



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 3, 2017 – 05:07 PM EDT

PDB ID : 2W9L
Title : CANINE ADENOVIRUS TYPE 2 FIBRE HEAD IN COMPLEX WITH CAR
DOMAIN D1 AND SIALIC ACID
Authors : Seiradake, E.; Henaff, D.; Wodrich, H.; Billet, O.; Perreau, M.; Hippert, C.;
Mennechet, F.; Schoehn, G.; Lortat-Jacob, H.; Dreja, H.; Ibanes, S.; Kalatzis,
V.; Wang, J.P.; Finberg, R.W.; Cusack, S.; Kremer, E.J.
Deposited on : unknown
Resolution : 2.91 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20029824
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) : rb-20029824

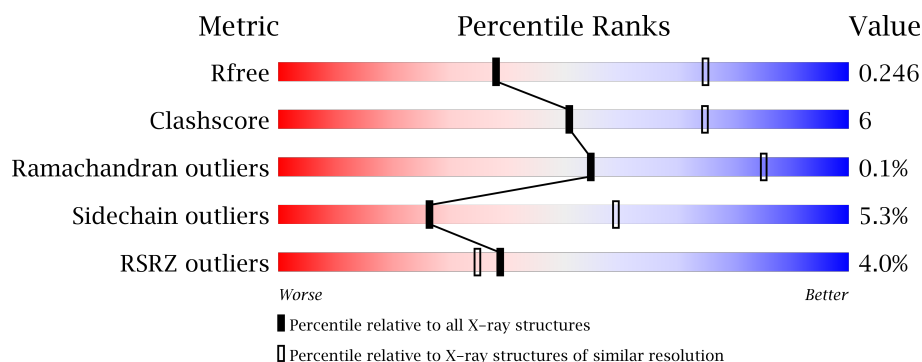
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.91 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	1813 (2.94-2.90)
Clashscore	112137	2045 (2.94-2.90)
Ramachandran outliers	110173	1997 (2.94-2.90)
Sidechain outliers	110143	1999 (2.94-2.90)
RSRZ outliers	101464	1825 (2.94-2.90)

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 ≥ 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	124	<div> <div>25%</div> <div> <div></div> <div>74%</div> <div>16%</div> <div>• 6%</div> </div> </div>
1	B	124	<div> <div>25%</div> <div> <div></div> <div>60%</div> <div>31%</div> <div>• 6%</div> </div> </div>
1	G	124	<div> <div>4%</div> <div> <div></div> <div>78%</div> <div>21%</div> <div>•</div> </div> </div>
1	J	124	<div> <div>7%</div> <div> <div></div> <div>78%</div> <div>20%</div> <div>••</div> </div> </div>
1	K	124	<div> <div>5%</div> <div> <div></div> <div>72%</div> <div>25%</div> <div>••</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	O	124	
1	P	124	
1	T	124	
1	V	124	
1	X	124	
1	Y	124	
1	Z	124	
2	C	197	
2	D	197	
2	E	197	
2	F	197	
2	H	197	
2	I	197	
2	L	197	
2	M	197	
2	N	197	
2	Q	197	
2	R	197	
2	S	197	

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
4	GL0	C	602	X	-	-	-
4	GL0	D	602	X	-	-	-
4	GL0	L	602	X	-	-	-
4	GL0	R	602	X	-	-	-
4	GL0	S	602	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	GAL	H	602	X	-	-	-
5	GAL	I	602	X	-	-	-
5	GAL	Q	602	X	-	-	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 28671 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 COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	117	Total	C	N	O	S	0	0	0
			914	581	147	183	3			
1	B	117	Total	C	N	O	S	0	0	0
			914	583	147	181	3			
1	G	123	Total	C	N	O	S	0	0	0
			959	611	156	189	3			
1	J	123	Total	C	N	O	S	0	0	0
			959	611	156	189	3			
1	K	123	Total	C	N	O	S	0	0	0
			963	615	156	189	3			
1	O	118	Total	C	N	O	S	0	0	0
			917	587	145	182	3			
1	P	123	Total	C	N	O	S	0	0	0
			959	611	156	189	3			
1	T	119	Total	C	N	O	S	0	0	0
			928	591	149	185	3			
1	V	121	Total	C	N	O	S	0	0	0
			944	600	154	187	3			
1	X	123	Total	C	N	O	S	0	0	0
			959	611	156	189	3			
1	Y	119	Total	C	N	O	S	0	0	0
			928	591	149	185	3			
1	Z	117	Total	C	N	O	S	0	0	0
			914	581	147	183	3			

- Molecule 2 is a protein called FIBRE PROTEIN.

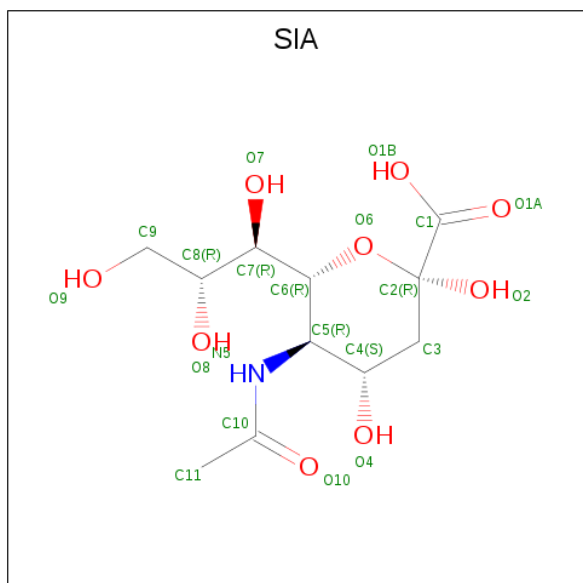
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	182	Total	C	N	O	S	0	0	0
			1406	892	239	266	9			
2	D	182	Total	C	N	O	S	0	0	0
			1406	892	239	266	9			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	182	Total	C	N	O	S	0	0	0
			1406	892	239	266	9			
2	F	182	Total	C	N	O	S	0	0	0
			1406	892	239	266	9			
2	H	182	Total	C	N	O	S	0	0	0
			1406	892	239	266	9			
2	I	182	Total	C	N	O	S	0	0	0
			1406	892	239	266	9			
2	L	182	Total	C	N	O	S	0	0	0
			1406	892	239	266	9			
2	M	182	Total	C	N	O	S	0	0	0
			1406	892	239	266	9			
2	N	182	Total	C	N	O	S	0	0	0
			1406	892	239	266	9			
2	Q	182	Total	C	N	O	S	0	0	0
			1406	892	239	266	9			
2	R	182	Total	C	N	O	S	0	0	0
			1406	892	239	266	9			
2	S	182	Total	C	N	O	S	0	0	0
			1406	892	239	266	9			

- Molecule 3 is O-SIALIC ACID (three-letter code: SIA) (formula: $C_{11}H_{19}NO_9$).



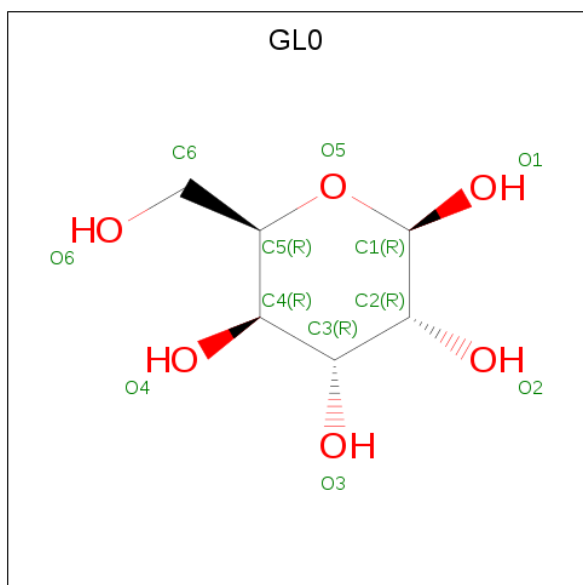
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	C	1	Total	C	N	O	0	0
			21	11	1	9		

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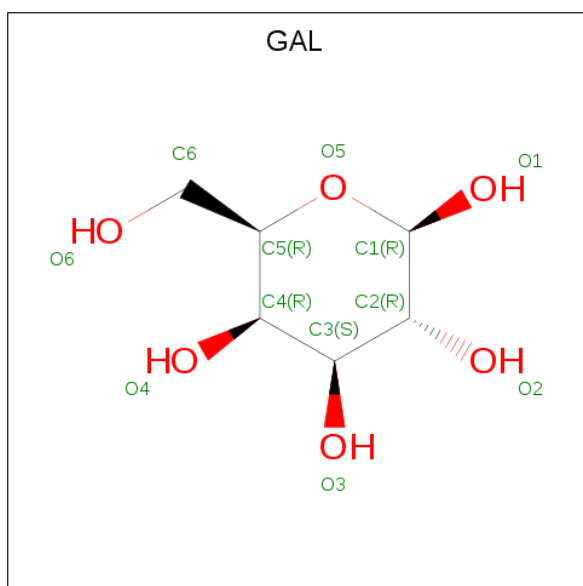
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	D	1	Total	C	N	O	0	0
			21	11	1	9		
3	E	1	Total	C	N	O	0	0
			21	11	1	9		
3	F	1	Total	C	N	O	0	0
			21	11	1	9		
3	H	1	Total	C	N	O	0	0
			21	11	1	9		
3	I	1	Total	C	N	O	0	0
			21	11	1	9		
3	L	1	Total	C	N	O	0	0
			21	11	1	9		
3	M	1	Total	C	N	O	0	0
			21	11	1	9		
3	N	1	Total	C	N	O	0	0
			21	11	1	9		
3	Q	1	Total	C	N	O	0	0
			21	11	1	9		
3	R	1	Total	C	N	O	0	0
			21	11	1	9		
3	S	1	Total	C	N	O	0	0
			21	11	1	9		

- Molecule 4 is beta-D-gulopyranose (three-letter code: GL0) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			11	6	5		
4	D	1	Total	C	O	0	0
			11	6	5		
4	F	1	Total	C	O	0	0
			11	6	5		
4	L	1	Total	C	O	0	0
			11	6	5		
4	N	1	Total	C	O	0	0
			11	6	5		
4	R	1	Total	C	O	0	0
			11	6	5		
4	S	1	Total	C	O	0	0
			11	6	5		

- Molecule 5 is BETA-D-GALACTOSE (three-letter code: GAL) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	E	1	Total	C	O	0	0
			11	6	5		
5	H	1	Total	C	O	0	0
			11	6	5		
5	I	1	Total	C	O	0	0
			11	6	5		
5	M	1	Total	C	O	0	0
			11	6	5		
5	Q	1	Total	C	O	0	0
			11	6	5		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	2	Total O 2 2	0	0
6	B	4	Total O 4 4	0	0
6	C	5	Total O 5 5	0	0
6	D	5	Total O 5 5	0	0
6	E	4	Total O 4 4	0	0
6	F	12	Total O 12 12	0	0
6	G	9	Total O 9 9	0	0
6	H	9	Total O 9 9	0	0
6	I	10	Total O 10 10	0	0
6	J	2	Total O 2 2	0	0
6	K	1	Total O 1 1	0	0
6	L	11	Total O 11 11	0	0
6	M	14	Total O 14 14	0	0
6	N	17	Total O 17 17	0	0
6	O	5	Total O 5 5	0	0
6	P	1	Total O 1 1	0	0
6	Q	13	Total O 13 13	0	0
6	R	10	Total O 10 10	0	0
6	S	7	Total O 7 7	0	0
6	T	5	Total O 5 5	0	0
6	V	1	Total O 1 1	0	0

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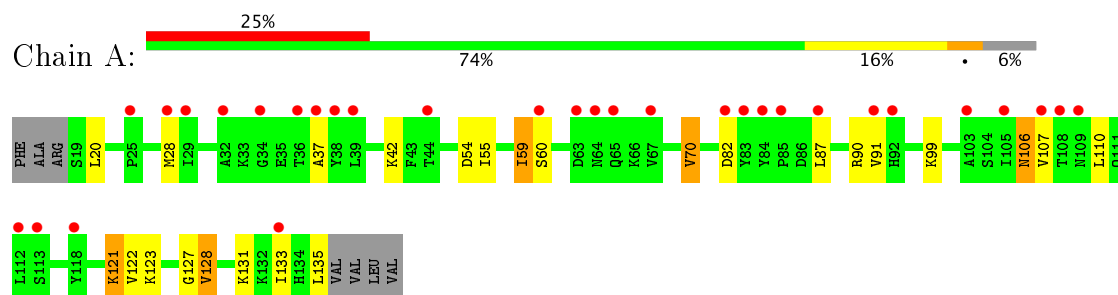
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	X	3	Total 3	O 3	0	0
6	Y	2	Total 2	O 2	0	0
6	Z	5	Total 5	O 5	0	0

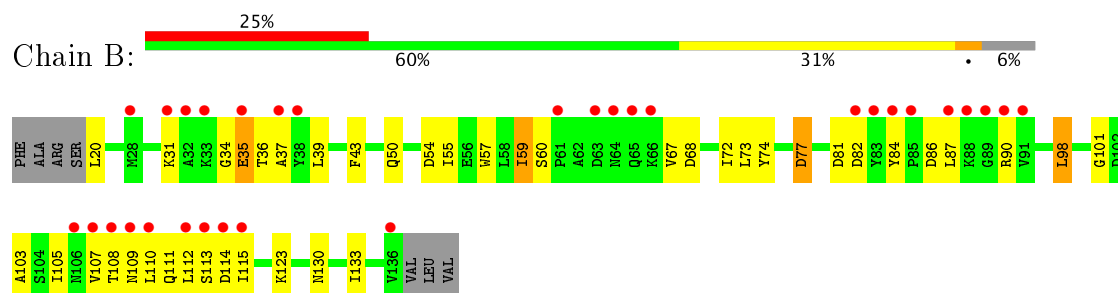
3 Residue-property plots [i](#)

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

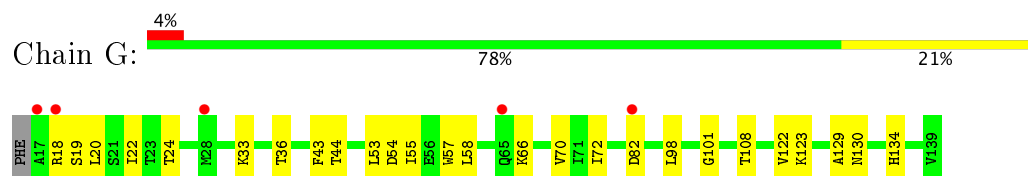
• Molecule 1: COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR



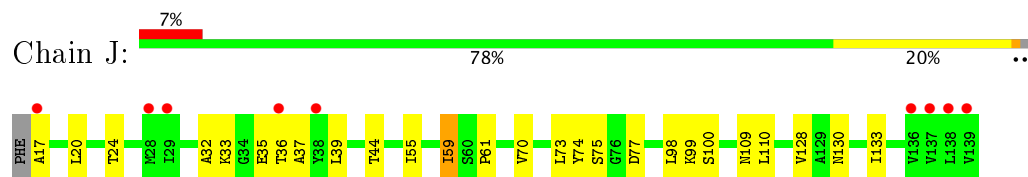
• Molecule 1: COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR



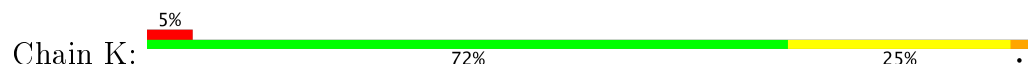
• Molecule 1: COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR

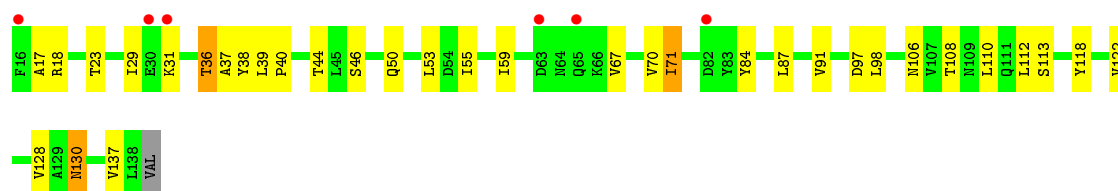


• Molecule 1: COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR

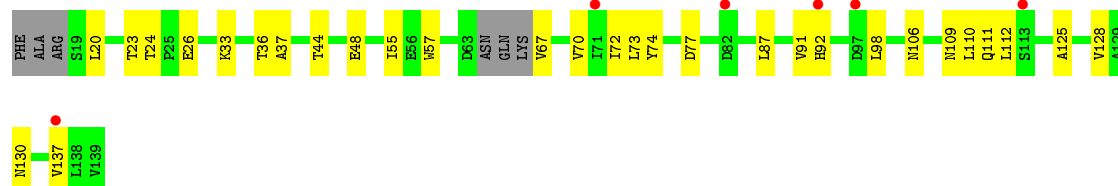


• Molecule 1: COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR

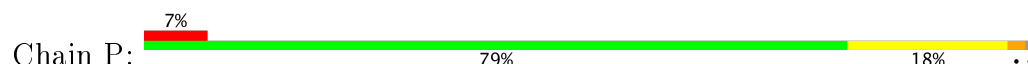




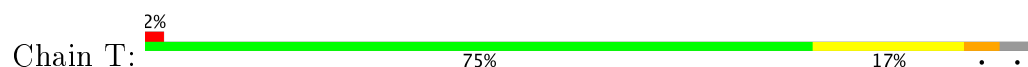
• Molecule 1: COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR



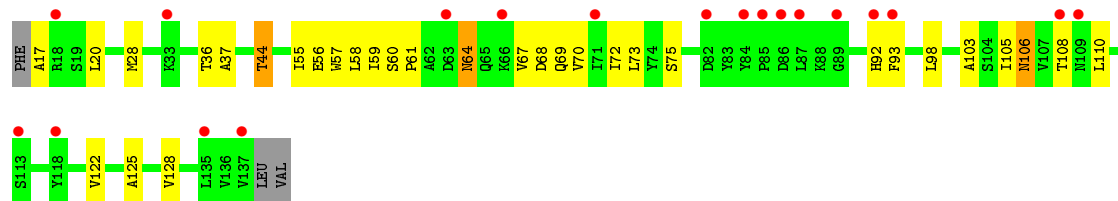
• Molecule 1: COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR



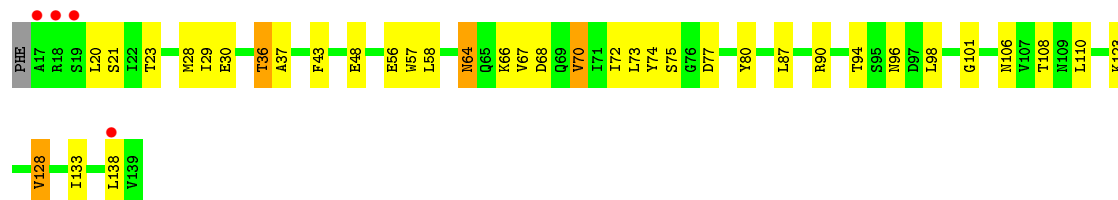
• Molecule 1: COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR



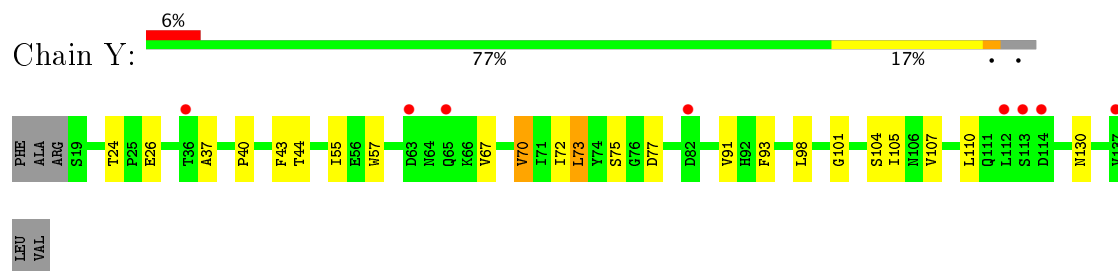
• Molecule 1: COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR



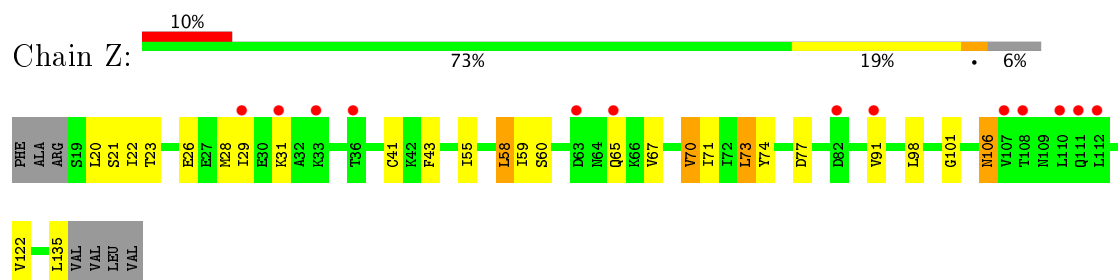
• Molecule 1: COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR



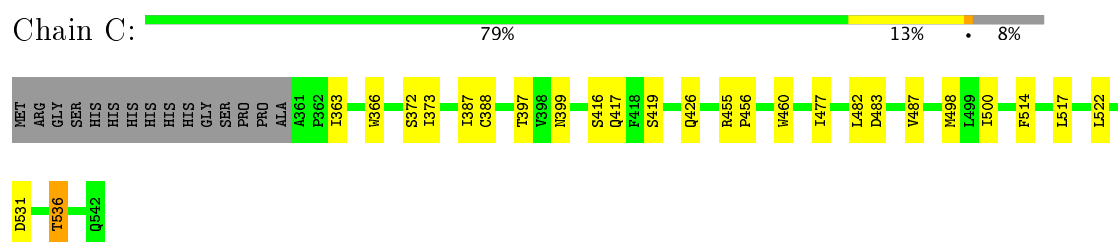
- Molecule 1: COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR



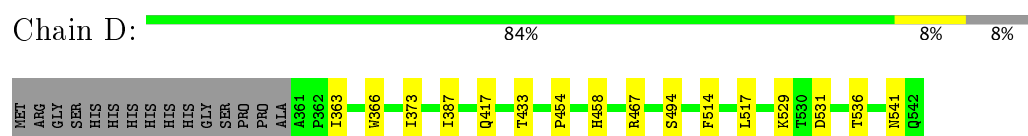
- Molecule 1: COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR



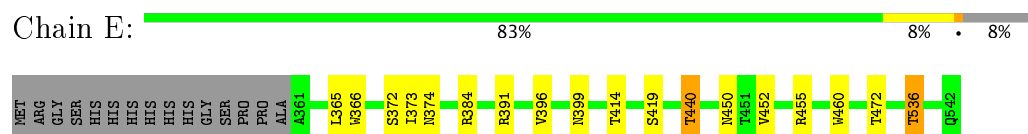
- Molecule 2: FIBRE PROTEIN



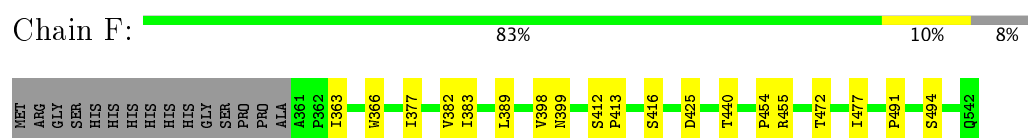
- Molecule 2: FIBRE PROTEIN



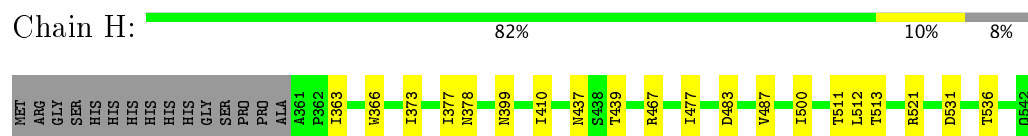
- Molecule 2: FIBRE PROTEIN



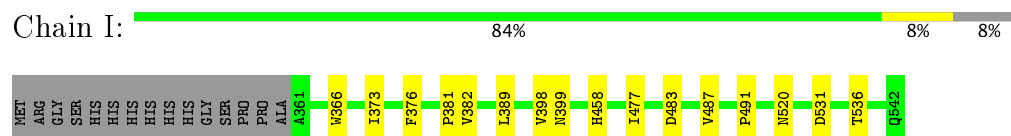
- Molecule 2: FIBRE PROTEIN



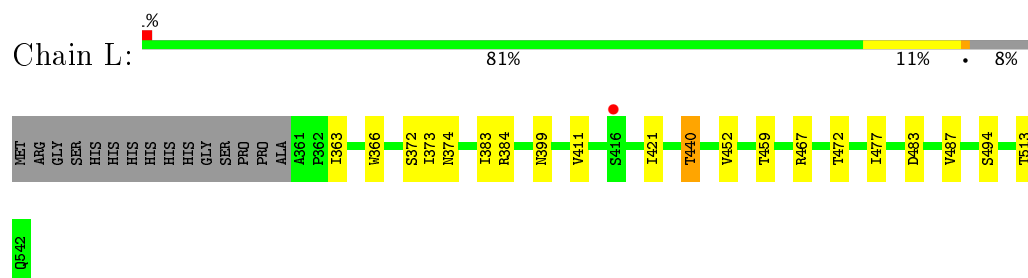
- Molecule 2: FIBRE PROTEIN



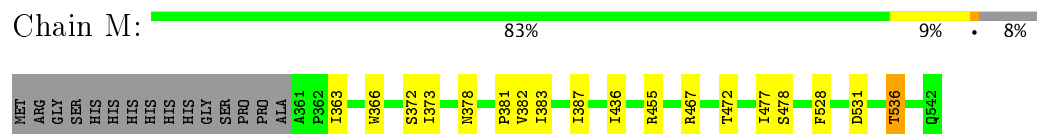
- Molecule 2: FIBRE PROTEIN



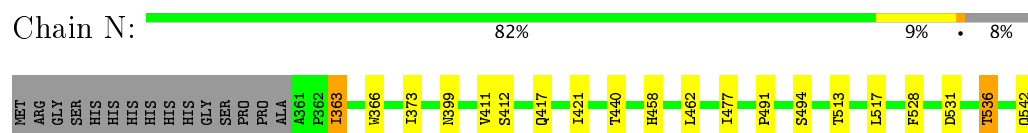
- Molecule 2: FIBRE PROTEIN



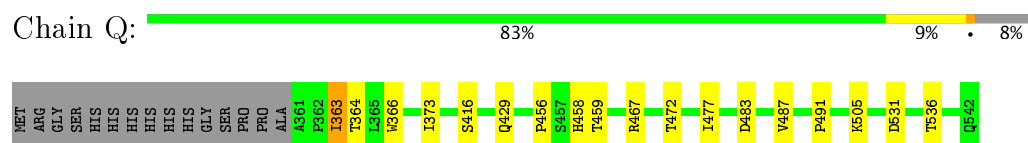
- Molecule 2: FIBRE PROTEIN



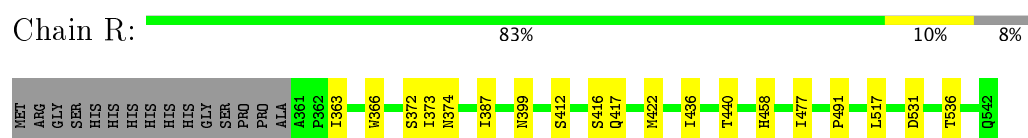
- Molecule 2: FIBRE PROTEIN



- Molecule 2: FIBRE PROTEIN



- Molecule 2: FIBRE PROTEIN



- Molecule 2: FIBRE PROTEIN

Chain S:

84%

9%

8%



4 Data and refinement statistics

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, α , β , γ	221.15Å 221.15Å 391.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.63 – 2.91 49.61 – 2.91	Depositor EDS
% Data completeness (in resolution range)	99.0 (49.63-2.91) 99.0 (49.61-2.91)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.15 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.197 , 0.254 0.196 , 0.246	Depositor DCC
R_{free} test set	1031 reflections (0.99%)	DCC
Wilson B-factor (Å ²)	46.5	Xtriage
Anisotropy	0.395	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 56.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	28671	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.13% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: GL0, SIA, GAL

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	0.48	0/932	0.62	0/1264
1	B	0.56	0/932	0.75	0/1265
1	G	0.51	0/977	0.67	0/1326
1	J	0.49	0/977	0.66	0/1326
1	K	0.52	0/982	0.67	0/1332
1	O	0.52	0/934	0.61	0/1268
1	P	0.46	0/977	0.62	0/1326
1	T	0.45	0/946	0.64	0/1284
1	V	0.46	0/962	0.62	0/1305
1	X	0.49	0/977	0.63	0/1326
1	Y	0.53	0/946	0.63	0/1284
1	Z	0.49	0/932	0.63	0/1264
2	C	0.55	1/1441 (0.1%)	0.68	0/1964
2	D	0.49	0/1441	0.66	0/1964
2	E	0.49	0/1441	0.63	0/1964
2	F	0.53	0/1441	0.65	0/1964
2	H	0.52	0/1441	0.65	0/1964
2	I	0.48	0/1441	0.63	0/1964
2	L	0.50	0/1441	0.66	0/1964
2	M	0.52	0/1441	0.66	0/1964
2	N	0.54	0/1441	0.67	0/1964
2	Q	0.49	0/1441	0.65	0/1964
2	R	0.53	0/1441	0.66	0/1964
2	S	0.49	0/1441	0.65	0/1964
All	All	0.51	1/28766 (0.0%)	0.65	0/39138

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	G	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	388	CYS	CB-SG	-6.00	1.72	1.82

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	G	82	ASP	Peptide

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	914	0	910	21	0
1	B	914	0	914	55	0
1	G	959	0	966	13	0
1	J	959	0	966	18	0
1	K	963	0	966	19	0
1	O	917	0	920	15	0
1	P	959	0	966	18	0
1	T	928	0	928	20	0
1	V	944	0	946	23	0
1	X	959	0	966	20	0
1	Y	928	0	928	13	0
1	Z	914	0	910	19	0
2	C	1406	0	1382	16	0
2	D	1406	0	1382	10	0
2	E	1406	0	1382	16	0
2	F	1406	0	1382	11	0
2	H	1406	0	1382	16	0
2	I	1406	0	1382	18	0
2	L	1406	0	1382	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	M	1406	0	1382	10	0
2	N	1406	0	1382	20	0
2	Q	1406	0	1382	13	0
2	R	1406	0	1382	15	0
2	S	1406	0	1382	16	0
3	C	21	0	17	0	0
3	D	21	0	17	0	0
3	E	21	0	17	1	0
3	F	21	0	17	0	0
3	H	21	0	17	0	0
3	I	21	0	17	0	0
3	L	21	0	17	0	0
3	M	21	0	17	0	0
3	N	21	0	17	0	0
3	Q	21	0	17	0	0
3	R	21	0	17	1	0
3	S	21	0	17	0	0
4	C	11	0	10	0	0
4	D	11	0	10	0	0
4	F	11	0	10	0	0
4	L	11	0	10	0	0
4	N	11	0	10	0	0
4	R	11	0	10	0	0
4	S	11	0	10	0	0
5	E	11	0	10	0	0
5	H	11	0	8	0	0
5	I	11	0	8	1	0
5	M	11	0	9	0	0
5	Q	11	0	8	0	0
6	A	2	0	0	0	0
6	B	4	0	0	1	0
6	C	5	0	0	0	0
6	D	5	0	0	2	0
6	E	4	0	0	2	0
6	F	12	0	0	3	0
6	G	9	0	0	3	0
6	H	9	0	0	1	0
6	I	10	0	0	2	0
6	J	2	0	0	1	0
6	K	1	0	0	1	0
6	L	11	0	0	3	0
6	M	14	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	N	17	0	0	4	0
6	O	5	0	0	0	0
6	P	1	0	0	0	0
6	Q	13	0	0	7	0
6	R	10	0	0	2	0
6	S	7	0	0	0	0
6	T	5	0	0	2	0
6	V	1	0	0	0	0
6	X	3	0	0	1	0
6	Y	2	0	0	0	0
6	Z	5	0	0	2	0
All	All	28671	0	28187	368	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 6.

All (368) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:458:HIS:CD2	6:N:703:HOH:O	1.84	1.27
1:X:28:MET:HB3	6:X:203:HOH:O	1.48	1.14
1:B:90:ARG:HD2	1:B:108:THR:O	1.48	1.10
2:Q:467:ARG:HD2	6:Q:713:HOH:O	1.51	1.09
2:I:373:ILE:HD11	1:P:70:VAL:HG21	1.10	1.08
2:L:399:ASN:HD22	2:N:536:THR:HG22	1.25	1.02
1:B:36:THR:HA	1:B:107:VAL:O	1.58	1.01
1:B:90:ARG:HB3	1:B:108:THR:O	1.60	1.01
1:B:90:ARG:HD3	1:B:109:ASN:HB3	1.40	1.00
1:B:90:ARG:CD	1:B:109:ASN:HB3	1.96	0.95
2:D:467:ARG:HD2	6:D:703:HOH:O	1.63	0.95
2:M:536:THR:HG22	2:N:399:ASN:HD22	1.32	0.95
1:B:34:GLY:O	1:B:35:GLU:HB2	1.63	0.95
1:K:37:ALA:HB2	1:K:110:LEU:HD11	1.50	0.94
1:B:36:THR:HG23	1:B:107:VAL:O	1.67	0.93
1:B:36:THR:HG23	1:B:107:VAL:C	1.90	0.90
1:B:34:GLY:O	1:B:35:GLU:CB	2.18	0.90
2:M:536:THR:HG22	2:N:399:ASN:ND2	1.87	0.90
2:Q:531:ASP:OD2	2:S:477:ILE:HG22	1.71	0.89
6:G:2005:HOH:O	2:R:440:THR:HG22	1.72	0.89
2:H:536:THR:HG22	2:I:399:ASN:HD22	1.35	0.89
2:C:536:THR:HG22	2:H:399:ASN:HD22	1.38	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:536:THR:HG22	2:F:399:ASN:HD22	1.38	0.86
2:C:536:THR:HG22	2:H:399:ASN:ND2	1.90	0.86
2:H:467:ARG:HD2	6:H:708:HOH:O	1.74	0.86
5:I:602:GAL:H5	6:I:708:HOH:O	1.75	0.86
2:S:377:ILE:HG22	2:S:378:ASN:ND2	1.90	0.85
1:B:90:ARG:HA	1:B:108:THR:HB	1.60	0.84
1:B:36:THR:CG2	1:B:107:VAL:O	2.26	0.84
2:R:491:PRO:HD2	6:R:708:HOH:O	1.78	0.82
2:S:377:ILE:HG22	2:S:378:ASN:HD22	1.45	0.81
2:I:373:ILE:CD1	1:P:70:VAL:HG21	2.03	0.81
2:I:373:ILE:HD11	1:P:70:VAL:CG2	2.04	0.78
1:T:137:VAL:O	6:T:201:HOH:O	2.00	0.78
2:L:399:ASN:ND2	2:N:536:THR:HG22	1.98	0.77
1:P:139:VAL:O	1:P:139:VAL:HG12	1.85	0.77
2:E:536:THR:HG22	2:F:399:ASN:ND2	2.00	0.76
2:H:536:THR:HG22	2:I:399:ASN:ND2	2.01	0.76
1:K:55:ILE:HD12	1:K:122:VAL:HG22	1.67	0.76
1:B:90:ARG:CD	1:B:108:THR:O	2.32	0.75
2:E:373:ILE:HD12	1:O:73:LEU:HD11	1.68	0.75
2:L:531:ASP:OD2	2:N:477:ILE:HG22	1.87	0.74
2:N:491:PRO:HD2	6:N:706:HOH:O	1.87	0.73
2:C:399:ASN:HD22	2:I:536:THR:HG22	1.53	0.73
2:N:373:ILE:HD11	1:Y:70:VAL:HG11	1.71	0.72
1:A:121:LYS:HD3	6:Q:707:HOH:O	1.89	0.72
1:O:37:ALA:HB2	1:O:110:LEU:HD11	1.69	0.72
2:F:454:PRO:HD2	6:F:710:HOH:O	1.89	0.72
2:H:477:ILE:HG22	2:I:531:ASP:OD2	1.90	0.72
1:J:98:LEU:C	1:J:98:LEU:HD23	2.10	0.72
1:B:36:THR:CA	1:B:107:VAL:O	2.36	0.71
1:J:99:LYS:HE2	6:J:2002:HOH:O	1.91	0.70
1:B:55:ILE:HD13	1:B:103:ALA:HB2	1.73	0.69
1:P:17:ALA:HB1	1:P:45:LEU:O	1.93	0.69
2:Q:477:ILE:HG22	2:R:531:ASP:OD2	1.94	0.68
1:Y:55:ILE:HD12	1:Y:98:LEU:HD21	1.75	0.68
1:A:59:ILE:HD12	1:A:60:SER:N	2.08	0.68
2:M:536:THR:CG2	2:N:399:ASN:HD22	2.05	0.68
1:T:36:THR:HB	1:T:108:THR:HA	1.75	0.68
1:B:90:ARG:O	1:B:108:THR:N	2.27	0.67
1:B:86:ASP:OD2	1:B:113:SER:HB2	1.94	0.67
1:K:53:LEU:HD11	1:K:55:ILE:HD11	1.75	0.67
1:B:108:THR:HG22	1:B:109:ASN:N	2.09	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:37:ALA:HB2	1:V:110:LEU:HD11	1.77	0.66
1:P:55:ILE:CD1	1:P:122:VAL:HG13	2.25	0.66
1:V:92:HIS:CE1	1:V:106:ASN:HD21	2.12	0.66
1:P:55:ILE:HD12	1:P:122:VAL:HG22	1.78	0.66
2:L:399:ASN:HD22	2:N:536:THR:CG2	2.04	0.66
2:M:382:VAL:HG23	2:M:383:ILE:HG12	1.77	0.66
1:B:110:LEU:HD12	1:B:114:ASP:OD2	1.95	0.65
2:E:373:ILE:HD11	1:O:70:VAL:HG21	1.78	0.65
1:A:121:LYS:HE2	6:Q:707:HOH:O	1.96	0.64
1:Z:98:LEU:CD1	6:Z:204:HOH:O	2.45	0.64
1:A:55:ILE:HD12	1:A:122:VAL:HG22	1.80	0.64
2:H:521:ARG:HH21	2:I:491:PRO:HB3	1.63	0.64
1:V:56:GLU:HB3	1:V:73:LEU:HD12	1.80	0.64
1:V:36:THR:HG22	1:V:108:THR:HA	1.79	0.63
2:N:531:ASP:OD1	6:N:701:HOH:O	2.16	0.62
2:C:399:ASN:ND2	2:I:536:THR:HG22	2.13	0.62
1:T:60:SER:HB3	1:T:67:VAL:HG23	1.81	0.62
2:L:421:ILE:HG12	2:L:513:THR:HG23	1.81	0.62
2:F:377:ILE:HD12	2:F:382:VAL:HG21	1.82	0.62
1:Z:58:LEU:HD12	1:Z:58:LEU:N	2.15	0.61
1:B:110:LEU:CD1	1:B:114:ASP:OD2	2.47	0.61
2:C:536:THR:CG2	2:H:399:ASN:HD22	2.12	0.61
2:L:467:ARG:HD2	6:L:2011:HOH:O	2.00	0.61
1:X:29:ILE:HD12	1:X:133:ILE:HG21	1.83	0.61
2:L:477:ILE:HG22	2:M:531:ASP:OD2	2.00	0.61
1:A:37:ALA:HB2	1:A:110:LEU:HD11	1.83	0.61
1:B:90:ARG:HD2	1:B:109:ASN:HB3	1.80	0.61
1:G:57:TRP:HB2	1:G:72:ILE:HG22	1.81	0.61
1:X:123:LYS:HG2	1:X:128:VAL:HG13	1.83	0.60
1:B:90:ARG:HD3	1:B:109:ASN:CB	2.26	0.60
2:R:536:THR:HG22	2:S:399:ASN:ND2	2.15	0.60
1:B:90:ARG:CA	1:B:108:THR:HB	2.32	0.60
1:B:90:ARG:CB	1:B:108:THR:O	2.42	0.60
1:J:55:ILE:CD1	1:J:98:LEU:HD21	2.32	0.60
1:K:17:ALA:HB2	1:K:44:THR:HG21	1.84	0.59
2:C:531:ASP:OD2	2:I:477:ILE:HG22	2.02	0.59
1:O:55:ILE:HD12	1:O:98:LEU:HD21	1.82	0.59
1:Y:93:PHE:HA	1:Y:105:ILE:HG22	1.84	0.59
1:T:123:LYS:HG2	1:T:128:VAL:HG13	1.84	0.59
1:T:57:TRP:HB2	1:T:72:ILE:HG22	1.84	0.59
1:B:34:GLY:O	1:B:35:GLU:CG	2.50	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:74:TYR:CE1	1:B:98:LEU:HD22	2.38	0.59
2:C:373:ILE:HD11	1:T:70:VAL:HG11	1.84	0.59
2:D:458:HIS:HB3	6:I:709:HOH:O	2.03	0.58
1:J:39:LEU:HD22	1:J:133:ILE:HG21	1.85	0.58
1:X:94:THR:HG22	1:X:106:ASN:HD22	1.67	0.58
1:V:67:VAL:HG22	1:V:68:ASP:OD1	2.02	0.58
1:B:67:VAL:HG12	1:B:68:ASP:OD2	2.04	0.58
1:J:37:ALA:HB2	1:J:110:LEU:HD11	1.84	0.58
1:Y:37:ALA:HB2	1:Y:110:LEU:HD11	1.86	0.58
2:Q:491:PRO:HD2	6:Q:702:HOH:O	2.04	0.57
1:A:55:ILE:CD1	1:A:122:VAL:HG22	2.35	0.57
1:P:123:LYS:HG2	1:P:128:VAL:HG13	1.85	0.57
2:L:374:ASN:HB2	2:L:440:THR:HG21	1.84	0.57
1:A:106:ASN:HD22	1:A:106:ASN:C	2.06	0.57
1:K:71:ILE:HG22	1:K:84:TYR:CB	2.35	0.57
2:L:483:ASP:O	2:L:487:VAL:HG22	2.05	0.57
1:A:70:VAL:HG11	2:Q:373:ILE:HD11	1.86	0.57
1:T:20:LEU:HD12	1:T:21:SER:N	2.20	0.57
1:G:70:VAL:HG21	2:R:373:ILE:HD11	1.86	0.56
6:D:705:HOH:O	2:I:458:HIS:HB3	2.05	0.56
1:J:17:ALA:CB	1:J:44:THR:HG21	2.35	0.56
1:X:67:VAL:HG12	1:X:68:ASP:OD1	2.05	0.56
1:O:112:LEU:HD23	1:O:137:VAL:HG12	1.88	0.56
1:B:39:LEU:HD12	1:B:105:ILE:HD11	1.88	0.56
2:Q:363:ILE:HD13	2:Q:364:THR:N	2.21	0.56
1:K:31:LYS:O	1:K:137:VAL:HA	2.05	0.56
1:X:36:THR:HB	1:X:108:THR:HA	1.88	0.56
1:B:108:THR:CG2	1:B:109:ASN:N	2.69	0.55
1:V:60:SER:OG	1:V:67:VAL:HG23	2.06	0.55
1:B:73:LEU:CD2	2:D:373:ILE:HD12	2.37	0.55
2:S:411:VAL:HG13	2:S:528:PHE:HB2	1.88	0.55
1:Z:98:LEU:HD12	6:Z:204:HOH:O	2.07	0.55
1:A:87:LEU:HD23	1:A:90:ARG:NH2	2.22	0.55
2:E:373:ILE:CD1	1:O:73:LEU:HD11	2.37	0.55
2:M:477:ILE:HG22	2:N:531:ASP:OD2	2.05	0.55
1:Y:55:ILE:CD1	1:Y:98:LEU:HD21	2.37	0.55
2:R:458:HIS:HD2	6:R:705:HOH:O	1.89	0.55
2:D:536:THR:HG22	2:E:399:ASN:HD22	1.72	0.54
2:S:421:ILE:HG12	2:S:513:THR:HG23	1.89	0.54
2:N:373:ILE:CD1	1:Y:70:VAL:HG11	2.37	0.54
2:H:511:THR:O	2:H:512:LEU:HD23	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:115:ILE:HA	6:B:201:HOH:O	2.07	0.54
1:B:90:ARG:HB3	1:B:108:THR:C	2.26	0.54
6:G:2005:HOH:O	2:R:440:THR:CG2	2.44	0.54
2:S:373:ILE:HD11	1:Z:70:VAL:HG11	1.90	0.54
1:X:74:TYR:CZ	1:X:77:ASP:HA	2.43	0.54
1:A:110:LEU:HD21	1:A:135:LEU:HD21	1.90	0.54
1:G:33:LYS:NZ	6:G:2001:HOH:O	2.39	0.54
1:T:98:LEU:C	1:T:98:LEU:HD23	2.27	0.54
1:G:54:ASP:HB3	1:G:123:LYS:HB2	1.90	0.53
2:H:437:ASN:OD1	2:H:439:THR:HB	2.08	0.53
1:P:36:THR:HG21	1:P:108:THR:HG22	1.91	0.53
1:X:37:ALA:HB2	1:X:110:LEU:HD11	1.90	0.53
1:K:59:ILE:HD13	1:K:118:TYR:CZ	2.44	0.52
1:Z:59:ILE:O	1:Z:59:ILE:HG23	2.09	0.52
2:Q:505:LYS:HD2	6:Q:709:HOH:O	2.08	0.52
1:V:17:ALA:HB2	1:V:44:THR:HG21	1.90	0.52
2:R:374:ASN:HA	2:R:440:THR:HG21	1.91	0.52
2:C:482:LEU:HD12	2:C:522:LEU:HD21	1.92	0.52
2:I:373:ILE:HB	1:P:73:LEU:HD11	1.92	0.52
2:N:458:HIS:HD2	6:N:703:HOH:O	1.47	0.51
1:G:22:ILE:HG13	1:G:129:ALA:HB1	1.92	0.51
2:F:389:LEU:CD2	2:F:398:VAL:HG22	2.40	0.51
1:B:34:GLY:C	1:B:35:GLU:HG3	2.30	0.51
1:B:90:ARG:CD	1:B:109:ASN:CB	2.81	0.51
1:X:43:PHE:CZ	1:X:101:GLY:HA2	2.45	0.51
1:G:53:LEU:HD11	1:G:55:ILE:HD11	1.93	0.51
2:H:483:ASP:O	2:H:487:VAL:HG22	2.10	0.51
1:P:87:LEU:HD23	1:P:90:ARG:NH2	2.25	0.51
2:Q:458:HIS:CE1	2:Q:459:THR:HG23	2.46	0.51
1:V:93:PHE:HA	1:V:105:ILE:HG22	1.93	0.51
1:J:32:ALA:HB3	1:J:35:GLU:HG2	1.93	0.51
1:X:56:GLU:OE2	1:X:58:LEU:HD21	2.11	0.51
2:H:536:THR:CG2	2:I:399:ASN:HD22	2.16	0.51
1:X:30:GLU:HG2	1:X:138:LEU:HD11	1.93	0.51
1:B:34:GLY:O	1:B:35:GLU:HG3	2.12	0.50
2:E:452:VAL:O	1:O:125:ALA:HB1	2.11	0.50
1:K:70:VAL:HG12	6:K:2001:HOH:O	2.11	0.50
1:K:36:THR:HB	1:K:108:THR:HA	1.94	0.50
1:B:39:LEU:HB3	1:B:133:ILE:HD12	1.93	0.50
1:B:54:ASP:HB3	1:B:123:LYS:HB2	1.93	0.50
1:V:106:ASN:HD22	1:V:106:ASN:C	2.14	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:31:LYS:HG3	1:B:37:ALA:HB2	1.92	0.50
1:Y:98:LEU:HD23	1:Y:98:LEU:C	2.32	0.50
1:J:98:LEU:O	1:J:98:LEU:HD23	2.11	0.50
2:R:536:THR:HG22	2:S:399:ASN:HD22	1.75	0.50
1:Z:29:ILE:HG22	1:Z:31:LYS:CE	2.41	0.50
1:Z:55:ILE:HG12	1:Z:122:VAL:HG22	1.94	0.50
1:A:123:LYS:HG2	1:A:128:VAL:HG22	1.94	0.49
2:L:440:THR:HG22	6:L:2003:HOH:O	2.12	0.49
2:S:477:ILE:O	2:S:477:ILE:HG23	2.12	0.49
1:B:86:ASP:OD2	1:B:113:SER:CB	2.59	0.49
1:O:57:TRP:HB2	1:O:72:ILE:HG22	1.94	0.49
1:K:130:ASN:OD1	1:K:130:ASN:N	2.46	0.49
1:J:32:ALA:HB3	1:J:35:GLU:CG	2.41	0.49
1:O:20:LEU:C	1:O:20:LEU:HD23	2.33	0.49
2:R:387:ILE:HD11	2:R:436:ILE:HD13	1.93	0.49
1:A:121:LYS:CD	6:Q:707:HOH:O	2.56	0.49
2:C:477:ILE:HG22	2:H:531:ASP:OD2	2.13	0.49
1:T:20:LEU:C	1:T:20:LEU:HD12	2.32	0.49
1:B:57:TRP:HB2	1:B:72:ILE:HG22	1.95	0.49
1:J:74:TYR:CZ	1:J:77:ASP:HA	2.47	0.49
1:V:93:PHE:CD1	1:V:98:LEU:HD21	2.48	0.49
1:J:98:LEU:CD2	1:J:98:LEU:C	2.81	0.49
1:K:71:ILE:HG22	1:K:84:TYR:HB2	1.95	0.49
2:D:531:ASP:OD2	2:F:477:ILE:HG22	2.13	0.49
2:S:373:ILE:HD12	1:Z:73:LEU:CD2	2.43	0.49
1:A:91:VAL:HG13	1:A:107:VAL:HG22	1.95	0.49
1:B:43:PHE:CZ	1:B:101:GLY:HA2	2.48	0.49
1:O:87:LEU:HD22	1:O:91:VAL:CG2	2.43	0.48
2:C:373:ILE:CD1	1:T:70:VAL:HG11	2.43	0.48
2:E:374:ASN:HB2	2:E:440:THR:HG21	1.95	0.48
2:Q:429:GLN:HE21	2:Q:456:PRO:CB	2.26	0.48
1:B:84:TYR:CD2	1:B:87:LEU:HD12	2.48	0.48
1:V:20:LEU:HD11	1:V:122:VAL:HG12	1.93	0.48
1:V:59:ILE:HG22	1:V:69:GLN:O	2.13	0.48
2:C:387:ILE:HD13	2:C:514:PHE:CE2	2.48	0.48
2:C:483:ASP:O	2:C:487:VAL:HG22	2.14	0.48
2:F:382:VAL:HG23	2:F:383:ILE:HG12	1.95	0.48
2:E:455:ARG:HB3	6:E:703:HOH:O	2.13	0.48
1:V:17:ALA:HB2	1:V:44:THR:CG2	2.43	0.48
1:T:31:LYS:HD2	1:T:37:ALA:HA	1.95	0.48
1:P:36:THR:CG2	1:P:108:THR:HG22	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:20:LEU:HD11	1:Z:122:VAL:HG12	1.96	0.48
2:L:363:ILE:HD12	2:L:459:THR:OG1	2.14	0.47
1:Z:29:ILE:HG22	1:Z:31:LYS:HE2	1.96	0.47
2:H:377:ILE:HG22	2:H:378:ASN:ND2	2.28	0.47
1:Y:43:PHE:CZ	1:Y:101:GLY:HA2	2.49	0.47
2:N:363:ILE:C	2:N:363:ILE:HD13	2.34	0.47
1:P:55:ILE:HD13	1:P:122:VAL:HG13	1.94	0.47
1:B:74:TYR:CZ	1:B:77:ASP:HA	2.49	0.47
1:K:87:LEU:HB3	1:K:91:VAL:HG23	1.97	0.47
2:Q:363:ILE:C	2:Q:363:ILE:HD13	2.35	0.47
6:L:2001:HOH:O	1:V:73:LEU:HD11	2.15	0.47
1:T:28:MET:HE2	1:T:28:MET:CA	2.45	0.47
1:B:74:TYR:CZ	1:B:98:LEU:HD22	2.50	0.47
2:Q:483:ASP:O	2:Q:487:VAL:HG22	2.14	0.47
2:R:477:ILE:HG22	2:S:531:ASP:OD2	2.14	0.47
1:T:31:LYS:O	1:T:137:VAL:HA	2.15	0.47
2:L:383:ILE:HD12	2:L:528:PHE:HE2	1.80	0.47
1:X:87:LEU:HD23	1:X:90:ARG:NH2	2.30	0.47
1:Z:43:PHE:CZ	1:Z:101:GLY:HA2	2.49	0.47
1:T:57:TRP:CH2	1:T:120:CYS:HB2	2.50	0.47
1:B:109:ASN:O	1:B:111:GLN:HG2	2.15	0.46
1:X:20:LEU:HD23	1:X:21:SER:N	2.30	0.46
1:J:36:THR:HG22	1:J:109:ASN:H	1.81	0.46
1:T:95:SER:HB3	6:T:202:HOH:O	2.16	0.46
1:O:112:LEU:HD23	1:O:137:VAL:CG1	2.45	0.46
1:G:36:THR:HG21	1:G:108:THR:HG22	1.98	0.46
1:Z:106:ASN:HD22	1:Z:106:ASN:HA	1.63	0.46
1:P:55:ILE:HD11	1:P:122:VAL:HG13	1.95	0.46
1:V:58:LEU:HD23	1:V:70:VAL:HA	1.97	0.46
2:M:373:ILE:HD11	1:X:70:VAL:HG21	1.97	0.46
1:A:131:LYS:HE3	1:A:133:ILE:HD11	1.97	0.46
2:I:483:ASP:O	2:I:487:VAL:HG22	2.16	0.46
1:V:61:PRO:HG2	1:V:64:ASN:HB2	1.96	0.46
2:C:417:GLN:HB2	2:C:517:LEU:HD23	1.98	0.45
1:V:20:LEU:C	1:V:20:LEU:HD23	2.37	0.45
1:A:54:ASP:HB3	1:A:123:LYS:HB2	1.98	0.45
2:E:536:THR:CG2	2:F:399:ASN:HD22	2.20	0.45
2:N:417:GLN:HB2	2:N:517:LEU:HD23	1.98	0.45
1:P:55:ILE:O	1:P:73:LEU:HD23	2.16	0.45
2:I:520:ASN:H	2:I:520:ASN:HD22	1.64	0.45
1:A:87:LEU:HB3	1:A:91:VAL:HG23	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:36:THR:CG2	1:G:108:THR:HG22	2.46	0.45
2:E:455:ARG:CB	6:E:703:HOH:O	2.64	0.45
2:E:419:SER:O	3:E:601:SIA:O9	2.35	0.45
2:R:417:GLN:HB2	2:R:517:LEU:HD23	1.99	0.45
1:A:121:LYS:CE	6:Q:707:HOH:O	2.61	0.45
1:J:55:ILE:HD12	1:J:98:LEU:HD21	1.99	0.45
2:H:500:ILE:HB	2:H:513:THR:HB	1.99	0.45
1:X:64:ASN:HD22	1:X:66:LYS:H	1.65	0.45
1:B:36:THR:HG23	1:B:108:THR:N	2.32	0.44
1:T:60:SER:CB	1:T:67:VAL:HG23	2.45	0.44
1:V:57:TRP:HB2	1:V:72:ILE:HG22	2.00	0.44
1:X:73:LEU:HD11	1:X:80:TYR:HB2	2.00	0.44
1:K:38:TYR:O	1:K:40:PRO:HD3	2.17	0.44
1:Y:24:THR:HG22	1:Y:26:GLU:O	2.18	0.44
2:E:365:LEU:HD21	2:E:460:TRP:CD2	2.53	0.44
1:B:59:ILE:HD13	1:B:60:SER:N	2.33	0.44
1:K:55:ILE:CD1	1:K:122:VAL:HG13	2.48	0.44
1:V:59:ILE:O	1:V:59:ILE:HG23	2.18	0.44
1:A:20:LEU:HD11	1:A:122:VAL:HG12	2.00	0.44
2:M:383:ILE:HD12	2:M:528:PHE:HE2	1.81	0.44
1:X:57:TRP:HB2	1:X:72:ILE:HG22	2.00	0.44
2:L:373:ILE:HD11	1:V:70:VAL:HG21	1.99	0.43
1:K:59:ILE:HG22	1:K:71:ILE:HG23	1.99	0.43
1:G:57:TRP:O	1:G:58:LEU:HD23	2.19	0.43
2:N:373:ILE:HB	1:Y:73:LEU:HD11	2.00	0.43
2:H:373:ILE:HD11	1:J:70:VAL:HG11	2.00	0.43
1:J:17:ALA:HB3	1:J:44:THR:HG21	1.99	0.43
1:B:84:TYR:HD2	1:B:87:LEU:HD12	1.84	0.43
1:B:50:GLN:HB2	2:D:454:PRO:HG2	2.00	0.43
1:J:59:ILE:HD13	1:J:61:PRO:HD3	2.00	0.43
1:X:43:PHE:CE1	1:X:101:GLY:HA2	2.54	0.43
1:X:94:THR:CG2	1:X:106:ASN:HD22	2.32	0.43
1:K:71:ILE:HG22	1:K:84:TYR:CG	2.54	0.43
2:N:462:LEU:HD21	2:N:542:GLN:HB2	2.01	0.43
1:O:91:VAL:HA	1:O:106:ASN:O	2.18	0.43
1:G:98:LEU:HD23	1:G:98:LEU:C	2.40	0.43
2:Q:429:GLN:HE21	2:Q:456:PRO:HB3	1.84	0.43
2:S:373:ILE:HD12	1:Z:73:LEU:HD21	2.01	0.42
1:B:20:LEU:HD23	1:B:20:LEU:C	2.39	0.42
1:B:35:GLU:O	1:B:110:LEU:N	2.47	0.42
2:D:541:ASN:ND2	2:E:450:ASN:OD1	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:17:ALA:HB2	1:J:44:THR:HG21	2.01	0.42
2:R:416:SER:OG	3:R:601:SIA:H113	2.19	0.42
2:C:373:ILE:HD11	1:T:70:VAL:HG21	2.01	0.42
1:X:20:LEU:HD23	1:X:20:LEU:C	2.39	0.42
1:A:87:LEU:HB3	1:A:91:VAL:CG2	2.49	0.42
1:B:90:ARG:HD2	1:B:108:THR:C	2.30	0.42
2:F:491:PRO:HD2	6:F:701:HOH:O	2.18	0.42
1:K:98:LEU:HD23	1:K:98:LEU:C	2.40	0.42
2:N:411:VAL:HG13	2:N:528:PHE:HB2	2.01	0.42
1:Y:57:TRP:HB2	1:Y:72:ILE:HG22	2.01	0.42
1:A:59:ILE:HD12	1:A:60:SER:H	1.84	0.42
2:S:466:ASN:OD1	2:S:469:VAL:HG23	2.20	0.42
1:Z:20:LEU:HD23	1:Z:21:SER:N	2.35	0.42
1:G:43:PHE:CZ	1:G:101:GLY:HA2	2.54	0.42
1:Z:60:SER:OG	1:Z:67:VAL:HG23	2.19	0.42
2:D:417:GLN:HB2	2:D:517:LEU:HD23	2.02	0.41
1:G:55:ILE:CD1	1:G:122:VAL:HG13	2.50	0.41
1:V:55:ILE:HD13	1:V:103:ALA:HB2	2.02	0.41
1:O:24:THR:HG22	1:O:26:GLU:O	2.21	0.41
1:P:55:ILE:CD1	1:P:122:VAL:HG22	2.48	0.41
1:P:98:LEU:HD23	1:P:98:LEU:C	2.41	0.41
1:T:98:LEU:HD23	1:T:99:LYS:N	2.34	0.41
1:Z:22:ILE:HD13	1:Z:41:CYS:SG	2.60	0.41
1:B:90:ARG:NH2	1:B:111:GLN:HG3	2.36	0.41
2:F:425:ASP:HA	6:F:706:HOH:O	2.19	0.41
1:Y:40:PRO:HA	1:Y:104:SER:OG	2.20	0.41
1:B:73:LEU:HD23	2:D:373:ILE:HD12	2.02	0.41
2:L:452:VAL:O	1:V:125:ALA:HB1	2.21	0.41
1:A:127:GLY:O	1:A:128:VAL:HG23	2.21	0.41
1:G:19:SER:OG	1:G:20:LEU:N	2.53	0.41
2:I:376:PHE:CZ	2:I:381:PRO:HG3	2.56	0.41
2:I:520:ASN:H	2:I:520:ASN:ND2	2.19	0.41
1:J:24:THR:O	1:J:24:THR:HG22	2.20	0.41
1:O:55:ILE:HB	1:O:74:TYR:HB3	2.03	0.41
2:Q:536:THR:HG22	2:R:399:ASN:HD22	1.86	0.41
2:S:373:ILE:CD1	1:Z:70:VAL:HG11	2.51	0.41
2:N:421:ILE:HG12	2:N:513:THR:HG23	2.03	0.41
1:T:37:ALA:HB2	1:T:110:LEU:HD11	2.02	0.41
1:K:29:ILE:HD12	1:K:39:LEU:HD23	2.03	0.41
2:F:413:PRO:HB2	2:M:378:ASN:HB3	2.02	0.41
2:E:414:THR:HG21	2:S:378:ASN:CB	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:91:VAL:HG12	1:Y:107:VAL:HG22	2.03	0.41
1:Z:74:TYR:CZ	1:Z:77:ASP:HA	2.56	0.41
1:B:108:THR:CG2	1:B:109:ASN:H	2.34	0.41
2:R:422:MET:HG2	2:R:436:ILE:HB	2.03	0.41
1:T:53:LEU:HD12	1:T:54:ASP:H	1.86	0.41
1:V:56:GLU:CB	1:V:73:LEU:HD12	2.49	0.41
2:D:387:ILE:HD13	2:D:514:PHE:CE2	2.55	0.40
1:O:36:THR:HG22	1:O:109:ASN:H	1.85	0.40
1:P:29:ILE:O	1:P:135:LEU:HD12	2.21	0.40
2:S:430:LEU:HD21	2:S:437:ASN:C	2.41	0.40
2:E:391:ARG:HB2	2:E:396:VAL:HG22	2.03	0.40
1:Z:29:ILE:O	1:Z:135:LEU:HD12	2.22	0.40
2:C:498:MET:CE	2:C:500:ILE:HD11	2.52	0.40
2:I:389:LEU:HD22	2:I:398:VAL:HG22	2.02	0.40
2:M:387:ILE:HD11	2:M:436:ILE:HD13	2.04	0.40
1:B:72:ILE:HG13	1:B:81:ASP:HB3	2.02	0.40
2:C:456:PRO:HA	2:C:460:TRP:CZ2	2.57	0.40
1:K:29:ILE:HD12	1:K:39:LEU:CD2	2.51	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	115/124 (93%)	104 (90%)	11 (10%)	0	100	100
1	B	115/124 (93%)	104 (90%)	10 (9%)	1 (1%)	20	53
1	G	121/124 (98%)	110 (91%)	11 (9%)	0	100	100
1	J	121/124 (98%)	113 (93%)	8 (7%)	0	100	100
1	K	121/124 (98%)	107 (88%)	14 (12%)	0	100	100
1	O	114/124 (92%)	106 (93%)	8 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	P	121/124 (98%)	111 (92%)	8 (7%)	2 (2%)	11	35
1	T	117/124 (94%)	104 (89%)	13 (11%)	0	100	100
1	V	119/124 (96%)	113 (95%)	6 (5%)	0	100	100
1	X	121/124 (98%)	116 (96%)	5 (4%)	0	100	100
1	Y	117/124 (94%)	113 (97%)	4 (3%)	0	100	100
1	Z	115/124 (93%)	104 (90%)	10 (9%)	1 (1%)	20	53
2	C	180/197 (91%)	171 (95%)	9 (5%)	0	100	100
2	D	180/197 (91%)	172 (96%)	8 (4%)	0	100	100
2	E	180/197 (91%)	171 (95%)	9 (5%)	0	100	100
2	F	180/197 (91%)	169 (94%)	11 (6%)	0	100	100
2	H	180/197 (91%)	170 (94%)	10 (6%)	0	100	100
2	I	180/197 (91%)	172 (96%)	8 (4%)	0	100	100
2	L	180/197 (91%)	171 (95%)	9 (5%)	0	100	100
2	M	180/197 (91%)	170 (94%)	10 (6%)	0	100	100
2	N	180/197 (91%)	171 (95%)	9 (5%)	0	100	100
2	Q	180/197 (91%)	171 (95%)	9 (5%)	0	100	100
2	R	180/197 (91%)	170 (94%)	10 (6%)	0	100	100
2	S	180/197 (91%)	170 (94%)	10 (6%)	0	100	100
All	All	3577/3852 (93%)	3353 (94%)	220 (6%)	4 (0%)	55	85

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	35	GLU
1	P	63	ASP
1	Z	65	GLN
1	P	24	THR

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	104/110 (94%)	95 (91%)	9 (9%)	12	34
1	B	104/110 (94%)	98 (94%)	6 (6%)	23	55
1	G	109/110 (99%)	103 (94%)	6 (6%)	25	57
1	J	109/110 (99%)	101 (93%)	8 (7%)	16	42
1	K	109/110 (99%)	96 (88%)	13 (12%)	6	17
1	O	105/110 (96%)	95 (90%)	10 (10%)	10	29
1	P	109/110 (99%)	99 (91%)	10 (9%)	11	31
1	T	106/110 (96%)	97 (92%)	9 (8%)	12	34
1	V	107/110 (97%)	101 (94%)	6 (6%)	25	56
1	X	109/110 (99%)	100 (92%)	9 (8%)	13	36
1	Y	106/110 (96%)	99 (93%)	7 (7%)	19	48
1	Z	104/110 (94%)	95 (91%)	9 (9%)	12	34
2	C	159/171 (93%)	150 (94%)	9 (6%)	24	55
2	D	159/171 (93%)	154 (97%)	5 (3%)	45	79
2	E	159/171 (93%)	153 (96%)	6 (4%)	38	72
2	F	159/171 (93%)	151 (95%)	8 (5%)	28	61
2	H	159/171 (93%)	156 (98%)	3 (2%)	62	87
2	I	159/171 (93%)	157 (99%)	2 (1%)	73	92
2	L	159/171 (93%)	152 (96%)	7 (4%)	33	66
2	M	159/171 (93%)	150 (94%)	9 (6%)	24	55
2	N	159/171 (93%)	153 (96%)	6 (4%)	38	72
2	Q	159/171 (93%)	155 (98%)	4 (2%)	53	83
2	R	159/171 (93%)	155 (98%)	4 (2%)	53	83
2	S	159/171 (93%)	156 (98%)	3 (2%)	62	87
All	All	3189/3372 (95%)	3021 (95%)	168 (5%)	26	59

All (168) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	MET
1	A	42	LYS
1	A	59	ILE
1	A	70	VAL
1	A	82	ASP
1	A	99	LYS

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Mol	Chain	Res	Type
1	A	106	ASN
1	A	121	LYS
1	A	128	VAL
1	B	59	ILE
1	B	77	ASP
1	B	82	ASP
1	B	98	LEU
1	B	112	LEU
1	B	130	ASN
2	C	363	ILE
2	C	366	TRP
2	C	372	SER
2	C	397	THR
2	C	416	SER
2	C	419	SER
2	C	426	GLN
2	C	455	ARG
2	C	536	THR
2	D	363	ILE
2	D	366	TRP
2	D	433	THR
2	D	494	SER
2	D	529	LYS
2	E	366	TRP
2	E	372	SER
2	E	384	ARG
2	E	440	THR
2	E	472	THR
2	E	536	THR
2	F	363	ILE
2	F	366	TRP
2	F	412	SER
2	F	416	SER
2	F	440	THR
2	F	455	ARG
2	F	472	THR
2	F	494	SER
1	G	18	ARG
1	G	24	THR
1	G	44	THR
1	G	66	LYS
1	G	130	ASN

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Mol	Chain	Res	Type
1	G	134	HIS
2	H	363	ILE
2	H	366	TRP
2	H	410	ILE
2	I	366	TRP
2	I	382	VAL
1	J	20	LEU
1	J	33	LYS
1	J	59	ILE
1	J	73	LEU
1	J	75	SER
1	J	100	SER
1	J	128	VAL
1	J	130	ASN
1	K	18	ARG
1	K	23	THR
1	K	36	THR
1	K	46	SER
1	K	50	GLN
1	K	67	VAL
1	K	71	ILE
1	K	97	ASP
1	K	106	ASN
1	K	112	LEU
1	K	113	SER
1	K	128	VAL
1	K	130	ASN
2	L	366	TRP
2	L	372	SER
2	L	384	ARG
2	L	411	VAL
2	L	440	THR
2	L	472	THR
2	L	494	SER
2	M	363	ILE
2	M	366	TRP
2	M	372	SER
2	M	381	PRO
2	M	455	ARG
2	M	467	ARG
2	M	472	THR
2	M	478	SER

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Mol	Chain	Res	Type
2	M	536	THR
2	N	363	ILE
2	N	366	TRP
2	N	412	SER
2	N	440	THR
2	N	494	SER
2	N	536	THR
1	O	23	THR
1	O	33	LYS
1	O	44	THR
1	O	48	GLU
1	O	67	VAL
1	O	77	ASP
1	O	92	HIS
1	O	111	GLN
1	O	128	VAL
1	O	130	ASN
1	P	21	SER
1	P	46	SER
1	P	65	GLN
1	P	67	VAL
1	P	77	ASP
1	P	82	ASP
1	P	98	LEU
1	P	106	ASN
1	P	108	THR
1	P	128	VAL
2	Q	363	ILE
2	Q	366	TRP
2	Q	416	SER
2	Q	472	THR
2	R	363	ILE
2	R	366	TRP
2	R	372	SER
2	R	412	SER
2	S	363	ILE
2	S	366	TRP
2	S	372	SER
1	T	20	LEU
1	T	28	MET
1	T	36	THR
1	T	58	LEU

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Mol	Chain	Res	Type
1	T	59	ILE
1	T	66	LYS
1	T	70	VAL
1	T	128	VAL
1	T	130	ASN
1	V	28	MET
1	V	44	THR
1	V	64	ASN
1	V	75	SER
1	V	106	ASN
1	V	128	VAL
1	X	23	THR
1	X	36	THR
1	X	48	GLU
1	X	64	ASN
1	X	70	VAL
1	X	75	SER
1	X	96	ASN
1	X	98	LEU
1	X	128	VAL
1	Y	44	THR
1	Y	67	VAL
1	Y	70	VAL
1	Y	73	LEU
1	Y	75	SER
1	Y	77	ASP
1	Y	130	ASN
1	Z	23	THR
1	Z	26	GLU
1	Z	28	MET
1	Z	58	LEU
1	Z	70	VAL
1	Z	71	ILE
1	Z	73	LEU
1	Z	91	VAL
1	Z	106	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (54) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	69	GLN
1	A	106	ASN

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Mol	Chain	Res	Type
1	A	111	GLN
1	A	134	HIS
2	C	378	ASN
2	C	399	ASN
2	D	378	ASN
2	D	399	ASN
2	E	399	ASN
2	F	399	ASN
1	G	119	GLN
1	G	130	ASN
2	H	378	ASN
2	H	399	ASN
2	I	378	ASN
2	I	399	ASN
2	I	520	ASN
1	J	130	ASN
1	K	50	GLN
1	K	106	ASN
2	L	378	ASN
2	L	399	ASN
2	L	429	GLN
2	M	399	ASN
2	M	542	GLN
2	N	378	ASN
2	N	399	ASN
2	N	458	HIS
1	O	50	GLN
1	O	111	GLN
1	O	130	ASN
1	P	64	ASN
1	P	65	GLN
1	P	119	GLN
2	Q	399	ASN
2	Q	429	GLN
2	Q	542	GLN
2	R	399	ASN
2	R	520	ASN
2	S	378	ASN
2	S	399	ASN
1	T	109	ASN
1	T	130	ASN
1	V	64	ASN

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Mol	Chain	Res	Type
1	V	92	HIS
1	X	64	ASN
1	X	96	ASN
1	X	106	ASN
1	X	119	GLN
1	X	134	HIS
1	Y	111	GLN
1	Y	130	ASN
1	Z	106	ASN
1	Z	119	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 ⓘ

24 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	$\# Z > 2$
3	SIA	C	601	4	18,21,21	1.10	1 (5%)	19,31,31	1.23	2 (10%)
4	GL0	C	602	3	11,11,12	1.04	0	10,15,17	2.46	3 (30%)
3	SIA	D	601	4	18,21,21	1.27	2 (11%)	19,31,31	1.51	3 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	GL0	D	602	3	11,11,12	1.14	0	10,15,17	1.98	3 (30%)
3	SIA	E	601	5	18,21,21	1.39	2 (11%)	19,31,31	1.92	7 (36%)
5	GAL	E	602	3	11,11,12	0.93	1 (9%)	10,15,17	0.75	0
3	SIA	F	601	4	18,21,21	1.49	2 (11%)	19,31,31	0.98	1 (5%)
4	GL0	F	602	3	11,11,12	1.46	3 (27%)	10,15,17	3.20	2 (20%)
3	SIA	H	601	5	18,21,21	1.25	1 (5%)	19,31,31	1.58	2 (10%)
5	GAL	H	602	3	11,11,12	30.78	1 (9%)	13,15,17	13.69	2 (15%)
3	SIA	I	601	5	18,21,21	1.36	1 (5%)	19,31,31	1.32	3 (15%)
5	GAL	I	602	3	11,11,12	30.90	1 (9%)	13,15,17	13.26	4 (30%)
3	SIA	L	601	4	18,21,21	1.91	3 (16%)	19,31,31	1.39	2 (10%)
4	GL0	L	602	3	11,11,12	0.97	0	10,15,17	1.65	1 (10%)
3	SIA	M	601	5	18,21,21	1.19	1 (5%)	19,31,31	2.02	5 (26%)
5	GAL	M	602	3	11,11,12	23.86	2 (18%)	13,15,17	10.87	6 (46%)
3	SIA	N	601	4	18,21,21	1.82	1 (5%)	19,31,31	1.24	2 (10%)
4	GL0	N	602	3	11,11,12	1.13	0	10,15,17	2.81	2 (20%)
3	SIA	Q	601	5	18,21,21	1.47	1 (5%)	19,31,31	1.28	3 (15%)
5	GAL	Q	602	3	11,11,12	30.92	1 (9%)	13,15,17	13.32	4 (30%)
3	SIA	R	601	4	18,21,21	1.15	2 (11%)	19,31,31	1.65	4 (21%)
4	GL0	R	602	3	11,11,12	1.00	1 (9%)	10,15,17	2.80	2 (20%)
3	SIA	S	601	4	18,21,21	1.03	1 (5%)	19,31,31	1.16	2 (10%)
4	GL0	S	602	3	11,11,12	0.82	0	10,15,17	2.22	2 (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
3	SIA	C	601	4	-	0/14/38/38	0/1/1/1
4	GL0	C	602	3	1/1/4/5	0/2/18/22	1/1/1/1
3	SIA	D	601	4	-	0/14/38/38	0/1/1/1
4	GL0	D	602	3	1/1/4/5	0/2/18/22	0/1/1/1
3	SIA	E	601	5	-	0/14/38/38	0/1/1/1
5	GAL	E	602	3	-	0/2/18/22	0/1/1/1
3	SIA	F	601	4	-	0/14/38/38	0/1/1/1
4	GL0	F	602	3	-	0/2/18/22	1/1/1/1
3	SIA	H	601	5	-	0/14/38/38	0/1/1/1
5	GAL	H	602	3	1/1/4/5	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SIA	I	601	5	-	0/14/38/38	0/1/1/1
5	GAL	I	602	3	1/1/4/5	0/2/19/22	0/1/1/1
3	SIA	L	601	4	-	0/14/38/38	0/1/1/1
4	GL0	L	602	3	1/1/4/5	0/2/18/22	0/1/1/1
3	SIA	M	601	5	-	0/14/38/38	0/1/1/1
5	GAL	M	602	3	-	0/2/19/22	0/1/1/1
3	SIA	N	601	4	-	0/14/38/38	0/1/1/1
4	GL0	N	602	3	-	0/2/18/22	1/1/1/1
3	SIA	Q	601	5	-	0/14/38/38	0/1/1/1
5	GAL	Q	602	3	1/1/4/5	0/2/19/22	0/1/1/1
3	SIA	R	601	4	-	0/14/38/38	0/1/1/1
4	GL0	R	602	3	1/1/4/5	0/2/18/22	0/1/1/1
3	SIA	S	601	4	-	0/14/38/38	0/1/1/1
4	GL0	S	602	3	1/1/4/5	0/2/18/22	0/1/1/1

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	602	GL0	C3-C2	-2.48	1.48	1.52
4	F	602	GL0	C3-C4	-2.25	1.49	1.52
4	R	602	GL0	C1-C2	2.04	1.54	1.52
3	D	601	SIA	O6-C2	2.07	1.45	1.43
3	R	601	SIA	C3-C2	2.09	1.54	1.51
5	M	602	GAL	O5-C1	2.19	1.47	1.43
4	F	602	GL0	C1-C2	2.23	1.54	1.52
3	E	601	SIA	C3-C2	2.24	1.54	1.51
3	F	601	SIA	O6-C2	2.25	1.45	1.43
5	E	602	GAL	C1-C2	2.28	1.54	1.52
3	L	601	SIA	O6-C2	2.89	1.46	1.43
3	L	601	SIA	C3-C2	3.05	1.55	1.51
3	C	601	SIA	O2-C2	3.68	1.43	1.39
3	S	601	SIA	O2-C2	3.84	1.44	1.39
3	R	601	SIA	O2-C2	4.00	1.44	1.39
3	M	601	SIA	O2-C2	4.04	1.44	1.39
3	D	601	SIA	O2-C2	4.37	1.44	1.39
3	H	601	SIA	O2-C2	4.61	1.44	1.39
3	E	601	SIA	O2-C2	5.14	1.45	1.39
3	I	601	SIA	O2-C2	5.18	1.45	1.39
3	F	601	SIA	O2-C2	5.64	1.45	1.39
3	Q	601	SIA	O2-C2	5.72	1.46	1.39
3	L	601	SIA	O2-C2	6.59	1.46	1.39
3	N	601	SIA	O2-C2	6.97	1.47	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	M	602	GAL	O3-C3	79.08	3.25	1.43
5	H	602	GAL	O3-C3	102.06	3.77	1.43
5	I	602	GAL	O3-C3	102.48	3.78	1.43
5	Q	602	GAL	O3-C3	102.54	3.79	1.43

All (67) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	H	602	GAL	O3-C3-C2	-48.63	21.56	110.02
5	I	602	GAL	O3-C3-C2	-47.20	24.15	110.02
5	Q	602	GAL	O3-C3-C2	-47.12	24.30	110.02
5	M	602	GAL	O3-C3-C2	-35.50	45.44	110.02
5	M	602	GAL	O3-C3-C4	-14.04	79.81	110.36
4	F	602	GL0	C3-C4-C5	-8.64	99.48	110.82
4	R	602	GL0	C3-C4-C5	-7.93	100.42	110.82
5	H	602	GAL	O3-C3-C4	-7.87	93.23	110.36
5	Q	602	GAL	O3-C3-C4	-7.49	94.06	110.36
4	N	602	GL0	C3-C4-C5	-7.48	101.00	110.82
5	I	602	GAL	O3-C3-C4	-6.57	96.07	110.36
4	S	602	GL0	C3-C4-C5	-6.26	102.61	110.82
4	C	602	GL0	C3-C4-C5	-6.12	102.79	110.82
3	M	601	SIA	O2-C2-C3	-5.73	101.73	109.41
4	D	602	GL0	C3-C4-C5	-4.90	104.39	110.82
5	Q	602	GAL	C3-C4-C5	-4.76	101.83	110.22
3	E	601	SIA	O2-C2-C3	-4.75	103.05	109.41
4	L	602	GL0	C3-C4-C5	-4.30	105.17	110.82
3	M	601	SIA	C4-C5-N5	-3.05	104.12	110.40
3	E	601	SIA	C4-C5-N5	-3.00	104.22	110.40
3	M	601	SIA	O9-C9-C8	-2.68	105.20	111.11
5	I	602	GAL	C3-C4-C5	-2.64	105.57	110.22
3	R	601	SIA	C4-C5-N5	-2.61	105.02	110.40
3	D	601	SIA	C4-C5-N5	-2.57	105.10	110.40
3	E	601	SIA	O7-C7-C6	-2.51	103.85	109.46
3	C	601	SIA	C4-C5-N5	-2.42	105.41	110.40
3	N	601	SIA	C9-C8-C7	-2.18	107.56	112.41
3	I	601	SIA	O2-C2-C3	-2.17	106.51	109.41
3	C	601	SIA	O4-C4-C5	-2.17	105.83	110.40
3	Q	601	SIA	C4-C5-N5	-2.11	106.05	110.40
3	E	601	SIA	C4-C5-C6	-2.04	103.52	108.89
5	M	602	GAL	C3-C4-C5	-2.04	106.63	110.22
3	N	601	SIA	O8-C8-C7	2.01	114.09	109.09
3	Q	601	SIA	O6-C6-C7	2.12	110.50	107.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	601	SIA	O6-C6-C7	2.14	110.53	107.41
4	D	602	GL0	O5-C1-C2	2.26	113.70	110.03
5	Q	602	GAL	C2-C3-C4	2.26	114.82	110.88
3	I	601	SIA	O6-C6-C7	2.27	110.71	107.41
3	F	601	SIA	O6-C6-C7	2.28	110.74	107.41
3	S	601	SIA	O6-C6-C7	2.32	110.79	107.41
3	M	601	SIA	O6-C6-C7	2.38	110.88	107.41
3	I	601	SIA	O2-C2-O6	2.39	114.91	109.88
4	D	602	GL0	C1-O5-C5	2.42	117.75	113.39
3	H	601	SIA	O6-C6-C7	2.49	111.05	107.41
3	E	601	SIA	O7-C7-C8	2.58	115.20	108.82
5	I	602	GAL	C2-C3-C4	2.59	115.40	110.88
4	S	602	GL0	O5-C5-C6	2.64	112.75	106.41
3	E	601	SIA	O2-C2-O6	2.68	115.51	109.88
4	C	602	GL0	O5-C5-C6	2.70	112.87	106.41
3	R	601	SIA	O6-C6-C7	2.91	111.66	107.41
4	R	602	GL0	O5-C5-C6	2.95	113.48	106.41
3	R	601	SIA	O2-C2-O6	3.02	116.22	109.88
3	Q	601	SIA	O2-C2-O6	3.13	116.47	109.88
3	S	601	SIA	O2-C2-O6	3.22	116.66	109.88
3	L	601	SIA	O2-C2-C3	3.37	113.92	109.41
3	M	601	SIA	O2-C2-O6	3.40	117.03	109.88
3	D	601	SIA	O2-C2-O6	3.43	117.10	109.88
3	L	601	SIA	O6-C6-C7	3.46	112.46	107.41
3	D	601	SIA	O6-C6-C7	3.49	112.50	107.41
5	M	602	GAL	O5-C1-C2	3.51	116.30	110.79
3	R	601	SIA	O2-C2-C3	3.54	114.15	109.41
4	C	602	GL0	C1-O5-C5	3.74	120.14	113.39
4	N	602	GL0	C1-O5-C5	3.80	120.25	113.39
4	F	602	GL0	C1-O5-C5	3.87	120.37	113.39
5	M	602	GAL	C2-C3-C4	4.42	118.58	110.88
3	H	601	SIA	O2-C2-O6	4.80	119.96	109.88
5	M	602	GAL	C1-O5-C5	6.23	120.75	112.17

All (8) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	C	602	GL0	C3
4	R	602	GL0	C3
4	L	602	GL0	C3
4	D	602	GL0	C3
5	Q	602	GAL	C3

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Mol	Chain	Res	Type	Atom
5	I	602	GAL	C3
4	S	602	GL0	C3
5	H	602	GAL	C3

There are no torsion outliers.

All (3) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	N	602	GL0	C1-C2-C3-C4-C5-O5
4	F	602	GL0	C1-C2-C3-C4-C5-O5
4	C	602	GL0	C1-C2-C3-C4-C5-O5

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	601	SIA	1	0
5	I	602	GAL	1	0
3	R	601	SIA	1	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 ⓘ

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	117/124 (94%)	1.27	31 (26%) 1 0	36, 40, 43, 44	0
1	B	117/124 (94%)	1.23	31 (26%) 1 0	27, 35, 40, 42	0
1	G	123/124 (99%)	0.26	5 (4%) 38 33	35, 40, 44, 47	0
1	J	123/124 (99%)	0.54	9 (7%) 16 12	35, 40, 44, 47	0
1	K	123/124 (99%)	0.44	6 (4%) 30 27	35, 40, 44, 48	0
1	O	118/124 (95%)	0.58	6 (5%) 29 25	37, 40, 43, 43	0
1	P	123/124 (99%)	0.79	9 (7%) 16 12	36, 40, 43, 46	0
1	T	119/124 (95%)	0.53	2 (1%) 70 68	37, 40, 43, 45	0
1	V	121/124 (97%)	0.74	19 (15%) 2 1	36, 40, 43, 47	0
1	X	123/124 (99%)	0.41	4 (3%) 47 41	36, 40, 44, 47	0
1	Y	119/124 (95%)	0.52	8 (6%) 19 14	35, 40, 43, 45	0
1	Z	117/124 (94%)	0.76	13 (11%) 6 4	37, 40, 43, 44	0
2	C	182/197 (92%)	-0.10	0 100 100	38, 40, 42, 46	0
2	D	182/197 (92%)	-0.12	0 100 100	39, 40, 42, 44	0
2	E	182/197 (92%)	-0.18	0 100 100	38, 40, 42, 44	0
2	F	182/197 (92%)	-0.20	0 100 100	39, 40, 42, 47	0
2	H	182/197 (92%)	-0.17	0 100 100	39, 40, 42, 46	0
2	I	182/197 (92%)	-0.16	0 100 100	39, 40, 42, 44	0
2	L	182/197 (92%)	-0.06	1 (0%) 90 90	39, 40, 42, 45	0
2	M	182/197 (92%)	-0.15	0 100 100	39, 40, 41, 44	0
2	N	182/197 (92%)	-0.21	0 100 100	39, 40, 42, 47	0
2	Q	182/197 (92%)	-0.04	0 100 100	39, 40, 42, 45	0
2	R	182/197 (92%)	-0.19	0 100 100	39, 40, 42, 45	0
2	S	182/197 (92%)	-0.12	0 100 100	39, 40, 42, 45	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	3627/3852 (94%)	0.18	144 (3%) 39 35	27, 40, 43, 48	0

All (144) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	109	ASN	8.2
1	B	32	ALA	6.1
1	B	136	VAL	5.9
1	B	65	GLN	5.2
1	B	112	LEU	4.9
1	B	64	ASN	4.7
1	B	63	ASP	4.6
1	B	83	TYR	4.4
1	Z	63	ASP	4.3
1	A	65	GLN	4.1
1	B	114	ASP	4.1
1	P	112	LEU	3.9
1	J	28	MET	3.8
1	G	17	ALA	3.7
1	P	108	THR	3.7
1	Z	110	LEU	3.6
1	B	108	THR	3.6
1	A	118	TYR	3.6
1	V	137	VAL	3.5
1	Z	112	LEU	3.5
1	B	28	MET	3.5
1	B	91	VAL	3.4
1	V	85	PRO	3.4
1	P	107	VAL	3.4
1	K	30	GLU	3.4
1	A	107	VAL	3.3
1	P	82	ASP	3.3
1	V	82	ASP	3.3
1	V	109	ASN	3.3
1	A	36	THR	3.2
1	B	106	ASN	3.2
1	A	112	LEU	3.2
1	K	63	ASP	3.1
1	X	18	ARG	3.1
1	J	29	ILE	3.1
1	A	37	ALA	3.0
1	A	91	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
1	Y	112	LEU	3.0
1	B	35	GLU	3.0
1	V	108	THR	3.0
1	A	84	TYR	3.0
1	Y	82	ASP	3.0
1	V	92	HIS	3.0
1	G	65	GLN	3.0
1	A	113	SER	2.9
1	A	103	ALA	2.9
1	Z	31	LYS	2.9
1	O	113	SER	2.9
1	V	113	SER	2.9
1	P	111	GLN	2.9
1	A	39	LEU	2.8
1	X	138	LEU	2.8
1	B	107	VAL	2.8
1	B	84	TYR	2.8
1	A	108	THR	2.8
1	A	82	ASP	2.8
1	K	82	ASP	2.8
1	A	85	PRO	2.7
1	P	86	ASP	2.7
1	B	33	LYS	2.7
1	Z	82	ASP	2.7
1	A	28	MET	2.7
1	A	34	GLY	2.7
1	V	66	LYS	2.7
1	Z	91	VAL	2.7
1	G	28	MET	2.6
1	A	92	HIS	2.6
1	A	83	TYR	2.6
1	T	64	ASN	2.6
1	J	138	LEU	2.6
1	G	18	ARG	2.6
1	V	84	TYR	2.6
1	A	87	LEU	2.5
1	Z	107	VAL	2.5
1	T	66	LYS	2.5
1	B	89	GLY	2.5
1	J	17	ALA	2.4
1	X	19	SER	2.4
1	J	136	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	K	31	LYS	2.4
1	Z	65	GLN	2.4
1	V	18	ARG	2.4
1	O	71	ILE	2.4
1	Y	137	VAL	2.4
1	A	105	ILE	2.4
1	K	16	PHE	2.4
1	Y	63	ASP	2.4
2	L	416	SER	2.3
1	Z	111	GLN	2.3
1	O	97	ASP	2.3
1	B	31	LYS	2.3
1	V	33	LYS	2.3
1	A	109	ASN	2.3
1	B	88	LYS	2.3
1	O	82	ASP	2.3
1	B	115	ILE	2.3
1	Y	113	SER	2.3
1	J	137	VAL	2.3
1	P	63	ASP	2.3
1	V	93	PHE	2.3
1	Z	108	THR	2.3
1	V	89	GLY	2.3
1	Z	33	LYS	2.2
1	A	67	VAL	2.2
1	V	86	ASP	2.2
1	A	133	ILE	2.2
1	V	87	LEU	2.2
1	J	38	TYR	2.2
1	A	29	ILE	2.2
1	Y	36	THR	2.2
1	P	139	VAL	2.2
1	V	135	LEU	2.2
1	K	65	GLN	2.2
1	O	137	VAL	2.2
1	V	71	ILE	2.2
1	B	87	LEU	2.2
1	B	37	ALA	2.2
1	A	32	ALA	2.1
1	A	64	ASN	2.1
1	A	60	SER	2.1
1	Z	36	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	38	TYR	2.1
1	B	38	TYR	2.1
1	V	118	TYR	2.1
1	B	113	SER	2.1
1	B	66	LYS	2.1
1	Y	114	ASP	2.1
1	B	90	ARG	2.1
1	B	61	PRO	2.1
1	J	36	THR	2.1
1	Y	65	GLN	2.1
1	O	92	HIS	2.1
1	A	25	PRO	2.1
1	P	17	ALA	2.1
1	G	82	ASP	2.0
1	Z	29	ILE	2.0
1	A	44	THR	2.0
1	A	63	ASP	2.0
1	V	63	ASP	2.0
1	X	17	ALA	2.0
1	J	139	VAL	2.0
1	B	82	ASP	2.0
1	B	85	PRO	2.0
1	B	110	LEU	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(\AA^2)	Q<0.9
3	SIA	D	601	21/21	0.94	0.28	1.51	41,46,54,58	0
3	SIA	H	601	21/21	0.95	0.20	0.58	33,38,41,46	0
3	SIA	M	601	21/21	0.94	0.18	0.35	31,34,39,45	0
3	SIA	C	601	21/21	0.96	0.22	0.31	34,37,39,45	0
3	SIA	F	601	21/21	0.96	0.20	0.28	36,40,45,51	0
3	SIA	L	601	21/21	0.95	0.23	0.04	36,39,43,50	0
3	SIA	E	601	21/21	0.96	0.21	-0.31	32,40,42,48	0
3	SIA	I	601	21/21	0.96	0.19	-0.32	31,36,43,50	0
3	SIA	S	601	21/21	0.95	0.19	-0.34	42,44,49,54	0
3	SIA	Q	601	21/21	0.95	0.20	-0.46	38,42,48,53	0
3	SIA	N	601	21/21	0.95	0.14	-1.22	31,35,38,43	0
3	SIA	R	601	21/21	0.96	0.14	-2.76	31,37,43,48	0
4	GL0	C	602	11/12	0.85	0.28	-	51,53,54,55	0
4	GL0	R	602	11/12	0.76	0.28	-	55,57,59,60	0
4	GL0	F	602	11/12	0.86	0.32	-	57,60,63,63	0
5	GAL	E	602	11/12	0.88	0.29	-	51,53,54,54	0
4	GL0	L	602	11/12	0.65	0.32	-	56,59,60,61	0
5	GAL	Q	602	11/12	0.78	0.28	-	59,61,64,65	0
4	GL0	N	602	11/12	0.86	0.22	-	49,51,56,58	0
5	GAL	M	602	11/12	0.80	0.21	-	50,52,56,56	0
5	GAL	I	602	11/12	0.79	0.29	-	57,60,64,65	0
4	GL0	S	602	11/12	0.78	0.29	-	60,62,63,64	0
5	GAL	H	602	11/12	0.88	0.24	-	49,51,53,54	0
4	GL0	D	602	11/12	0.59	0.44	-	65,68,69,69	0

6.5 Other polymers

There are no such residues in this entry.