



# Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 10:08 am BST

PDB ID : 4HDA  
Title : Crystal structure of human Sirt5 in complex with Fluor-de-Lys peptide and resveratrol  
Authors : Gertz, M.; Steegborn, C.  
Deposited on : 2012-10-02  
Resolution : 2.60 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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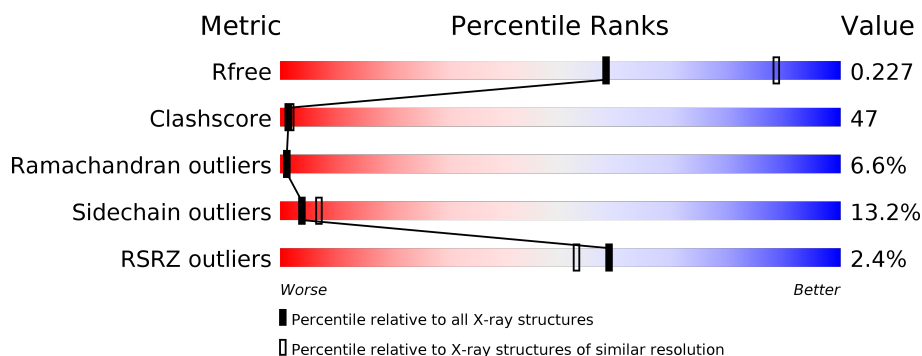
The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

i

## X-RAY DIFFRACTION

A.



<b>Metric</b>	<b>Whole archive (#Entries)</b>	<b>Similar resolution (#Entries, resolution range(Å))</b>
$R_{free}$	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

Mol	Chain	Length	Quality of chain
1	A	275	<div> <div> <div></div> <div>3%</div> </div> <div> <div></div> <div>40%</div> </div> <div> <div></div> <div>47%</div> </div> <div> <div></div> <div>10%</div> </div> <div> <div></div> <div>• •</div> </div> </div>
1	B	275	<div> <div> <div></div> <div>2%</div> </div> <div> <div></div> <div>37%</div> </div> <div> <div></div> <div>50%</div> </div> <div> <div></div> <div>9%</div> </div> <div> <div></div> <div>• •</div> </div> </div>
2	F	4	<div> <div> <div></div> <div>50%</div> </div> <div> <div></div> <div>25%</div> </div> <div> <div></div> <div>25%</div> </div> </div>

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	FDL	F	4	-	-	X	-

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4189 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 NAD-dependent protein deacylase sirtuin-5, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	267	Total	C	N	O	S	0	0	0
			2047	1291	373	371	12			
1	B	270	Total	C	N	O	S	0	0	0
			2064	1301	376	375	12			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	28	GLY	-	EXPRESSION TAG	UNP Q9NXA8
A	29	ILE	-	EXPRESSION TAG	UNP Q9NXA8
A	30	ASP	-	EXPRESSION TAG	UNP Q9NXA8
A	31	PRO	-	EXPRESSION TAG	UNP Q9NXA8
A	32	PHE	-	EXPRESSION TAG	UNP Q9NXA8
A	33	THR	-	EXPRESSION TAG	UNP Q9NXA8
B	28	GLY	-	EXPRESSION TAG	UNP Q9NXA8
B	29	ILE	-	EXPRESSION TAG	UNP Q9NXA8
B	30	ASP	-	EXPRESSION TAG	UNP Q9NXA8
B	31	PRO	-	EXPRESSION TAG	UNP Q9NXA8
B	32	PHE	-	EXPRESSION TAG	UNP Q9NXA8
B	33	THR	-	EXPRESSION TAG	UNP Q9NXA8

- Molecule 2 is a protein called Fluor-de-Lys peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	F	3	Total	C	N	O	0	0	0
			44	30	8	6			

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

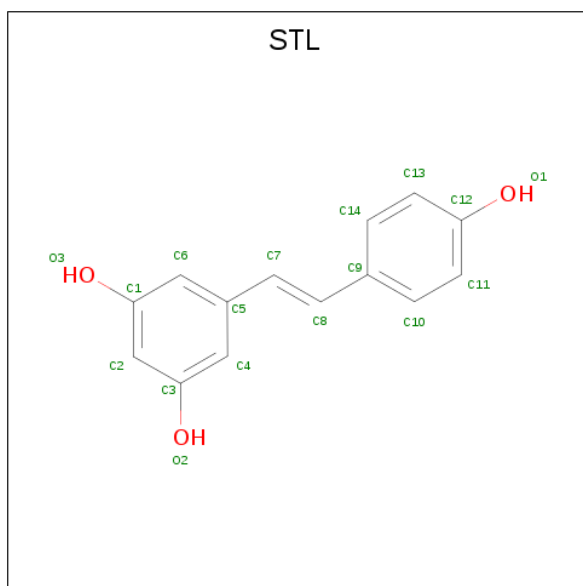
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Zn	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		

- Molecule 4 is RESVERATROL (three-letter code: STL) (formula:  $C_{14}H_{12}O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			17	14	3		

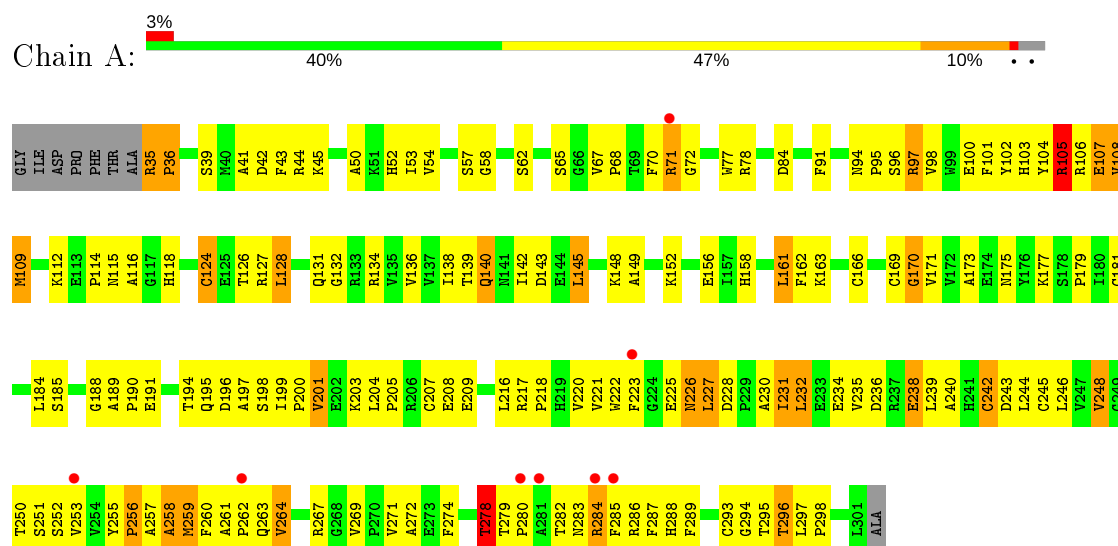
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	10	Total	O	0	0
			10	10		
5	B	5	Total	O	0	0
			5	5		

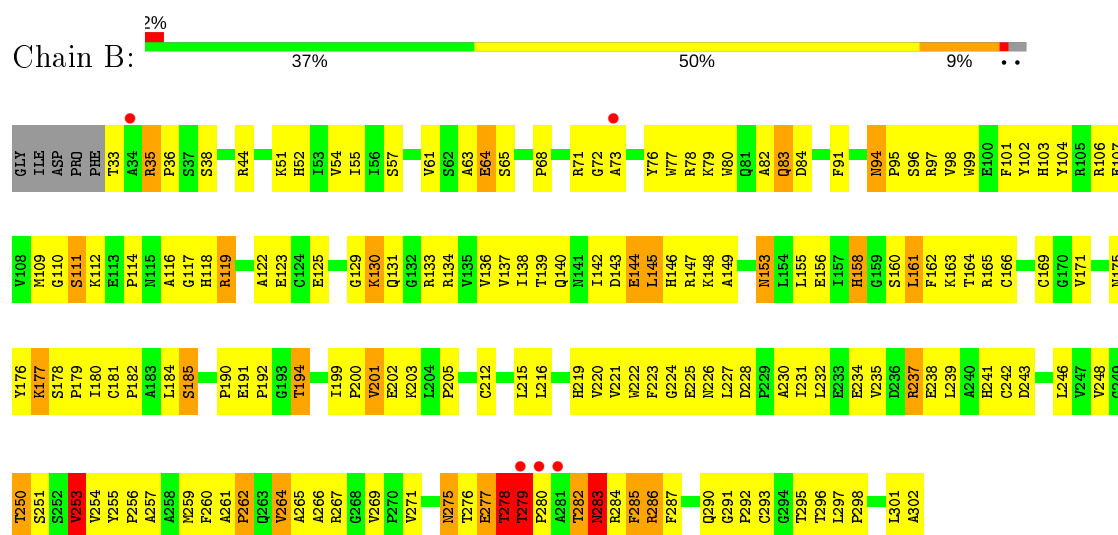
### 3 Residue-property plots

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: NAD-dependent protein deacylase sirtuin-5, mitochondrial



- Molecule 1: NAD-dependent protein deacylase sirtuin-5, mitochondrial



- Molecule 2: Fluor-de-Lys peptide





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	41.30Å 112.69Å 55.89Å 90.00° 90.05° 90.00°	Depositor
Resolution (Å)	38.78 – 2.60 38.78 – 2.60	Depositor EDS
% Data completeness (in resolution range)	97.7 (38.78-2.60) 92.4 (38.78-2.60)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.66 (at 2.61Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, $R_{free}$	0.199 , 0.252 0.177 , 0.227	Depositor DCC
$R_{free}$ test set	760 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	34.1	Xtriage
Anisotropy	0.650	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 21.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.42$ , $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	0.448 for h,-k,-l	Xtriage
Reported twinning fraction	0.521 for h,-k,-l	Depositor
Outliers	0 of 15353 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	4189	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.60% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: STL, ZN, FDL

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	0.33	0/2100	0.59	0/2850
1	B	0.31	0/2117	0.62	0/2874
2	F	0.50	0/19	0.63	0/23
All	All	0.32	0/4236	0.61	0/5747

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

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	2047	0	2014	208	0
1	B	2064	0	2031	189	0
2	F	44	0	41	35	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	B	17	0	9	2	0
5	A	10	0	0	0	0
5	B	5	0	0	0	0
All	All	4189	0	4095	390	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 47.

All (390) 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:A:255:TYR:CD2	1:A:256:PRO:HA	1.79	1.16
2:F:4:FDL:H16	2:F:4:FDL:O	1.51	1.08
1:A:264:VAL:HG21	1:A:271:VAL:HG23	1.38	1.03
2:F:2:HIS:O	2:F:3:LYS:HB2	1.60	0.97
1:A:255:TYR:CD2	1:A:256:PRO:CA	2.47	0.97
1:A:35:ARG:HG3	1:A:36:PRO:CD	1.94	0.96
1:B:282:THR:O	1:B:283:ASN:HB2	1.67	0.94
1:A:54:VAL:HG23	1:A:242:CYS:HB2	1.49	0.92
1:B:78:ARG:HD2	1:B:80:TRP:CZ3	2.05	0.91
1:A:227:LEU:HB3	1:A:232:LEU:HD11	1.51	0.90
1:B:129:GLY:O	1:B:131:GLN:N	2.06	0.88
1:A:242:CYS:O	1:A:267:ARG:NH2	2.07	0.88
1:A:226:ASN:HB2	2:F:2:HIS:O	1.74	0.87
1:B:223:PHE:CD1	2:F:4:FDL:H13	2.09	0.87
1:A:262:PRO:HG2	1:B:280:PRO:HB2	1.57	0.86
1:A:255:TYR:CG	1:A:256:PRO:HA	2.12	0.85
1:A:262:PRO:HG2	1:B:280:PRO:CB	2.06	0.84
1:A:35:ARG:HG3	1:A:36:PRO:HD3	1.57	0.84
1:A:293:CYS:HB3	1:A:297:LEU:HD12	1.59	0.83
1:B:52:HIS:HA	1:B:134:ARG:HB3	1.59	0.83
1:B:119:ARG:HG3	1:B:119:ARG:HH11	1.44	0.82
1:A:255:TYR:CE2	1:A:256:PRO:HB3	2.16	0.81
1:B:72:GLY:H	4:B:402:STL:H10	1.44	0.80
1:A:35:ARG:N	1:A:36:PRO:HD2	1.97	0.80
1:A:226:ASN:H	2:F:2:HIS:HB3	1.48	0.78
1:B:78:ARG:HD2	1:B:80:TRP:HZ3	1.48	0.77
1:A:262:PRO:HB3	1:B:280:PRO:HA	1.65	0.77
1:A:227:LEU:HB3	1:A:232:LEU:CD1	2.14	0.77
1:A:228:ASP:HB3	1:A:231:ILE:HB	1.67	0.77
1:B:83:GLN:HA	1:B:223:PHE:HE2	1.49	0.75
1:B:82:ALA:O	1:B:84:ASP:N	2.19	0.75
2:F:4:FDL:O	2:F:4:FDL:H7	1.86	0.75
2:F:2:HIS:O	2:F:2:HIS:CD2	2.40	0.75
1:B:83:GLN:HA	1:B:223:PHE:CE2	2.21	0.75
1:B:52:HIS:CD2	1:B:242:CYS:HA	2.22	0.75
1:A:252:SER:HB2	1:A:283:ASN:HD22	1.52	0.74
1:A:207:CYS:SG	1:A:209:GLU:HB2	2.27	0.74
1:A:262:PRO:HB2	1:B:280:PRO:HB3	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:128:LEU:HA	1:A:131:GLN:HB2	1.69	0.74
1:A:226:ASN:CB	2:F:3:LYS:HB2	2.17	0.74
1:A:54:VAL:HG23	1:A:242:CYS:CB	2.17	0.74
1:A:293:CYS:HB3	1:A:297:LEU:CD1	2.17	0.74
1:A:258:ALA:HB1	1:B:253:VAL:HG12	1.70	0.73
1:A:267:ARG:HE	1:A:269:VAL:HG21	1.52	0.73
1:B:181:CYS:SG	1:B:205:PRO:HD3	2.29	0.73
1:A:104:TYR:CE1	1:A:190:PRO:HG3	2.24	0.73
1:B:226:ASN:HA	2:F:2:HIS:HA	1.71	0.72
1:A:226:ASN:HB3	2:F:3:LYS:HB2	1.71	0.72
1:A:71:ARG:HD2	1:A:223:PHE:HZ	1.54	0.72
1:B:285:PHE:O	1:B:286:ARG:HD2	1.90	0.71
2:F:4:FDL:O	2:F:4:FDL:CAS	2.25	0.71
1:A:225:GLU:HG2	2:F:2:HIS:CG	2.26	0.71
1:B:104:TYR:CE1	1:B:190:PRO:HG3	2.26	0.70
1:A:142:ILE:O	1:A:161:LEU:HD22	1.92	0.70
1:B:106:ARG:HG2	1:B:161:LEU:HD12	1.73	0.70
1:A:54:VAL:CG2	1:A:242:CYS:CB	2.70	0.69
1:A:240:ALA:O	1:A:267:ARG:NH1	2.24	0.69
1:A:255:TYR:HB2	1:B:284:ARG:HH12	1.57	0.69
1:B:78:ARG:N	1:B:190:PRO:O	2.26	0.68
1:A:70:PHE:O	1:A:72:GLY:N	2.27	0.68
1:B:158:HIS:CE1	2:F:4:FDL:H15	2.28	0.67
1:B:285:PHE:C	1:B:286:ARG:HD2	2.14	0.67
1:B:279:THR:HB	1:B:280:PRO:HD3	1.77	0.67
1:B:224:GLY:H	2:F:3:LYS:HD3	1.60	0.66
1:A:252:SER:CB	1:A:283:ASN:HD22	2.08	0.66
1:A:226:ASN:CB	2:F:3:LYS:CB	2.72	0.66
1:A:54:VAL:CG2	1:A:242:CYS:HB2	2.24	0.66
1:A:262:PRO:CB	1:B:280:PRO:HA	2.26	0.66
1:A:103:HIS:CE1	1:A:179:PRO:HB3	2.32	0.65
1:A:166:CYS:HA	1:A:216:LEU:HD23	1.78	0.65
2:F:4:FDL:O	2:F:4:FDL:CAI	2.38	0.65
1:A:226:ASN:HB3	2:F:3:LYS:CB	2.26	0.64
1:A:35:ARG:HG3	1:A:36:PRO:N	2.12	0.64
1:A:106:ARG:HG2	1:A:161:LEU:O	1.98	0.64
1:B:293:CYS:O	1:B:297:LEU:HB2	1.97	0.64
1:B:297:LEU:HD22	1:B:301:LEU:CD1	2.28	0.64
1:A:107:GLU:O	1:A:109:MET:N	2.31	0.64
1:A:222:TRP:O	1:A:225:GLU:HB2	1.97	0.64
1:B:144:GLU:HG2	1:B:148:LYS:HG3	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:264:VAL:HG13	1:B:269:VAL:HG12	1.80	0.64
1:A:239:LEU:HD12	1:A:263:GLN:OE1	1.98	0.64
1:A:264:VAL:HG21	1:A:271:VAL:CG2	2.22	0.64
1:B:109:MET:O	1:B:111:SER:N	2.30	0.63
1:A:252:SER:OG	1:A:261:ALA:HB2	1.99	0.63
1:B:77:TRP:N	1:B:80:TRP:O	2.32	0.63
1:A:255:TYR:CD2	1:A:256:PRO:CB	2.81	0.62
1:A:71:ARG:CZ	1:A:223:PHE:CE1	2.83	0.62
1:A:136:VAL:HG21	1:A:238:GLU:OE1	2.00	0.62
1:A:253:VAL:HG11	1:A:282:THR:H	1.63	0.62
1:B:199:ILE:HG23	1:B:203:LYS:CB	2.30	0.61
1:A:169:CYS:O	1:A:171:VAL:N	2.33	0.61
1:B:57:SER:HB3	1:B:139:THR:HB	1.83	0.61
1:B:223:PHE:CE1	2:F:4:FDL:H13	2.34	0.61
1:A:105:ARG:HG2	1:A:161:LEU:HD12	1.82	0.61
2:F:2:HIS:O	2:F:2:HIS:HD2	1.81	0.61
1:B:119:ARG:CG	1:B:119:ARG:HH11	2.11	0.61
1:B:80:TRP:CH2	1:B:97:ARG:NE	2.69	0.61
1:A:262:PRO:CB	1:B:280:PRO:HB3	2.31	0.61
1:B:227:LEU:HD23	1:B:232:LEU:HD23	1.83	0.60
1:A:255:TYR:CD2	1:A:256:PRO:HB3	2.37	0.60
1:B:177:LYS:O	1:B:180:ILE:HA	2.01	0.60
1:B:129:GLY:C	1:B:131:GLN:H	2.05	0.60
1:A:199:ILE:CG2	1:A:203:LYS:HB2	2.32	0.60
1:B:106:ARG:HA	1:B:161:LEU:HD11	1.84	0.60
1:B:147:ARG:NH2	1:B:156:GLU:OE1	2.35	0.60
1:A:103:HIS:HE1	1:A:179:PRO:HB3	1.66	0.59
1:A:78:ARG:HH21	1:A:188:GLY:C	2.06	0.59
1:A:235:VAL:O	1:A:239:LEU:HG	2.03	0.59
1:A:283:ASN:OD1	1:A:284:ARG:N	2.35	0.59
1:A:245:CYS:C	1:A:246:LEU:HD12	2.22	0.59
1:B:35:ARG:H	1:B:36:PRO:HD2	1.67	0.59
1:B:51:LYS:N	1:B:243:ASP:OD2	2.35	0.59
1:A:139:THR:O	1:A:156:GLU:HA	2.03	0.59
1:A:258:ALA:O	1:A:260:PHE:N	2.36	0.59
1:A:267:ARG:HE	1:A:269:VAL:CG2	2.15	0.59
1:B:114:PRO:HG2	1:B:149:ALA:HB2	1.84	0.59
1:B:264:VAL:HG12	1:B:265:ALA:N	2.17	0.59
1:A:262:PRO:CG	1:B:280:PRO:CB	2.79	0.59
1:B:136:VAL:HG13	1:B:153:ASN:HB3	1.85	0.59
1:A:94:ASN:HB3	1:A:97:ARG:HG2	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:191:GLU:O	1:B:194:THR:OG1	2.21	0.58
1:A:227:LEU:CB	1:A:232:LEU:HD11	2.29	0.58
1:B:73:ALA:O	1:B:76:TYR:HE1	1.86	0.58
1:A:200:PRO:HG2	1:A:203:LYS:HE2	1.86	0.58
1:B:76:TYR:HB3	1:B:80:TRP:O	2.03	0.58
1:B:106:ARG:CG	1:B:161:LEU:HD12	2.33	0.58
1:B:169:CYS:HB3	1:B:212:CYS:SG	2.43	0.58
1:A:261:ALA:N	1:A:262:PRO:CD	2.67	0.57
1:B:261:ALA:HB3	1:B:262:PRO:CD	2.35	0.57
1:A:248:VAL:CG1	1:A:274:PHE:HB2	2.33	0.57
1:A:258:ALA:O	1:A:262:PRO:HD3	2.04	0.57
1:A:226:ASN:CB	2:F:2:HIS:O	2.50	0.57
1:A:54:VAL:HG21	1:A:242:CYS:HB3	1.86	0.57
1:A:91:PHE:O	1:A:95:PRO:HG3	2.05	0.57
1:A:71:ARG:HD2	1:A:223:PHE:CZ	2.38	0.56
1:A:226:ASN:HB2	2:F:2:HIS:C	2.26	0.56
1:A:71:ARG:CD	1:A:223:PHE:HZ	2.18	0.56
1:A:78:ARG:HG2	1:A:191:GLU:O	2.06	0.56
1:B:94:ASN:O	1:B:98:VAL:HG23	2.06	0.56
1:A:235:VAL:HG12	1:A:236:ASP:N	2.20	0.56
1:B:276:THR:O	1:B:277:GLU:CB	2.54	0.56
1:A:104:TYR:O	1:A:107:GLU:HB2	2.06	0.55
1:A:36:PRO:HA	1:A:285:PHE:O	2.06	0.55
1:A:255:TYR:HA	1:A:257:ALA:H	1.70	0.55
1:B:250:THR:HG23	1:B:251:SER:N	2.21	0.55
1:A:288:HIS:CE1	1:A:289:PHE:O	2.59	0.55
1:B:129:GLY:C	1:B:131:GLN:N	2.59	0.55
1:B:118:HIS:O	1:B:119:ARG:C	2.44	0.55
1:B:94:ASN:O	1:B:96:SER:N	2.39	0.55
1:A:226:ASN:HB2	2:F:3:LYS:HB2	1.89	0.55
1:A:114:PRO:HB3	1:A:149:ALA:HB2	1.89	0.55
1:A:108:VAL:HG12	1:A:112:LYS:HE2	1.87	0.55
1:B:199:ILE:HG23	1:B:203:LYS:HB3	1.89	0.55
1:A:106:ARG:HH22	1:A:175:ASN:C	2.11	0.54
1:B:253:VAL:HG21	1:B:280:PRO:O	2.07	0.54
1:B:64:GLU:OE2	1:B:292:PRO:HA	2.07	0.54
1:A:169:CYS:O	1:A:170:GLY:C	2.45	0.54
1:B:54:VAL:CG2	1:B:242:CYS:HB3	2.37	0.54
1:A:54:VAL:CG2	1:A:242:CYS:HB3	2.38	0.54
1:B:261:ALA:N	1:B:262:PRO:HD2	2.22	0.54
1:A:52:HIS:CE1	1:A:134:ARG:HB3	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:44:ARG:NH1	1:B:302:ALA:HB3	2.22	0.54
1:B:179:PRO:HB2	1:B:181:CYS:O	2.08	0.54
1:A:199:ILE:HG23	1:A:203:LYS:HD2	1.90	0.54
1:A:271:VAL:HG12	1:A:271:VAL:O	2.08	0.54
1:B:107:GLU:HA	1:B:107:GLU:OE2	2.08	0.54
1:A:252:SER:HB2	1:A:283:ASN:ND2	2.20	0.54
1:B:144:GLU:OE1	1:B:147:ARG:HD2	2.07	0.53
1:A:207:CYS:SG	1:A:209:GLU:CB	2.97	0.53
1:A:264:VAL:CG2	1:A:271:VAL:HG23	2.25	0.53
1:A:225:GLU:HG2	2:F:2:HIS:ND1	2.23	0.53
1:A:198:SER:O	1:A:200:PRO:HD3	2.08	0.53
1:A:261:ALA:HB3	1:A:262:PRO:HD3	1.89	0.53
1:B:290:GLN:HG2	1:B:291:GLY:N	2.22	0.53
1:B:239:LEU:HD11	1:B:260:PHE:HD1	1.74	0.53
1:B:44:ARG:HH12	1:B:302:ALA:C	2.12	0.53
1:B:35:ARG:HB2	1:B:36:PRO:HD3	1.91	0.53
1:B:166:CYS:HA	1:B:216:LEU:HD23	1.89	0.53
1:A:262:PRO:CB	1:B:280:PRO:CB	2.86	0.53
1:A:226:ASN:N	2:F:2:HIS:HB3	2.21	0.53
1:B:251:SER:HB3	1:B:275:ASN:ND2	2.23	0.52
1:A:248:VAL:HG12	1:A:274:PHE:HB2	1.91	0.52
1:B:78:ARG:HG2	1:B:79:LYS:H	1.74	0.52
1:A:58:GLY:HA3	1:A:250:THR:H	1.73	0.52
1:A:248:VAL:HG12	1:A:293:CYS:SG	2.49	0.52
1:B:201:VAL:CG1	1:B:215:LEU:HD22	2.40	0.52
1:A:278:THR:HG23	1:A:279:THR:H	1.75	0.52
1:A:94:ASN:ND2	1:A:97:ARG:HB3	2.24	0.52
1:A:62:SER:OG	1:A:143:ASP:OD2	2.19	0.52
1:A:142:ILE:HD12	1:A:161:LEU:HD13	1.91	0.52
1:B:54:VAL:HG23	1:B:242:CYS:CB	2.39	0.52
1:B:119:ARG:O	1:B:123:GLU:HG3	2.09	0.52
1:B:275:ASN:N	1:B:275:ASN:OD1	2.43	0.52
1:B:72:GLY:N	4:B:402:STL:H10	2.20	0.52
1:B:63:ALA:C	1:B:65:SER:H	2.14	0.51
1:A:294:GLY:O	1:A:298:PRO:HG2	2.11	0.51
1:A:272:ALA:HA	1:A:287:PHE:HB2	1.91	0.51
1:B:54:VAL:HG23	1:B:242:CYS:HB3	1.90	0.51
1:A:105:ARG:HB3	1:A:161:LEU:HD12	1.93	0.51
1:A:258:ALA:C	1:A:260:PHE:H	2.14	0.51
1:B:285:PHE:O	1:B:285:PHE:CD1	2.63	0.51
1:B:199:ILE:HG23	1:B:203:LYS:HB2	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:169:CYS:SG	1:B:171:VAL:HB	2.52	0.50
1:B:63:ALA:O	1:B:65:SER:N	2.44	0.50
1:A:105:ARG:CG	1:A:161:LEU:HD12	2.41	0.50
1:A:239:LEU:CD1	1:A:263:GLN:OE1	2.59	0.50
1:B:239:LEU:HD11	1:B:260:PHE:CD1	2.45	0.50
1:A:225:GLU:HA	2:F:2:HIS:HB3	1.94	0.50
1:A:226:ASN:CB	2:F:3:LYS:HB3	2.41	0.50
1:B:82:ALA:C	1:B:84:ASP:H	2.15	0.50
1:A:71:ARG:CZ	1:A:223:PHE:HE1	2.24	0.50
1:A:109:MET:HA	1:A:112:LYS:HG2	1.94	0.50
1:A:225:GLU:HG2	2:F:2:HIS:CB	2.40	0.50
1:B:265:ALA:C	1:B:267:ARG:H	2.16	0.50
1:A:264:VAL:HG23	1:A:269:VAL:HB	1.94	0.50
1:B:176:TYR:O	1:B:177:LYS:C	2.49	0.50
1:B:61:VAL:CG2	1:B:248:VAL:HG23	2.42	0.50
1:A:251:SER:OG	1:A:252:SER:N	2.45	0.49
1:B:91:PHE:O	1:B:95:PRO:HD3	2.12	0.49
1:B:235:VAL:O	1:B:238:GLU:N	2.45	0.49
1:B:255:TYR:HD1	1:B:256:PRO:HA	1.77	0.49
1:B:199:ILE:CG2	1:B:203:LYS:CB	2.90	0.49
1:A:217:ARG:CZ	1:A:222:TRP:CZ3	2.96	0.49
1:A:262:PRO:CB	1:B:280:PRO:CA	2.90	0.49
1:B:182:PRO:O	1:B:185:SER:HB2	2.13	0.49
1:B:199:ILE:CG2	1:B:203:LYS:HB3	2.43	0.49
1:A:57:SER:HA	1:A:248:VAL:HG23	1.94	0.49
1:A:39:SER:C	1:A:41:ALA:H	2.16	0.49
1:B:257:ALA:C	1:B:259:MET:H	2.16	0.49
1:B:80:TRP:CZ3	1:B:97:ARG:HD2	2.48	0.49
1:B:224:GLY:H	2:F:3:LYS:CD	2.24	0.49
1:A:226:ASN:CG	2:F:3:LYS:HB3	2.33	0.48
1:A:50:ALA:CB	1:A:244:LEU:HB2	2.43	0.48
1:B:227:LEU:CD2	1:B:232:LEU:HD23	2.43	0.48
1:A:142:ILE:O	1:A:161:LEU:CD2	2.61	0.48
1:A:145:LEU:HD12	1:A:145:LEU:HA	1.70	0.48
1:A:222:TRP:O	1:A:225:GLU:CB	2.61	0.48
1:A:50:ALA:HB1	1:A:244:LEU:HB2	1.95	0.48
1:A:124:CYS:O	1:A:128:LEU:HG	2.14	0.48
1:A:200:PRO:HD2	1:A:203:LYS:HE3	1.94	0.48
1:A:258:ALA:C	1:A:260:PHE:N	2.66	0.48
1:A:279:THR:O	1:A:280:PRO:C	2.51	0.48
1:B:109:MET:CE	1:B:145:LEU:CD1	2.92	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:71:ARG:NH1	1:B:82:ALA:CB	2.77	0.48
1:B:276:THR:HG22	1:B:291:GLY:C	2.34	0.48
1:A:262:PRO:HG2	1:B:280:PRO:HB3	1.95	0.47
1:B:222:TRP:O	1:B:225:GLU:HB2	2.14	0.47
1:A:261:ALA:O	1:A:264:VAL:HG13	2.13	0.47
1:A:103:HIS:O	1:A:107:GLU:HG2	2.15	0.47
1:B:231:ILE:O	1:B:235:VAL:HG23	2.13	0.47
1:A:258:ALA:O	1:A:262:PRO:CD	2.62	0.47
1:A:42:ASP:O	1:A:45:LYS:HB3	2.14	0.47
1:B:109:MET:CE	1:B:145:LEU:HD11	2.43	0.47
1:A:246:LEU:HD12	1:A:246:LEU:N	2.29	0.47
1:B:103:HIS:O	1:B:106:ARG:HB2	2.14	0.47
1:A:228:ASP:OD1	1:A:230:ALA:HB3	2.15	0.47
1:B:125:GLU:OE1	1:B:153:ASN:HB2	2.14	0.47
1:B:255:TYR:CD1	1:B:256:PRO:HA	2.50	0.47
1:A:42:ASP:O	1:A:45:LYS:N	2.45	0.47
1:B:160:SER:HB3	1:B:163:LYS:HD2	1.96	0.47
1:A:251:SER:O	1:A:257:ALA:HB3	2.15	0.47
1:A:255:TYR:HE2	1:A:256:PRO:HB3	1.73	0.47
1:B:276:THR:O	1:B:277:GLU:HB3	2.15	0.47
1:B:297:LEU:HD22	1:B:301:LEU:HD11	1.96	0.47
1:A:179:PRO:HG2	1:A:185:SER:HB2	1.97	0.46
1:B:112:LYS:N	1:B:112:LYS:HD3	2.29	0.46
1:A:243:ASP:C	1:A:243:ASP:OD2	2.54	0.46
1:A:71:ARG:NH1	1:A:223:PHE:CE1	2.83	0.46
1:B:116:ALA:O	1:B:117:GLY:C	2.53	0.46
1:A:98:VAL:O	1:A:101:PHE:N	2.49	0.46
1:A:200:PRO:HB2	1:A:203:LYS:HG3	1.97	0.46
1:B:52:HIS:CA	1:B:134:ARG:HB3	2.39	0.46
1:B:223:PHE:HE1	2:F:4:FDL:O	1.98	0.46
1:A:106:ARG:NH1	1:A:162:PHE:HA	2.31	0.46
1:A:166:CYS:HA	1:A:216:LEU:CD2	2.45	0.46
1:A:217:ARG:HB2	1:A:218:PRO:CD	2.45	0.46
1:A:227:LEU:CD2	1:A:232:LEU:HD11	2.45	0.46
1:B:138:ILE:HD13	1:B:235:VAL:HG22	1.98	0.46
1:B:264:VAL:HG12	1:B:271:VAL:CG2	2.46	0.46
1:A:177:LYS:HB3	1:A:177:LYS:HE2	1.67	0.46
1:A:181:CYS:SG	1:A:184:LEU:HD12	2.56	0.46
1:B:264:VAL:HG13	1:B:269:VAL:CG1	2.43	0.46
1:B:275:ASN:O	1:B:290:GLN:HA	2.15	0.46
1:B:83:GLN:HG3	1:B:223:PHE:CE2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:238:GLU:O	1:A:242:CYS:HB3	2.16	0.46
2:F:3:LYS:HD2	2:F:4:FDL:N	2.31	0.46
1:B:228:ASP:OD2	1:B:230:ALA:HB3	2.16	0.46
1:B:106:ARG:HG2	1:B:161:LEU:CD1	2.45	0.46
1:B:246:LEU:HD21	1:B:301:LEU:HD21	1.97	0.45
1:A:234:GLU:O	1:A:238:GLU:HG2	2.16	0.45
1:A:248:VAL:HG13	1:A:274:PHE:HB2	1.98	0.45
1:B:165:ARG:NH1	1:B:219:HIS:ND1	2.64	0.45
1:B:264:VAL:CG1	1:B:271:VAL:CG2	2.94	0.45
1:A:158:HIS:O	1:A:220:VAL:HA	2.17	0.45
1:B:71:ARG:NH1	1:B:82:ALA:HB3	2.32	0.45
1:B:223:PHE:CD1	2:F:3:LYS:HE3	2.52	0.45
1:A:204:LEU:HB3	1:A:205:PRO:CD	2.47	0.45
1:A:70:PHE:HE2	1:A:105:ARG:HD2	1.82	0.45
1:B:139:THR:OG1	1:B:140:GLN:N	2.50	0.45
1:B:292:PRO:HB2	1:B:295:THR:OG1	2.17	0.45
1:A:205:PRO:HB2	1:A:216:LEU:HB2	1.99	0.45
1:B:199:ILE:CG2	1:B:203:LYS:HB2	2.47	0.45
1:A:207:CYS:SG	1:A:209:GLU:CG	3.06	0.44
1:B:181:CYS:SG	1:B:184:LEU:HD12	2.57	0.44
1:B:155:LEU:HD22	1:B:234:GLU:OE2	2.16	0.44
1:B:142:ILE:HD13	2:F:4:FDL:H22	1.99	0.44
1:B:237:ARG:O	1:B:241:HIS:HB2	2.18	0.44
1:A:102:TYR:HA	1:A:105:ARG:HB2	2.00	0.44
1:A:70:PHE:CE2	1:A:105:ARG:HD2	2.53	0.44
1:B:106:ARG:CG	1:B:161:LEU:CD1	2.96	0.44
1:A:114:PRO:HG3	1:A:148:LYS:HB2	1.99	0.43
1:A:35:ARG:O	1:A:36:PRO:C	2.56	0.43
1:A:43:PHE:CD2	1:A:43:PHE:C	2.91	0.43
1:B:286:ARG:HB3	1:B:287:PHE:H	1.52	0.43
1:B:143:ASP:OD1	1:B:145:LEU:HB2	2.18	0.43
1:A:105:ARG:HG2	1:A:161:LEU:CD1	2.45	0.43
1:A:106:ARG:NH2	1:A:175:ASN:O	2.46	0.43
1:A:200:PRO:CG	1:A:203:LYS:HE2	2.48	0.43
2:F:4:FDL:H6	2:F:4:FDL:H1	1.81	0.43
1:A:105:ARG:O	1:A:106:ARG:C	2.57	0.43
1:A:252:SER:CB	1:A:283:ASN:ND2	2.80	0.43
1:A:294:GLY:O	1:A:298:PRO:CG	2.67	0.43
1:B:94:ASN:C	1:B:96:SER:N	2.72	0.43
1:A:54:VAL:HG21	1:A:238:GLU:O	2.19	0.43
1:B:297:LEU:N	1:B:298:PRO:CD	2.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:191:GLU:CD	1:A:191:GLU:N	2.72	0.43
1:A:35:ARG:N	1:A:36:PRO:CD	2.76	0.43
1:A:70:PHE:C	1:A:72:GLY:N	2.72	0.43
1:B:144:GLU:O	1:B:146:HIS:N	2.51	0.43
1:A:158:HIS:HA	1:A:221:VAL:CG2	2.49	0.43
1:B:101:PHE:O	1:B:101:PHE:CD1	2.72	0.43
1:B:259:MET:C	1:B:260:PHE:CD1	2.92	0.43
1:B:277:GLU:O	1:B:278:THR:C	2.56	0.43
1:B:98:VAL:O	1:B:102:TYR:HD1	2.02	0.43
1:A:98:VAL:O	1:A:101:PHE:HB3	2.18	0.42
1:B:279:THR:HB	1:B:280:PRO:CD	2.45	0.42
1:B:82:ALA:C	1:B:84:ASP:N	2.69	0.42
1:B:78:ARG:HG3	1:B:192:PRO:HA	2.01	0.42
1:A:258:ALA:CB	1:B:253:VAL:HG12	2.44	0.42
1:A:39:SER:C	1:A:41:ALA:N	2.72	0.42
1:B:129:GLY:O	1:B:130:LYS:C	2.56	0.42
1:B:52:HIS:O	1:B:243:ASP:N	2.48	0.42
1:B:78:ARG:CA	1:B:190:PRO:O	2.67	0.42
1:A:53:ILE:HG12	1:A:244:LEU:HD23	2.01	0.42
1:B:145:LEU:HA	1:B:145:LEU:HD12	1.76	0.42
1:A:166:CYS:O	1:A:170:GLY:HA2	2.19	0.42
1:B:61:VAL:HG12	1:B:118:HIS:NE2	2.35	0.42
1:A:57:SER:N	1:A:138:ILE:O	2.40	0.42
1:B:162:PHE:HB3	1:B:175:ASN:O	2.20	0.42
1:A:97:ARG:HA	1:A:100:GLU:HG3	2.02	0.42
1:A:53:ILE:CG2	1:A:246:LEU:HD13	2.50	0.42
1:A:58:GLY:N	1:A:248:VAL:O	2.52	0.42
1:A:259:MET:SD	1:B:254:VAL:HA	2.60	0.42
1:B:35:ARG:HB3	1:B:285:PHE:O	2.19	0.42
1:A:115:ASN:H	1:A:118:HIS:HD2	1.66	0.41
1:A:116:ALA:HB3	1:A:294:GLY:HA2	2.02	0.41
1:A:54:VAL:HG21	1:A:242:CYS:CB	2.44	0.41
1:B:35:ARG:H	1:B:36:PRO:CD	2.33	0.41
1:A:191:GLU:H	1:A:191:GLU:CD	2.23	0.41
1:A:262:PRO:CG	1:B:280:PRO:HB3	2.47	0.41
1:A:199:ILE:HG23	1:A:203:LYS:HB2	2.01	0.41
1:A:248:VAL:HG11	1:A:297:LEU:HD11	2.02	0.41
1:B:94:ASN:C	1:B:96:SER:H	2.23	0.41
1:A:67:VAL:HA	1:A:68:PRO:HD3	1.72	0.41
1:B:292:PRO:O	1:B:296:THR:HG23	2.19	0.41
1:B:106:ARG:HH22	1:B:176:TYR:C	2.24	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:63:ALA:C	1:B:65:SER:N	2.73	0.41
1:B:175:ASN:OD1	1:B:175:ASN:C	2.59	0.41
1:B:221:VAL:HG12	1:B:222:TRP:N	2.35	0.41
1:B:238:GLU:O	1:B:239:LEU:C	2.59	0.41
1:B:251:SER:OG	1:B:280:PRO:O	2.32	0.41
1:B:55:ILE:O	1:B:137:VAL:HA	2.21	0.41
1:A:140:GLN:H	1:A:140:GLN:HG3	1.62	0.41
1:A:163:LYS:HA	1:A:173:ALA:O	2.21	0.41
1:A:294:GLY:O	1:A:298:PRO:CD	2.69	0.41
1:B:109:MET:HE2	1:B:145:LEU:HD13	2.01	0.41
1:A:259:MET:HB2	1:B:253:VAL:O	2.21	0.41
1:A:200:PRO:O	1:A:201:VAL:C	2.60	0.40
1:B:51:LYS:HA	1:B:133:ARG:HG2	2.03	0.40
1:B:165:ARG:HA	1:B:171:VAL:O	2.21	0.40
1:A:94:ASN:CB	1:A:97:ARG:HG2	2.50	0.40
1:B:78:ARG:CG	1:B:192:PRO:HA	2.51	0.40
1:B:253:VAL:HG21	1:B:280:PRO:C	2.41	0.40
1:B:223:PHE:HD1	2:F:3:LYS:HE3	1.86	0.40
1:B:119:ARG:O	1:B:122:ALA:HB3	2.21	0.40
1:B:248:VAL:HG11	1:B:297:LEU:HD11	2.03	0.40
1:B:297:LEU:O	1:B:298:PRO:C	2.59	0.40
1:B:71:ARG:HH12	1:B:82:ALA:HB1	1.86	0.40
1:A:189:ALA:HB3	1:A:194:THR:HG21	2.03	0.40
1:B:200:PRO:HD2	1:B:203:LYS:HE2	2.04	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	265/275 (96%)	206 (78%)	41 (16%)	18 (7%)	<b>1</b> <b>1</b>

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	268/275 (98%)	208 (78%)	44 (16%)	16 (6%)	1	1
2	F	1/4 (25%)	0	0	1 (100%)	0	0
All	All	534/554 (96%)	414 (78%)	85 (16%)	35 (7%)	1	1

All (35) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	36	PRO
1	A	65	SER
1	A	108	VAL
1	A	170	GLY
1	A	196	ASP
1	A	278	THR
1	B	83	GLN
1	B	130	LYS
1	B	277	GLU
1	B	279	THR
1	B	283	ASN
2	F	3	LYS
1	A	71	ARG
1	A	258	ALA
1	A	259	MET
1	A	295	THR
1	B	64	GLU
1	B	111	SER
1	A	105	ARG
1	A	127	ARG
1	A	132	GLY
1	B	35	ARG
1	B	110	GLY
1	B	266	ALA
1	B	278	THR
1	A	77	TRP
1	A	197	ALA
1	A	296	THR
1	B	177	LYS
1	A	107	GLU
1	A	256	PRO
1	B	153	ASN
1	B	253	VAL
1	B	262	PRO

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Mol	Chain	Res	Type
1	B	68	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	214/219 (98%)	185 (86%)	29 (14%)	3	6
1	B	215/219 (98%)	188 (87%)	27 (13%)	4	8
2	F	2/3 (67%)	1 (50%)	1 (50%)	0	0
All	All	431/441 (98%)	374 (87%)	57 (13%)	4	7

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	35	ARG
1	A	44	ARG
1	A	84	ASP
1	A	96	SER
1	A	97	ARG
1	A	105	ARG
1	A	109	MET
1	A	124	CYS
1	A	126	THR
1	A	128	LEU
1	A	140	GLN
1	A	145	LEU
1	A	152	LYS
1	A	161	LEU
1	A	195	GLN
1	A	201	VAL
1	A	208	GLU
1	A	226	ASN
1	A	227	LEU
1	A	231	ILE
1	A	232	LEU

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Mol	Chain	Res	Type
1	A	238	GLU
1	A	242	CYS
1	A	248	VAL
1	A	264	VAL
1	A	278	THR
1	A	284	ARG
1	A	286	ARG
1	A	296	THR
1	B	33	THR
1	B	38	SER
1	B	94	ASN
1	B	99	TRP
1	B	119	ARG
1	B	144	GLU
1	B	145	LEU
1	B	158	HIS
1	B	161	LEU
1	B	164	THR
1	B	178	SER
1	B	185	SER
1	B	194	THR
1	B	201	VAL
1	B	202	GLU
1	B	220	VAL
1	B	237	ARG
1	B	250	THR
1	B	253	VAL
1	B	264	VAL
1	B	275	ASN
1	B	278	THR
1	B	279	THR
1	B	282	THR
1	B	283	ASN
1	B	285	PHE
1	B	286	ARG
2	F	3	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	103	HIS
1	B	158	HIS

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Mol	Chain	Res	Type
1	B	226	ASN
1	B	283	ASN
2	F	2	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	FDL	F	4	-	24,26,26	1.68	2 (8%)	30,35,35	2.03	6 (20%)

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	FDL	F	4	-	-	4/16/16/16	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	4	FDL	CAL-CAD	-5.97	1.39	1.51
2	F	4	FDL	CAJ-NAM	-3.59	1.34	1.41

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	4	FDL	CAJ-NAM-C	-5.35	114.60	127.40
2	F	4	FDL	CAS-CB-CA	-4.31	99.48	113.35
2	F	4	FDL	C-CA-N	3.69	123.66	109.40
2	F	4	FDL	CB-CA-C	-3.37	103.55	110.85
2	F	4	FDL	O-C-NAM	-3.12	117.22	123.93
2	F	4	FDL	CAD-CAE-CAF	2.68	119.65	118.05

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	4	FDL	O-C-CA-CB
2	F	4	FDL	O-C-CA-N
2	F	4	FDL	NAM-C-CA-CB
2	F	4	FDL	O-C-NAM-CAJ

There are no ring outliers.

1 monomer is involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	4	FDL	11	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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	STL	B	402	-	18,18,18	1.53	3 (16%)	24,24,24	0.85	1 (4%)



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	STL	B	402	-	-	3/5/5/5	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	402	STL	C8-C7	4.24	1.52	1.31
4	B	402	STL	C9-C8	-3.23	1.38	1.47
4	B	402	STL	C5-C7	-3.11	1.38	1.47

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	402	STL	C9-C8-C7	-2.74	115.05	125.87

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	402	STL	C7-C8-C9-C14
4	B	402	STL	C7-C8-C9-C10
4	B	402	STL	C4-C5-C7-C8

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	402	STL	2	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [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	267/275 (97%)	-0.42	8 (2%) 50 43	19, 40, 69, 94	4 (1%)
1	B	270/275 (98%)	-0.58	5 (1%) 66 62	18, 37, 61, 79	1 (0%)
2	F	2/4 (50%)	1.04	0 100 100	56, 56, 56, 64	0
All	All	539/554 (97%)	-0.49	13 (2%) 59 53	18, 39, 66, 94	5 (0%)

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	253	VAL	6.0
1	B	281	ALA	5.9
1	A	280	PRO	4.3
1	A	285	PHE	3.8
1	A	281	ALA	3.7
1	B	279	THR	3.0
1	A	71	ARG	3.0
1	B	73	ALA	2.6
1	A	262	PRO	2.6
1	A	223	PHE	2.2
1	B	280	PRO	2.2
1	B	34	ALA	2.1
1	A	284	ARG	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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	B-factors( $\text{\AA}^2$ )	Q<0.9
2	FDL	F	4	25/25	0.80	0.38	48,65,74,77	0

### 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. 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	B-factors( $\text{\AA}^2$ )	Q<0.9
4	STL	B	402	17/17	0.86	0.32	45,62,75,75	0
3	ZN	A	401	1/1	1.00	0.11	34,34,34,34	0
3	ZN	B	401	1/1	1.00	0.12	29,29,29,29	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.