	19	ASN
1	B	33	GLN
1	B	61	ASN
1	B	95	GLN
1	B	182	ASN
1	B	216	GLN
1	C	15	ASN
1	C	19	ASN
1	C	33	GLN
1	C	61	ASN
1	C	95	GLN
1	C	182	ASN
1	C	216	GLN
1	D	15	ASN
1	D	19	ASN
1	D	33	GLN
1	D	61	ASN
1	D	95	GLN
1	D	182	ASN
1	D	216	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

Of 19 ligands modelled in this entry, 8 are monoatomic - leaving 11 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
4	SFP	A	244	-	52,72,72	3.12	18 (34%)	62,112,112	1.58	12 (19%)
4	SFP	A	245	-	52,72,72	2.61	16 (30%)	62,112,112	1.24	6 (9%)
4	SFP	A	248	-	52,72,72	2.57	16 (30%)	62,112,112	1.32	9 (14%)
4	SFP	A	249	-	52,72,72	2.65	16 (30%)	62,112,112	1.31	7 (11%)
4	SFP	B	237	-	52,72,72	2.54	16 (30%)	62,112,112	1.24	5 (8%)
4	SFP	B	238	-	52,72,72	2.69	18 (34%)	62,112,112	1.45	10 (16%)
4	SFP	B	243	-	52,72,72	2.36	14 (26%)	62,112,112	1.23	6 (9%)
4	SFP	C	239	-	52,72,72	2.66	17 (32%)	62,112,112	1.27	8 (12%)
4	SFP	C	240	-	52,72,72	2.51	15 (28%)	62,112,112	1.34	6 (9%)
4	SFP	D	241	-	52,72,72	2.71	17 (32%)	62,112,112	1.31	7 (11%)
4	SFP	D	242	-	52,72,72	2.59	16 (30%)	62,112,112	1.46	4 (6%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	SFP	A	244	-	-	0/36/90/90	0/4/9/9
4	SFP	A	245	-	-	0/36/90/90	0/4/9/9
4	SFP	A	248	-	-	0/36/90/90	0/4/9/9
4	SFP	A	249	-	-	0/36/90/90	0/4/9/9
4	SFP	B	237	-	-	0/36/90/90	0/4/9/9
4	SFP	B	238	-	-	0/36/90/90	0/4/9/9
4	SFP	B	243	-	-	0/36/90/90	0/4/9/9
4	SFP	C	239	-	-	0/36/90/90	0/4/9/9
4	SFP	C	240	-	-	0/36/90/90	0/4/9/9
4	SFP	D	241	-	-	0/36/90/90	0/4/9/9
4	SFP	D	242	-	-	0/36/90/90	0/4/9/9



All (179) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	238	SFP	C7-C8C	-2.57	1.39	1.45
4	B	238	SFP	C8-C8A	-2.33	1.40	1.45
4	A	244	SFP	C8-C7	-2.30	1.30	1.35
4	A	248	SFP	C8-C8A	-2.22	1.40	1.45
4	B	243	SFP	C8-C8A	-2.03	1.40	1.45
4	B	238	SFP	C4C-N4B	2.03	1.41	1.36
4	D	242	SFP	C4C-N4B	2.05	1.41	1.36
4	D	242	SFP	C30-C29	2.06	1.42	1.38
4	A	249	SFP	C4C-N4B	2.07	1.41	1.36
4	C	239	SFP	C4C-N4B	2.13	1.41	1.36
4	B	237	SFP	C14-C13	2.28	1.42	1.38
4	A	248	SFP	C30-C29	2.29	1.42	1.38
4	D	241	SFP	C8A-N8B	2.32	1.42	1.36
4	A	244	SFP	C8A-N8B	2.32	1.42	1.36
4	A	249	SFP	C30-C29	2.33	1.42	1.38
4	A	244	SFP	C4A-N4B	2.38	1.43	1.38
4	B	237	SFP	C32-C27	2.43	1.43	1.38
4	A	245	SFP	C13-C12	2.47	1.43	1.39
4	B	238	SFP	C30-C29	2.47	1.43	1.38
4	A	244	SFP	C4C-N4B	2.47	1.42	1.36
4	C	240	SFP	C32-C27	2.56	1.43	1.38
4	C	239	SFP	C13-C12	2.57	1.43	1.39
4	A	249	SFP	C14-C13	2.62	1.43	1.38
4	D	241	SFP	C30-C29	2.62	1.43	1.38
4	A	245	SFP	C30-C29	2.64	1.43	1.38
4	A	248	SFP	C29-C28	2.71	1.43	1.39
4	C	239	SFP	C14-C13	2.76	1.43	1.38
4	A	245	SFP	C11-C10	2.76	1.43	1.38
4	C	239	SFP	C30-C29	2.82	1.43	1.38
4	B	243	SFP	C13-C12	2.84	1.44	1.39
4	B	238	SFP	C14-C13	2.86	1.43	1.38
4	C	240	SFP	C13-C12	2.89	1.44	1.39
4	C	240	SFP	C20-CB	2.90	1.54	1.49
4	A	248	SFP	C13-C12	3.07	1.44	1.39
4	A	249	SFP	CC-C8C	3.13	1.42	1.37
4	A	245	SFP	CB-C4A	3.16	1.42	1.37
4	C	240	SFP	C27-C28	3.20	1.44	1.39
4	B	237	SFP	C27-C28	3.25	1.44	1.39
4	A	248	SFP	CC-C8C	3.26	1.42	1.37
4	A	245	SFP	C20-CB	3.30	1.54	1.49
4	D	241	SFP	C14-C13	3.35	1.44	1.38
4	C	240	SFP	CC-C8C	3.36	1.42	1.37

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	243	SFP	C20-CB	3.43	1.55	1.49
4	B	243	SFP	C24-CD	3.44	1.55	1.49
4	B	243	SFP	CB-C4A	3.45	1.43	1.37
4	A	245	SFP	C25-C24	3.49	1.45	1.39
4	A	249	SFP	C29-C28	3.50	1.45	1.39
4	D	241	SFP	C29-C28	3.56	1.45	1.39
4	D	242	SFP	C14-C13	3.56	1.45	1.38
4	B	238	SFP	CB-C4A	3.58	1.43	1.37
4	A	245	SFP	C15-C20	3.65	1.45	1.39
4	C	239	SFP	CC-C8C	3.68	1.43	1.37
4	B	237	SFP	C13-C12	3.70	1.45	1.39
4	A	249	SFP	CB-C4A	3.78	1.43	1.37
4	D	241	SFP	C13-C12	3.78	1.45	1.39
4	A	244	SFP	C25-C24	3.78	1.45	1.39
4	B	243	SFP	C29-C28	3.85	1.45	1.39
4	B	238	SFP	CC-C8C	3.86	1.43	1.37
4	B	238	SFP	C29-C28	3.87	1.45	1.39
4	D	242	SFP	C29-C28	3.87	1.45	1.39
4	B	243	SFP	CC-C8C	3.88	1.43	1.37
4	B	238	SFP	C19-C20	3.88	1.45	1.39
4	D	242	SFP	C19-C20	3.88	1.45	1.39
4	A	244	SFP	C13-C12	3.89	1.45	1.39
4	C	239	SFP	C20-CB	3.89	1.55	1.49
4	C	240	SFP	C25-C24	3.90	1.45	1.39
4	A	244	SFP	C19-C20	3.92	1.45	1.39
4	B	237	SFP	C15-C20	3.92	1.45	1.39
4	B	237	SFP	CC-C8C	3.93	1.43	1.37
4	D	242	SFP	CC-C8C	3.98	1.43	1.37
4	B	238	SFP	C20-CB	3.99	1.55	1.49
4	B	237	SFP	C25-C24	4.03	1.46	1.39
4	C	239	SFP	C27-C28	4.04	1.46	1.39
4	C	240	SFP	C19-C20	4.05	1.46	1.39
4	A	245	SFP	C27-C28	4.07	1.46	1.39
4	A	248	SFP	C15-C20	4.10	1.46	1.39
4	B	243	SFP	C15-C20	4.12	1.46	1.39
4	D	241	SFP	C15-C20	4.15	1.46	1.39
4	B	237	SFP	C29-C28	4.16	1.46	1.39
4	A	244	SFP	CC-C8C	4.21	1.44	1.37
4	C	240	SFP	C15-C20	4.22	1.46	1.39
4	C	240	SFP	C12-CC	4.23	1.56	1.49
4	B	238	SFP	C15-C20	4.26	1.46	1.39
4	A	245	SFP	C29-C28	4.28	1.46	1.39

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	241	SFP	C20-CB	4.30	1.56	1.49
4	D	242	SFP	C27-C28	4.31	1.46	1.39
4	B	243	SFP	C12-CC	4.33	1.56	1.49
4	B	237	SFP	C19-C20	4.37	1.46	1.39
4	A	248	SFP	C25-C24	4.38	1.46	1.39
4	D	241	SFP	C27-C28	4.40	1.46	1.39
4	B	243	SFP	C23-C24	4.43	1.46	1.39
4	C	239	SFP	C19-C20	4.43	1.46	1.39
4	C	239	SFP	C15-C20	4.45	1.46	1.39
4	B	237	SFP	C23-C24	4.47	1.46	1.39
4	D	241	SFP	C19-C20	4.48	1.46	1.39
4	D	242	SFP	C23-C24	4.49	1.46	1.39
4	B	237	SFP	C20-CB	4.49	1.56	1.49
4	A	248	SFP	C12-CC	4.53	1.56	1.49
4	A	249	SFP	C15-C20	4.54	1.46	1.39
4	C	239	SFP	C29-C28	4.54	1.46	1.39
4	A	248	SFP	C27-C28	4.54	1.46	1.39
4	D	242	SFP	C24-CD	4.55	1.56	1.49
4	A	249	SFP	C27-C28	4.55	1.46	1.39
4	A	248	SFP	C23-C24	4.55	1.46	1.39
4	B	238	SFP	C25-C24	4.57	1.46	1.39
4	D	242	SFP	CB-C4A	4.64	1.44	1.37
4	B	243	SFP	C19-C20	4.68	1.47	1.39
4	A	249	SFP	C23-C24	4.73	1.47	1.39
4	A	249	SFP	C25-C24	4.73	1.47	1.39
4	B	237	SFP	C12-CC	4.75	1.57	1.49
4	A	248	SFP	C20-CB	4.75	1.57	1.49
4	C	239	SFP	C12-CC	4.76	1.57	1.49
4	B	237	SFP	CB-C4A	4.77	1.45	1.37
4	B	238	SFP	C27-C28	4.81	1.47	1.39
4	D	241	SFP	CB-C4A	4.81	1.45	1.37
4	D	242	SFP	C25-C24	4.82	1.47	1.39
4	A	248	SFP	C19-C20	4.82	1.47	1.39
4	A	244	SFP	C30-C29	4.83	1.47	1.38
4	C	239	SFP	C23-C24	4.83	1.47	1.39
4	D	242	SFP	C12-CC	4.87	1.57	1.49
4	A	245	SFP	CC-C8C	4.88	1.45	1.37
4	A	244	SFP	C20-CB	4.94	1.57	1.49
4	A	245	SFP	C19-C20	4.98	1.47	1.39
4	C	240	SFP	C11-C12	4.98	1.47	1.39
4	D	241	SFP	C23-C24	4.99	1.47	1.39
4	A	249	SFP	C19-C20	5.01	1.47	1.39

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	241	SFP	C11-C12	5.02	1.47	1.39
4	A	249	SFP	C24-CD	5.03	1.57	1.49
4	D	241	SFP	C28-CA	5.04	1.57	1.49
4	B	238	SFP	C28-CA	5.05	1.57	1.49
4	C	240	SFP	C29-C28	5.05	1.47	1.39
4	C	239	SFP	C11-C12	5.06	1.47	1.39
4	A	244	SFP	C23-C24	5.08	1.47	1.39
4	D	242	SFP	C20-CB	5.08	1.57	1.49
4	D	242	SFP	C15-C20	5.09	1.47	1.39
4	A	244	SFP	C29-C28	5.10	1.47	1.39
4	B	243	SFP	C27-C28	5.10	1.47	1.39
4	A	248	SFP	C24-CD	5.13	1.57	1.49
4	C	239	SFP	C25-C24	5.15	1.47	1.39
4	B	243	SFP	C11-C12	5.15	1.47	1.39
4	A	244	SFP	CB-C4A	5.18	1.45	1.37
4	D	242	SFP	C11-C12	5.20	1.47	1.39
4	D	241	SFP	C25-C24	5.24	1.48	1.39
4	C	240	SFP	C24-CD	5.24	1.57	1.49
4	C	240	SFP	C23-C24	5.24	1.48	1.39
4	A	244	SFP	C12-CC	5.27	1.58	1.49
4	A	244	SFP	C11-C12	5.30	1.48	1.39
4	B	237	SFP	C11-C12	5.32	1.48	1.39
4	D	241	SFP	CC-C8C	5.33	1.45	1.37
4	B	238	SFP	C23-C24	5.33	1.48	1.39
4	A	244	SFP	C27-C28	5.34	1.48	1.39
4	A	248	SFP	C11-C12	5.37	1.48	1.39
4	C	239	SFP	CB-C4A	5.42	1.46	1.37
4	B	237	SFP	C24-CD	5.43	1.58	1.49
4	A	245	SFP	C23-C24	5.44	1.48	1.39
4	A	249	SFP	C12-CC	5.46	1.58	1.49
4	C	239	SFP	C24-CD	5.47	1.58	1.49
4	A	245	SFP	C11-C12	5.50	1.48	1.39
4	D	242	SFP	C28-CA	5.53	1.58	1.49
4	B	238	SFP	C12-CC	5.53	1.58	1.49
4	A	248	SFP	C28-CA	5.54	1.58	1.49
4	A	245	SFP	C12-CC	5.65	1.58	1.49
4	C	240	SFP	CB-C4A	5.65	1.46	1.37
4	A	245	SFP	C28-CA	5.67	1.58	1.49
4	A	249	SFP	C28-CA	5.67	1.58	1.49
4	B	237	SFP	C28-CA	5.67	1.58	1.49
4	D	241	SFP	C24-CD	5.70	1.58	1.49
4	A	248	SFP	CB-C4A	5.81	1.46	1.37

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	243	SFP	C28-CA	5.91	1.59	1.49
4	D	241	SFP	C12-CC	5.96	1.59	1.49
4	A	245	SFP	C24-CD	5.97	1.59	1.49
4	B	238	SFP	C11-C12	6.09	1.49	1.39
4	A	249	SFP	C11-C12	6.16	1.49	1.39
4	C	239	SFP	C28-CA	6.27	1.59	1.49
4	A	249	SFP	C20-CB	6.29	1.59	1.49
4	C	240	SFP	C28-CA	6.34	1.59	1.49
4	B	238	SFP	C24-CD	7.38	1.61	1.49
4	A	244	SFP	C24-CD	8.57	1.63	1.49
4	A	244	SFP	C28-CA	9.81	1.65	1.49

All (80) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	242	SFP	C11-C12-CC	-5.52	112.89	120.91
4	A	244	SFP	C27-C28-CA	-4.30	114.66	120.91
4	B	238	SFP	C27-C28-CA	-4.26	114.72	120.91
4	A	249	SFP	C27-C28-CA	-4.02	115.06	120.91
4	A	249	SFP	C11-C12-CC	-3.65	115.61	120.91
4	B	243	SFP	C23-C24-CD	-3.35	116.04	120.91
4	B	238	SFP	C11-C12-CC	-3.30	116.11	120.91
4	B	237	SFP	C11-C12-CC	-3.23	116.22	120.91
4	D	241	SFP	C27-C28-CA	-3.21	116.24	120.91
4	C	240	SFP	C29-C28-CA	-3.17	116.30	120.91
4	A	248	SFP	C27-C28-CA	-3.02	116.53	120.91
4	C	239	SFP	C11-C12-CC	-2.93	116.66	120.91
4	A	248	SFP	C19-C20-CB	-2.86	116.75	120.91
4	D	242	SFP	C14-C13-C12	-2.83	117.62	120.79
4	D	241	SFP	C2C-CD-C24	-2.76	113.25	121.34
4	C	239	SFP	C19-C20-CB	-2.74	116.93	120.91
4	D	241	SFP	C11-C12-CC	-2.61	117.11	120.91
4	A	245	SFP	C23-C24-CD	-2.53	117.23	120.91
4	C	240	SFP	C23-C24-CD	-2.53	117.23	120.91
4	A	248	SFP	C12-CC-C8C	-2.50	114.84	121.97
4	B	238	SFP	C19-C20-CB	-2.44	117.36	120.91
4	A	245	SFP	C20-CB-C4A	-2.41	115.10	121.97
4	A	244	SFP	C30-C29-C28	-2.40	118.10	120.79
4	B	237	SFP	C14-C13-C12	-2.33	118.18	120.79
4	A	244	SFP	C12-CC-C8C	-2.32	115.38	121.97
4	B	237	SFP	C19-C20-CB	-2.31	117.56	120.91
4	A	244	SFP	C20-CB-C4A	-2.27	115.49	121.97

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	238	SFP	C23-C24-CD	-2.27	117.61	120.91
4	A	248	SFP	C23-C24-CD	-2.23	117.67	120.91
4	C	240	SFP	C2A-CA-C28	-2.20	114.88	121.34
4	C	239	SFP	C16-C15-C20	-2.17	118.36	120.79
4	C	239	SFP	C2A-CA-C28	-2.17	114.98	121.34
4	B	243	SFP	C2C-CD-C24	-2.17	114.99	121.34
4	A	248	SFP	C2A-CA-C28	-2.16	115.00	121.34
4	A	244	SFP	C19-C20-CB	-2.13	117.82	120.91
4	C	240	SFP	C12-CC-C8C	-2.10	116.00	121.97
4	B	243	SFP	C20-CB-C4A	-2.10	116.00	121.97
4	D	241	SFP	C20-CB-C4A	-2.07	116.06	121.97
4	C	239	SFP	C12-CC-C8C	-2.06	116.11	121.97
4	D	241	SFP	C30-C29-C28	-2.05	118.50	120.79
4	D	241	SFP	C14-C13-C12	-2.04	118.51	120.79
4	B	238	SFP	C30-C29-C28	-2.03	118.52	120.79
4	A	249	SFP	C12-CC-C8C	-2.03	116.19	121.97
4	A	245	SFP	C27-C28-CA	-2.03	117.96	120.91
4	C	239	SFP	C27-C28-CA	-2.00	118.00	120.91
4	A	249	SFP	C3-C4-C4A	2.04	109.69	107.05
4	A	248	SFP	C15-C20-CB	2.06	123.90	120.91
4	B	237	SFP	C1-C2-C2A	2.10	109.03	107.37
4	A	245	SFP	C7-C8-C8A	2.11	109.78	107.05
4	A	248	SFP	C1-C2-C2A	2.12	109.04	107.37
4	D	242	SFP	C2-C1-C2C	2.12	109.05	107.37
4	B	243	SFP	C1-C2-C2A	2.16	109.07	107.37
4	A	248	SFP	C29-C28-CA	2.17	124.07	120.91
4	A	244	SFP	C15-C20-CB	2.17	124.07	120.91
4	B	237	SFP	C2-C1-C2C	2.18	109.09	107.37
4	A	245	SFP	C25-C24-CD	2.18	124.08	120.91
4	C	239	SFP	C1-C2-C2A	2.21	109.12	107.37
4	B	238	SFP	C25-C24-CD	2.27	124.21	120.91
4	B	238	SFP	C2-C1-C2C	2.37	109.25	107.37
4	A	244	SFP	C7-C8-C8A	2.44	110.21	107.05
4	C	239	SFP	C2-C1-C2C	2.45	109.31	107.37
4	B	243	SFP	C25-C24-CD	2.45	124.47	120.91
4	A	244	SFP	C2-C1-C2C	2.47	109.33	107.37
4	B	243	SFP	C2-C1-C2C	2.56	109.40	107.37
4	A	248	SFP	C2-C1-C2C	2.63	109.45	107.37
4	A	249	SFP	C2-C1-C2C	2.66	109.47	107.37
4	C	240	SFP	C27-C28-CA	2.72	124.86	120.91
4	B	238	SFP	C29-C28-CA	2.80	124.98	120.91
4	A	244	SFP	C4-C3-C4C	2.81	110.68	107.05

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	238	SFP	C7-C8-C8A	2.92	110.83	107.05
4	A	249	SFP	C29-C28-CA	2.98	125.25	120.91
4	B	238	SFP	C13-C12-CC	3.00	125.27	120.91
4	A	244	SFP	C1-C2-C2A	3.03	109.77	107.37
4	D	241	SFP	C2-C1-C2C	3.05	109.78	107.37
4	A	244	SFP	C32-C27-C28	3.10	124.26	120.79
4	C	240	SFP	C1-C2-C2A	3.19	109.89	107.37
4	A	249	SFP	C13-C12-CC	3.22	125.59	120.91
4	A	245	SFP	C2-C1-C2C	3.50	110.14	107.37
4	D	242	SFP	C13-C12-CC	4.88	128.01	120.91
4	A	244	SFP	C29-C28-CA	5.09	128.31	120.91

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

11 monomers are involved in 42 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	244	SFP	9	0
4	A	245	SFP	6	0
4	A	248	SFP	2	0
4	A	249	SFP	9	0
4	B	237	SFP	3	0
4	B	238	SFP	7	0
4	B	243	SFP	1	0
4	C	239	SFP	5	0
4	C	240	SFP	4	0
4	D	241	SFP	7	0
4	D	242	SFP	3	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	232/236 (98%)	-0.41	0	100 100	19, 47, 90, 165	0
1	B	232/236 (98%)	-0.41	0	100 100	12, 47, 92, 155	0
1	C	232/236 (98%)	-0.30	0	100 100	29, 70, 130, 177	0
1	D	232/236 (98%)	-0.27	2 (0%)	84 83	23, 69, 128, 176	0
All	All	928/944 (98%)	-0.35	2 (0%)	94 95	12, 57, 115, 177	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	97	PRO	2.7
1	D	37	LEU	2.2

### 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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
4	SFP	D	241	64/64	0.86	0.21	1.46	144,153,164,166	0
4	SFP	A	244	64/64	0.92	0.16	0.56	106,114,126,128	0
4	SFP	C	239	64/64	0.91	0.18	0.28	132,140,152,154	0
4	SFP	D	242	64/64	0.95	0.15	-0.07	99,107,119,121	0
4	SFP	A	248	64/64	0.97	0.16	-0.10	75,83,95,97	0
2	CA	D	248	1/1	1.00	0.14	-0.10	28,28,28,28	0
4	SFP	A	245	64/64	0.96	0.16	-0.15	70,78,90,92	0
4	SFP	B	243	64/64	0.97	0.15	-0.21	73,81,93,95	0
4	SFP	C	240	64/64	0.96	0.15	-0.21	86,94,106,108	0
4	SFP	A	249	64/64	0.97	0.17	-0.24	65,74,85,87	0
4	SFP	B	238	64/64	0.96	0.16	-0.33	72,81,92,94	0
2	CA	A	246	1/1	1.00	0.13	-0.45	20,20,20,20	0
4	SFP	B	237	64/64	0.96	0.14	-0.52	76,84,96,98	0
2	CA	C	252	1/1	0.99	0.11	-0.91	31,31,31,31	0
3	MN	C	253	1/1	1.00	0.12	-1.20	51,51,51,51	0
3	MN	D	249	1/1	1.00	0.12	-1.28	54,54,54,54	0
2	CA	B	250	1/1	1.00	0.12	-2.10	19,19,19,19	0
3	MN	B	251	1/1	1.00	0.10	-2.17	48,48,48,48	0
3	MN	A	247	1/1	1.00	0.10	-3.53	51,51,51,51	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.